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(54) Title: METHODS OF DIAGNOSIS OF OVARIAN CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF OVARIAN CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in ovarian cancer. Related methods and compositions that can be used for diagnosis and treatment of ovarian cancer are disclosed. Also described herein are methods that can be used to identify modulators of ovarian cancer.

# METHODS OF DIAGNOSIS OF OVARIAN CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF OVARIAN CANCER

#### CROSS-REFERENCES TO RELATED APPLICATIONS.

This application is related to USSN 60/299,234, filed June 18, 2001; USSN 60/315,287, filed August 27, 2001; USSN 60/317,544, filed September 5, 2001; USSN 60/350,666, filed November 13, 2001; and USSN 60/372,246, filed April 12, 2002, each of which is incorporated herein by reference for all purposes.

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#### FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in ovarian cancer; and to the use of such expression profiles and compositions in the diagnosis, prognosis, and therapy of ovarian cancer. The invention further relates to methods for identifying and using agents and/or targets that inhibit ovarian cancer.

#### **BACKGROUND OF THE INVENTION**

Ovarian cancer is the sixth most common cancer in women, accounting for 6% of all female cancers. It ranks fifth as the cause of cancer death in women. The American Cancer Society predicts that there will be about 23,100 new cases of ovarian cancer in this country in the year 2000 and about 14,000 women will die of the disease. Because many ovarian cancers cannot be detected early in their development, they account for a disproportionate number of fatal cancers, being responsible for almost half the deaths from cancer of the female genital tract; more deaths than any other reproductive organ cancer.

Most patients with epithelial ovarian cancer, the predominant form, are asymptomatic in early-stage disease and usually present with stage III or IV disease. Their five-year survival is less than 25%, with lower survival among African-American women. The minority of patients discovered with early-stage disease have a five-year survival rate of 80%-90%. See, Parker, et. al.. (1997) "Cancer Statistics, 1997" CA Cancer J. Clin. 47:5-27.

In the absence of a family history of ovarian cancer, lifetime risk of ovarian cancer is 1/70. Risk factors include familial cancer syndromes (risk of up to 82% by age 70 in women

with hereditary breast/ovarian syndrome); family history (1.4% lifetime risk with no affected relatives, 5% with one affected relative, 7% with two affected relatives; Kerlikowske, et.al. (1992) Obstet. Gynecol. 80:700-707); nulliparity; advancing age; obesity; personal history of breast, endometrial, or colorectal cancer; fewer pregnancies; or older age (>35 years) at first pregnancy. However, 95% of all ovarian cancers occur in women without risk factors. Use of hormonal contraceptives, oophorectomy, and tubal sterilization reduce risk of ovarian cancer (Kerlikowske, et. al. (1992) Obstet. Gynecol. 80:700-707; Grimes (1992) Am J. Obstet. Gynecol. 166:1950-1954; Hankinson, et. al. (1993) JAMA 270:2813-2818); however, even bilateral oophorectomy may not be completely effective in preventing ovarian cancer.

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Treatment of ovarian cancer consists largely of surgical oophorectomy, anti-hormone therapy, and/or chemotherapy. Although many ovarian cancer patients are effectively treated, the current therapies can all induce serious side effects which diminish quality of life. Deciding on a particular course of treatment is typically based on a variety of prognostic parameters and markers (Fitzgibbons, et al. (2000) <u>Arch. Pathol. Lab. Med.</u> 124:966-978; Hamilton and Piccart (2000) <u>Ann. Oncol.</u> 11:647-663), including genetic predisposition markers BRCA-1 and BRCA-2 (Robson (2000) <u>J. Clin. Oncol.</u> 18:113sup-118sup).

The identification of novel therapeutic targets and diagnostic markers is essential for improving the current treatment of ovarian cancer patients. Recent advances in molecular medicine have increased the interest in tumor-specific cell surface antigens that could serve as targets for various immunotherapeutic or small molecule strategies. Antigens suitable for immunotherapeutic strategies should be highly expressed in cancer tissues and ideally not expressed in normal adult tissues. Expression in tissues that are dispensable for life, however, may be tolerated. Examples of such antigens include Her2/neu and the B-cell antigen CD20. Humanized monoclonal antibodies directed to Her2/neu (Herceptin®/trastuzumab) are currently in use for the treatment of metastatic breast cancer. Ross and Fletcher (1998) Stem Cells 16:413-428. Similarly, anti-CD20 monoclonal antibodies (Rituxin®/rituximab) are used to effectively treat non-Hodgkin's lymphoma. Maloney, et al. (1997) Blood 90:2188-2195; Leget and Czuczman (1998) Curr. Opin. Oncol.

Potential immunotherapeutic targets have been identified for ovarian cancer. One such target is polymorphic epithelial mucin (MUC1). MUC1 is a transmembrane protein, present at the apical surface of glandular epithelial cells. It is often overexpressed in ovarian cancer, and typically exhibits an altered glycosylation pattern, resulting in an antigenically

distinct molecule, and is in early clinical trials as a vaccine target. Gilewski, et al. (2000) Clin. Cancer Res. 6:1693-1701; Scholl, et al. (2000) J. Immunother. 23:570-580. The tumor-expressed protein is often cleaved into the circulation, where it is detectable as the tumor marker, CA 15-3. See, e.g., Bon, et al. (1997) Clin. Chem. 43:585-593. However, many patients have tumors that express neither HER2 nor MUC-1; therefore, it is clear that other targets need to be identified to manage localized and metastatic disease.

Mutations in both BRCA1 and BRCA2 are associated with increased susceptibility to ovarian cancer. Mutations in BRCA1 occur in approximately 5 percent (95 percent confidence interval, 3 to 8 percent) of women in whom ovarian cancer is diagnosed before the age of 70 years. See Stratton, et al. (1997) N.E.J. Med. 336:1125-1130. And, in BRCA1 gene carriers, the risk for developing ovarian cancer is .63. See Easton (1995) Am. J. Hum. Genet. 56:267-xxx; and Elit (2001) Can. Fam. Physician 47:778-84.

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Other biochemical markers such as CA125 have been reported to be associated with ovarian cancer, but they are not absolute indicators of disease. Although roughly 85% of women with clinically apparent ovarian cancer have increased levels of CA125, CA125 is also increased during the first trimester of pregnancy, during menstruation, in the presence of non-cancerous illnesses, and in cancers of other sites.

While industry and academia have identified novel gene sequences, there has not been an equal effort exerted to identify the function of these novel sequences. The elucidation of a role for novel proteins and compounds in disease states for identification of therapeutic targets and diagnostic markers is essential for improving the current treatment of ovarian cancer patients. Accordingly, provided herein are molecular targets for therapeutic intervention in ovarian and other cancers. Additionally, provided herein are methods that can be used in diagnosis and prognosis of ovarian cancer. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate ovarian cancer.

#### SUMMARY OF THE INVENTION

The present invention therefore provides nucleotide sequences of genes that are upand down-regulated in ovarian cancer cells. Such genes are useful for diagnostic purposes,
and also as targets for screening for therapeutic compounds that modulate ovarian cancer,
such as hormones or antibodies. The methods of detecting nucleic acids of the invention or
their encoded proteins can be used for many purposes, e.g., early detection of ovarian
cancers, monitoring and early detection of relapse following treatment, monitoring response
to therapy, selecting patients for postoperative chemotherapy or radiation therapy, selecting
therapy, determining tumor prognosis, treatment, or response to treatment (of primary or
metastatic tumors), and early detection of pre-cancerous lesions. Other aspects of the
invention will become apparent to the skilled artisan by the following description of the
invention.

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In one aspect, the present invention provides a method of detecting an ovarian cancerassociated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26.

In one embodiment, the present invention provides a method of determining the level of an ovarian cancer associated transcript in a cell from a patient.

In one embodiment, the present invention provides a method of detecting an ovarian cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26.

In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1-26.

In one embodiment, the biological sample is a tissue sample. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label.

In one embodiment, the polynucleotide is immobilized on a solid surface.

In one embodiment, the patient is undergoing a therapeutic regimen to treat ovarian cancer. In another embodiment, the patient is suspected of having metastatic ovarian cancer.

In one embodiment, the patient is a human.

In one embodiment, the ovarian cancer associated transcript is mRNA.

In one embodiment, the method further comprises the step of amplifying nucleic acids

before the step of contacting the biological sample with the polynucleotide.

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In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of ovarian cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of an ovarian cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26, thereby monitoring the efficacy of the therapy. In a further embodiment, the patient has metastatic ovarian cancer. In a further embodiment, the patient has a drug resistant form of ovarian cancer.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the ovarian cancer-associated transcript to a level of the ovarian cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

Additionally, provided herein is a method of evaluating the effect of a candidate ovarian cancer drug comprising administering the drug to a patient and removing a cell sample from the patient. The expression profile of the cell is then determined. This method may further comprise comparing the expression profile to an expression profile of a healthy individual. In a preferred embodiment, said expression profile includes a gene of Tables 1-26.

In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1-26.

In one embodiment, an expression vector or cell comprises the isolated nucleic acid.

In one aspect, the present invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-26.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-26.

In one embodiment, the antibody is conjugated to an effector component, e.g., a fluorescent label, a radioisotope or a cytotoxic chemical.

In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

In one aspect, the present invention provides a method of detecting an ovarian cancer cell in a biological sample from a patient, the method comprising contacting the biological

sample with an antibody as described herein.

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In another aspect, the present invention provides a method of detecting antibodies specific to ovarian cancer in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprising a sequence from Tables 1-26.

In another aspect, the present invention provides a method for identifying a compound that modulates an ovarian cancer-associated polypeptide, the method comprising the steps of:
(i) contacting the compound with an ovarian cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26; and (ii) determining the functional effect of the compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect.

In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant.

In one embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting proliferation of an ovarian cancer-associated cell to treat ovarian cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified as described herein.

In one embodiment, the compound is an antibody.

In another aspect, the present invention provides a drug screening assay comprising the steps of: (i) administering a test compound to a mammal having ovarian cancer or to a cell sample isolated from; (ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell sample or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of ovarian cancer.

In one embodiment, the control is a mammal with ovarian cancer or a cell sample that has not been treated with the test compound. In another embodiment, the control is a normal cell or mammal, or is non-malignant tissue.

In one embodiment, the test compound is administered in varying amounts or

concentrations. In another embodiment, the test compound is administered for varying time periods. In another embodiment, the comparison can occur after addition or removal of the drug candidate.

In one embodiment, the levels of a plurality of polynucleotides that selectively hybridize to a sequence at least 80% identical to a sequence as shown in Tables 1-26 are individually compared to their respective levels in a control cell sample or mammal. In a preferred embodiment the plurality of polynucleotides is from three to ten.

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In another aspect, the present invention provides a method for treating a mammal having ovarian cancer comprising administering a compound identified by the assay described herein.

In another aspect, the present invention provides a pharmaceutical composition for treating a mammal having ovarian cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

In one aspect, the present invention provides a method of screening drug candidates by providing a cell expressing a gene that is up- and down-regulated as in an ovarian cancer. In one embodiment, a gene is selected from Tables 1-26. The method further includes adding a drug candidate to the cell and determining the effect of the drug candidate on the expression of the expression profile gene.

In one embodiment, the method of screening drug candidates includes comparing the level of expression in the absence of the drug candidate to the level of expression in the presence of the drug candidate, wherein the concentration of the drug candidate can vary when present, and wherein the comparison can occur after addition or removal of the drug candidate. In a preferred embodiment, the cell expresses at least two expression profile genes. The profile genes may show an increase or decrease.

Also provided is a method of evaluating the effect of a candidate ovarian cancer drug comprising administering the drug to a transgenic animal expressing or over-expressing the ovarian cancer modulatory, protein, or an animal lacking the ovarian cancer modulatory protein, for example as a result of a gene knockout.

Moreover, provided herein is a biochip comprising one or more nucleic acid segments of Tables 1-26, wherein the biochip comprises fewer than 1000 nucleic acid probes.

Preferably, at least two nucleic acid segments are included. More preferably, at least three nucleic acid segments are included.

Furthermore, a method of diagnosing a disorder associated with ovarian cancer is

provided. The method comprises determining the expression of a gene of Tables 1-26 in a first tissue type of a first individual, and comparing the distribution to the expression of the gene from a second normal tissue type from the first individual or a second unaffected individual. A difference in the expression indicates that the first individual has a disorder associated with ovarian cancer.

In a further embodiment, the biochip also includes a polynucleotide sequence of a gene that is not up- and down-regulated in ovarian cancer.

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In one embodiment a method for screening for a bioactive agent capable of interfering with the binding of an ovarian cancer modulating protein (ovarian cancer modulatory protein) or a fragment thereof and an antibody which binds to said ovarian cancer modulatory protein or fragment thereof. In a preferred embodiment, the method comprises combining an ovarian cancer modulatory protein or fragment thereof, a candidate bioactive agent and an antibody which binds to said ovarian cancer modulatory protein or fragment thereof. The method further includes determining the binding of said ovarian cancer modulatory protein or fragment thereof and said antibody. Wherein there is a change in binding, an agent is identified as an interfering agent. The interfering agent can be an agonist or an antagonist. Preferably, the agent inhibits ovarian cancer.

Also provided herein are methods of eliciting an immune response in an individual. In one embodiment a method provided herein comprises administering to an individual a composition comprising an ovarian cancer modulating protein, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from those of Tables 1-26.

Further provided herein are compositions capable of eliciting an immune response in an individual. In one embodiment, a composition provided herein comprises an ovarian cancer modulating protein, preferably encoded by a nucleic acid of Table 1-26 or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, said composition comprises a nucleic acid comprising a sequence encoding an ovarian cancer modulating protein, preferably selected from the nucleic acids of Tables 1-26, and a pharmaceutically acceptable carrier.

Also provided are methods of neutralizing the effect of an ovarian cancer protein, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization. In another embodiment, the protein is encoded by a nucleic acid selected from those of Tables 1-26.

In another aspect of the invention, a method of treating an individual for ovarian cancer is provided. In one embodiment, the method comprises administering to said individual an inhibitor of an ovarian cancer modulating protein. In another embodiment, the method comprises administering to a patient having ovarian cancer an antibody to an ovarian cancer modulating protein conjugated to a therapeutic moiety. Such a therapeutic moiety can be a cytotoxic agent or a radioisotope.

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#### DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and prognosis evaluation for ovarian cancer (OC), including metastatic ovarian cancer, as well as methods for screening for compositions which modulate ovarian cancer. Also provided are methods for treating ovarian cancer and related conditions, e.g., ovarian carcinoma (e.g., epithelial (including malignant serous tumors, malignant mucinous tumors, and malignant endometrioid tumors), germ cell (including teratomas, choriocarcinomas, polyembryomas, embryonal carcinoma, endodermal sinus tumor, dysgerminoma, and gonadoblastoma), and stromal carcinomas (e.g., granulosal stromal cell tumors)), fallopian tube carcinoma, and peritoneal carcinoma.

Tables 1-26 provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in ovarian cancer samples. Tables 1-26 also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster.

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#### **Definitions**

The term "ovarian cancer protein" or "ovarian cancer polynucleotide" or "ovarian cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologues that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a gene of Tables 1-26; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-26, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1-26 and conservatively modified variants thereof; or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-26. A polynucleotide or polypeptide

sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. An "ovarian cancer polypeptide" and an "ovarian cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" ovarian cancer protein or nucleic acid refers to an ovarian cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains all of the elements normally contained in one or more naturally occurring, wild type ovarian cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translation processing or splicing, including alternative splicing.

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"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of an ovarian cancer protein, polynucleotide or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or a bird; reptile; or fish. Livestock and domestic animals are of particular interest.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default

parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site http://www.ncbi.nlm.nih.gov/BLAST/ or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the compliment of a test sequence. The definition also includes sequences that have deletions and/or additions, as well as those that have substitutions, as well as naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

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For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of one of the number of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482-489, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443-453, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l. Acad. Sci. USA 85:2444-2448, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology Lippincott.

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) <u>Nuc. Acids Res.</u> 25:3389-3402 and Altschul, et al. (1990)

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J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a word length of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Nat'l Acad. Sci. USA 89:10915-919) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) Proc. Nat'l Acad. Sci. USA 90:5873-5887). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be large negative numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions, as described below. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

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A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells in vivo, and the like. Host cells may be prokaryotic cells such as E. coli, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells, such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant from the composition to be purified. In this sense, purification does not require that the purified compound be homogenous, e.g., 100% pure.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymers.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ-carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain the same basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refers to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that functions similarly to a naturally occurring amino acid.

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Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions, or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds, or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton (1984) Proteins Freeman).

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Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts, et al. (2001) Molecular Biology of the Cell (4th ed.) Garland Pub.; and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules Freeman. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of  $\beta$ -sheet and  $\alpha$ -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the non-covalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50, or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds,

although in some cases, nucleic acid analogs are included that may have at least one different linkage, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or Omethylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford University Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 of Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ASC Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

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A variety of references disclose such nucleic acid analogs, including, e.g., 15 phosphoramidate (Beaucage, et al. (1993) Tetrahedron 49:1925-1963 and references therein; Letsinger (1970) J. Org. Chem. 35:3800-3803; Sprinzl, et al. (1977) Eur. J. Biochem. 81:579-589; Letsinger, et al. (1986) Nucl. Acids Res. 14:3487-499; Sawai, et al. (1984) Chem. Lett. 805, Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; and Pauwels, et al. (1986), 20 Chemica Scripta 26:141-149), phosphorothioate (Mag, et al. (1991) Nucl. Acids Res. 19:1437-441; and U.S. Patent No. 5,644,048), phosphorodithioate (Brill, et al. (1989) J. Am. Chem. Soc. 111:2321-2322), O-methylphophoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford Univ. Press), and peptide nucleic acid backbones and linkages (see Egholm (1992) J. Am. Chem. Soc. 114:1895-897; Meier, et al. (1992) Angew. Chem. Int. Ed. Engl. 31:1008-1010; Nielsen (1993) Nature, 25 365:566-568; Carlsson, et al. (1996) Nature 380:207, each of which is incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:6097-101; non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141 and 4,469,863; Kiedrowshi, et al. (1991) Angew. Chem. Intl. Ed. English 30:423-426; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-30 4471; Jung, et al. (1994) Nucleoside and Nucleotide 13:1597; Chapters 2 and 3, in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ASC Symposium Series 580; Mesmaeker, et al. (1994) Bioorganic and Medicinal Chem. Lett. 4:395-398; Jeffs,

et al. (1994) <u>J. Biomolecular NMR</u> 34:17-xx; Horn, et al. (1996) <u>Tetrahedron Lett.</u> 37:743-xxx) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, in Sanghvi and Cook (eds. 1994) <u>Carbohydrate</u>

<u>Modifications in Antisense Research</u> ASC Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins, et al. (1995) <u>Chem. Soc. Rev. pp</u> 169-176). Several nucleic acid analogs are described in Rawls (p. 35 June 2, 1997) <u>C&E News</u>. Each of these references is hereby expressly incorporated by reference.

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Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T<sub>m</sub>) for mismatched versus perfectly matched base pairs. DNA and RNA typically exhibit a 2-4° C drop in T<sub>m</sub> for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic,

photochemical, biochemical, immunochemical, chemical, or other physical means. For example, useful labels include <sup>32</sup>P, fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide. The labels may be incorporated into the ovarian cancer nucleic acids, proteins and antibodies at any position. Any method known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter, et al. (1962) Nature 144:945-xxx; David, et al. (1974) Biochemistry 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth. 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

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An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or non-covalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, an enzyme or substrate, tags such as epitope tags, a toxin; activatable moieties, a chemotherapeutic agent; a lipase; an antibiotic; or a radioisotope emitting "hard" e.g., beta radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or non-covalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (e.g., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the

stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

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The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, e.g., using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention. Similarly, a "recombinant protein" is a protein made using recombinant techniques, e.g., through the expression of a recombinant nucleic acid as depicted above.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is defined as an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

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An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed operably linked to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Hybridization with Nucleic Probes (Laboratory Techniques in Biochemistry and Molecular Biology) (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T<sub>m</sub>) for the specific sequence at a defined ionic strength pH. The T<sub>m</sub> is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target

sequence at equilibrium (as the target sequences are present in excess, at T<sub>m</sub>, 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., 10 to 50 nucleotides) and at least about 60° C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32-48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50° C to about 65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90-95° C for 30-120 sec, an annealing phase lasting 30-120 sec, and an extension phase of about 72° C for 1-2 min. Protocols and guidelines for low and high stringency amplification reactions are available, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications Academic Press, N.Y.

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Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is at least twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided, e.g., Ausubel, et al. (ed. 1991 and supplements) Current Protocols in Molecular Biology Lippincott.

The phrase "functional effects" in the context of assays for testing compounds that

modulate activity of an ovarian cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the ovarian cancer protein or nucleic acid, e.g., a functional, physical, physiological, or chemical effect, such as the ability to decrease ovarian cancer. It includes ligand binding activity; cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis, and other characteristics of ovarian cancer cells. "Functional effects" include in vitro, in vivo, and ex vivo activities.

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By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of an ovarian cancer protein sequence, e.g., functional, enzymatic, physical, physiological, and chemical effects. Such functional effects can be measured by any means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the ovarian cancer protein; measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring cellular proliferation. Determination of the functional effect of a compound on ovarian cancer can also be performed using ovarian cancer assays known to those of skill in the art such as an in vitro assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis, and other characteristics of ovarian cancer cells. The functional effects can be evaluated by means known to those skilled in the art, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for ovarian cancer-associated sequences, measurement of RNA stability, or identification of downstream or reporter gene expression (CAT, luciferase, β-gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators", and "modulators" of ovarian cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using in vitro and in vivo assays of ovarian cancer polynucleotide and

polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of ovarian cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate ovarian cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of ovarian cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules, and the like. Assays for inhibitors and activators include, e.g., expressing the ovarian cancer protein in vitro, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of ovarian cancer can also be identified by incubating ovarian cancer cells with the test compound and determining increases or decreases in the expression of one or more ovarian cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50, or more ovarian cancer proteins, such as ovarian cancer proteins encoded by the sequences set out in Tables 1-26.

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Samples or assays comprising ovarian cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25% or less. Activation of an ovarian cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 1000-500% (e.g., 2-5 fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to a change in cell growth and proliferation characteristics in vitro or in vivo, e.g., cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, change in contact inhibition or density limitation of growth, loss of growth factor or serum requirements, change in cell morphology, gain or loss of immortalization, gain or loss of tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., pp. 231-241 in Freshney (1994) <u>Culture of Animal Cells: A Manual of Basic Technique</u> (3d ed.) Wiley-Liss.

"Tumor cell" refers to pre-cancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is typically associated with phenotypic changes, such as immortalization of cells, aberrant growth control, non-morphological changes, and/or malignancy. See, Freshney (1994) Culture of Animal Cells.

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"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See, e.g., Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V<sub>L</sub>) and variable heavy chain (V<sub>H</sub>) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce  $F(ab)'_2$ , a dimer of Fab which itself is a light chain joined to  $V_H$ - $C_H$ 1 by a disulfide bond. The  $F(ab)'_2$  may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the  $F(ab)'_2$  dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region. See Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven. While various antibody fragments are defined in terms of the digestion of an intact antibody,

one of skill will appreciate that such fragments may be synthesized de novo either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized de novo using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries. See, e.g., McCafferty, et al. (1990) Nature 348:552-554.

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For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many techniques known in the art can be used (see, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al., pp. 77-96 in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; Coligan (1991) Current Protocols in Immunology Lippincott; Harlow and Lane (1988) Antibodies: A Laboratory Manual CSH Press; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.) Academic Press. Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Transgenic mice, or other organisms, e.g., other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens. See, e.g., McCafferty, et al. (1990) Nature 348:552-554; and Marks, et al. (1992) Biotechnology 10:779-783.

A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a portion thereof, is altered, replaced or exchanged with a variable region having a different or altered antigen specificity.

#### Identification of ovarian cancer-associated sequences

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is

characteristic of the state of the cell. That is, normal tissue (e.g., normal ovarian or other tissue) may be distinguished from cancerous or metastatic cancerous tissue of the ovarian, or ovarian cancer tissue or metastatic ovarian cancerous tissue can be compared with tissue samples of ovarian and other tissues from surviving cancer patients. By comparing expression profiles of tissue in known different ovarian cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of a cancer.

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The identification of sequences that are differentially expressed in ovarian cancer versus non-ovarian cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate ovarian cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, does existing treatment induce expression of a target. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Metastatic tissue can also be analyzed to determine the stage of ovarian cancer in the tissue or origin of the primary tumor. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the ovarian cancer expression profile. This may be done by making biochips comprising sets of the important ovarian cancer genes, which can then be used in these screens. These methods can also be based on evaluating protein expression; that is, protein expression levels of the ovarian cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the ovarian cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense or RNAi nucleic acids, or the ovarian cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in ovarian cancer relative to normal tissues and/or non-malignant tissues, herein termed "ovarian cancer sequences." As outlined below, ovarian cancer sequences include those that are up-regulated (e.g., expressed at a higher level) in ovarian cancer, as well as those that are down-regulated (e.g., expressed at a lower level). In a preferred embodiment, the ovarian cancer sequences are from humans; however, as will be appreciated by those in the art, ovarian cancer sequences from other organisms may be useful

in animal models of disease and drug evaluation; thus, other ovarian cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (e.g., dogs, cats, etc.). Ovarian cancer sequences, e.g., counterpart genes, from other organisms may be obtained using the techniques outlined below.

Ovarian cancer sequences can include both nucleic acid and amino acid sequences. Ovarian cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids. Screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the ovarian cancer sequences, are also provided.

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An ovarian cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the ovarian cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

For identifying ovarian cancer-associated sequences, the ovarian cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing ovarian cancer samples with metastatic cancer samples from other cancers, such as lung, ovarian, gastrointestinal cancers, etc. Samples of different stages of ovarian cancer, e.g., survivor tissue, drug resistant states, and tissue undergoing metastasis, are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated for the preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal ovarian, but also including, and not limited to, lung, heart, brain, liver, ovarian, kidney, muscle, colon, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the ovarian cancer screen that are expressed in any significant amount in other tissues are removed from the profile, although in some embodiments, expression in non-essential tissues may be tolerated. That is, when screening for drugs, it is usually preferable that the target be disease specific, to minimize possible side

effects by interaction with target present in other organs.

In a preferred embodiment, ovarian cancer sequences are those that are up-regulated in ovarian cancer; that is, the expression of these genes is higher in the ovarian cancer tissue as compared to non-cancerous tissue. "Up-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. Other embodiments are directed to sequences up regulated in non-malignant conditions relative to normal.

Unigene cluster identification numbers and accession numbers herein refer to the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, et al. (1998) Nucl. Acids Res. 26:1-7; and http://www.ncbi.nlm.nih.gov/. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, e.g., FGENESH. See Salamov and Solovyev (2000) Genome Res. 10:516-522. In other situations, sequences have been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, ovarian cancer sequences are those that are down-regulated in ovarian cancer; that is, the expression of these genes is lower in ovarian cancer tissue as compared to non-cancerous tissue. "Down-regulation" as used herein often means at least about a two-fold change, preferably at least about a three-fold change, with at least about five-fold or higher being preferred.

#### Informatics

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The ability to identify genes that are over or under expressed in ovarian cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. Expression profiles can be used in diagnostic or prognostic evaluation of patients with ovarian cancer. Subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson (June 11-12, 1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA) or in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable

exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database, and can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

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The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent to those of skill in the art that similar databases can be assembled for any assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample undergoing ovarian cancer, e.g., the identification of ovarian cancer-associated sequences described herein, provide an abundance of information which can be correlated with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, and outcome data, among others. Although data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method

using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures.

Fundamentals of bioinformatics are provided, e.g., in Mount, et al. (2001)

Bioinformatics: Sequence and Genome Analysis CSH Press, NY; Durbin, et al. (eds. 1999)

Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids

Cambridge Univ. Press; Baxevanis and Oeullette (eds. 1998) Bioinformatics: A Practical

Guide to the Analysis of Genes and Proteins (2d ed.) Wiley-Liss; Rashidi and Buehler (1999)

Bioinformatics: Basic Applications in Biological Science and Medicine CRC Press; Setubal, et al. (eds 1997) Introduction to Computational Molecular Biology Brooks/Cole; Misener and Krawetz (eds. 2000) Bioinformatics: Methods and Protocols Humana Press; Higgins and Taylor (eds. 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical

Approach Oxford Univ. Press; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the Internet Eaton Pub.; Han and Kamber (2000) Data Mining: Concepts and Techniques Kaufmann Pub.; and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes Chap and Hall.

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

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In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for ovarian cancer. In another variation, assay records cross-tabulate one or more of the following parameters for a target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or

characteristic separation coordinate (e.g., electrophoretic or genomic position coordinates); (2) sample source; and (3) absolute and/or relative quantity of target species present in the sample.

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The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells)

composing a bit pattern encoding data acquired from an assay of the invention.

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The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SDRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, e.g., which typically comprises one or more of: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by methods of the inventions, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

#### Characteristics of ovarian cancer-associated proteins

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Ovarian cancer proteins of the present invention may be categorized as secreted proteins, transmembrane proteins, or intracellular proteins. In one embodiment, the ovarian cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or disregulated cellular processes. See, e.g., Alberts, et al. (eds. 1994) Molecular Biology of the Cell (3d ed.) Garland. For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity, and the like. Intracellular proteins can also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are often involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in proteinprotein interaction. For example, Src-homology-2 (SH2) domains bind tyrosinephosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to prolinerich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden. See, e.g., Bateman, et al. (2000) Nuc. Acids Res. 28:263-266; Sonnhammer, et al. (1997) Proteins 28:405-420; Bateman, et al. (1999) Nuc. Acids Res. 27:260-262; and Sonnhammer, et al. (1998) Nuc. Acids Res. 26:320-

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In another preferred embodiment, the ovarian cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous 15 transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged 20 amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site http://psort.nibb.ac.jp/). Important transmembrane protein receptors include, but are not limited to the insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor 25 receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, interleukin receptors, e.g., IL-1 receptor, IL-2 receptor, etc.

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their

cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules, or may be processed or shed to the blood stream. In this respect, they can mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

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Ovarian cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins in situ. Alternatively, antibodies can also label intracellular proteins, in which case samples are typically permeablized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment. Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful ovarian markers of disease.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the ovarian cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion into the blood stream), or exocrine (secretion, e.g., through a duct or to an adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, wax producing glands of the ear, etc.). Thus, secreted molecules often find use in modulating or altering numerous aspects of physiology. Ovarian cancer proteins that are secreted proteins are particularly preferred as good diagnostic markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be

antibody or small molecule therapeutic targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms, as protein or DNA vaccines.

### Use of ovarian cancer nucleic acids

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As described above, ovarian cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the ovarian cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

The ovarian cancer nucleic acid sequences of the invention, e.g., in Table 1-26, can be fragments of larger genes, e.g., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the ovarian cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, et al., supra. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, http://www.ncbi.nlm.nih.gov/UniGene/).

Once the ovarian cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire ovarian cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised as a linear nucleic acid segment, the recombinant ovarian cancer nucleic acid can be further-used as a probe to identify and isolate other ovarian cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant ovarian cancer nucleic acids and proteins.

The ovarian cancer nucleic acids of the present invention are useful in several ways. In a first embodiment, nucleic acid probes to the ovarian cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, vaccine, RNAi, and/or antisense applications. Alternatively, the ovarian cancer nucleic acids that include coding regions of ovarian cancer proteins can be put into expression vectors for the expression of ovarian cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to ovarian cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the ovarian cancer nucleic acids, e.g., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

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A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a particular target. The probes can be overlapping (e.g., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent

attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be

formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

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In general, the probes are attached to the biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, TeflonJ, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silicabased materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. See, e.g., WO0055627 Reusable Low Fluorescent Plastic Biochip.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxyl groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using

functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers as are known in the art; e.g., homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

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In this embodiment, oligonucleotides are synthesized as is known in the art, and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using well known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix GeneChip<sup>TM</sup> technology.

Often, amplification-based assays are performed to measure the expression level of ovarian cancer-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, an ovarian cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of ovarian cancer-associated RNA. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative PCR are available. See, e.g., Innis, et al.(1990) PCR Protocols: A Guide to Methods and Applications Academic Press.

In some embodiments, a TaqMan based assay is used to measure expression.

TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be

extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR; see Wu and Wallace (1989) <u>Genomics</u> 4:560-569; Landegren, et al. (1988) <u>Science</u> 241:1077-1980; and Barringer, et al. (1990) <u>Gene</u> 89:117-122), transcription amplification (Kwoh, et al. (1989) <u>Proc. Nat'l Acad. Sci. USA</u> 86:1173-1177), self-sustained sequence replication (Guatelli, et al. (1990) <u>Proc. Nat'l Acad. Sci. USA</u> 87:1874-1878), dot PCR, linker adapter PCR, etc.

# Expression of ovarian cancer proteins from nucleic acids

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In a preferred embodiment, ovarian cancer nucleic acids, e.g., encoding ovarian cancer proteins are used to make a variety of expression vectors to express ovarian cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known and are used to express proteins. See, e.g., Ausubel, supra; and Fernandez and Hoeffler (eds. 1999) Gene Expression Systems Academic Press. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the ovarian cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a pre-sequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a pre-protein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation; and two sequences may be operably linked when they are physically part of the same polymer. Generally,

"operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the ovarian cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

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In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences typically encode constitutive or inducible promoters. The promoters may be naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, an expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a procaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are available. See, e.g., Fernandez and Hoeffler, supra.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The ovarian cancer proteins of the present invention are produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding an ovarian cancer protein, under the appropriate conditions to induce or cause expression of the ovarian cancer protein. Conditions appropriate for ovarian cancer protein expression will vary with

the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculovirus systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

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Appropriate host cells include yeast, bacteria, archaebacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are Saccharomyces cerevisiae and other yeasts, E. coli, Bacillus subtilis, Sf9 cells, C129 cells, 293 cells, Neurospora, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

In a preferred embodiment, the ovarian cancer proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral and adenoviral systems. One expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048, both of which are hereby expressly incorporated by reference. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor 20 virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter. See, e.g., Fernandez and Hoeffler, supra. Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived form SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, ovarian cancer proteins are expressed in bacterial systems. Bacterial expression systems are well known in the art. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters

are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion 5 of the ovarian cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been 10 transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin, and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for Bacillus subtilis, E. coli, Streptococcus cremoris, and Streptococcus 15 lividans, among others. See Fernandez and Hoeffler, supra. The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as

In one embodiment, ovarian cancer proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

calcium chloride treatment, electroporation, and others.

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In a preferred embodiment, an ovarian cancer protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for Saccharomyces cerevisiae, Candida albicans and C. maltosa, Hansenula polymorpha, Kluyveromyces fragilis and K. lactis, Pichia guillerimondii and P. pastoris, Schizosaccharomyces pombe, and Yarrowia lipolytica.

The ovarian cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the ovarian cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the ovarian cancer protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the ovarian cancer protein is an ovarian cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In a preferred embodiment, the ovarian cancer protein is purified or isolated after expression. Ovarian cancer proteins may be isolated or purified in a variety of ways known to those skilled in the art depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the ovarian cancer protein may be purified using a standard anti-ovarian cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes (1982) Protein Purification Springer-Verlag. The degree of purification necessary will vary depending on the use of the ovarian cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the ovarian cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, etc.

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# Variants of ovarian cancer proteins

In one embodiment, the ovarian cancer proteins are derivative or variant ovarian cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative ovarian cancer peptide will often contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion, or deletion may occur at most any residue within the ovarian cancer peptide.

Also included within one embodiment of ovarian cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the ovarian cancer protein, using cassette or PCR mutagenesis or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant ovarian cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the ovarian cancer protein amino acid sequence. The variants typically exhibit the same

qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed ovarian cancer variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of ovarian cancer protein activities.

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Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be tolerated. Deletions range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the ovarian cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution relationships provided in the definition section.

The variants typically exhibit the same qualitative biological activity and will elicit the same immune response as the naturally-occurring analog, although variants also are selected to modify the characteristics of the ovarian cancer proteins as needed. Alternatively, the variant may be designed such that the biological activity of the ovarian cancer protein is altered. For example, glycosylation sites may be altered or removed.

Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those described above. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, e.g., serine or threonine is substituted for (or by) a hydrophobic residue, e.g., leucine, isoleucine, phenylalanine,

valine, or alanine; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g., lysine, arginine, or histidine, is substituted for (or by) an electronegative residue, e.g., glutamic or aspartic acid; (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine; or (e) a proline residue is incorporated or substituted, which changes the degree of rotational freedom of the peptidyl bond.

Covalent modifications of ovarian cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of an ovarian cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of an ovarian cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking ovarian cancer polypeptides to a water-insoluble support matrix or surface for use in the method for purifying anti-ovarian cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimidate.

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Other modifications include deamidation of glutamine and asparagine residues to the corresponding glutamic and aspartic acid residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serine, threonine, or tyrosine residues, methylation of the amino groups of the lysine, arginine, and histidine side chains (e.g., pp. 79-86, Creighton (1983) <u>Proteins: Structure and Molecular Properties</u> Freeman), acetylation of the N-terminal amine, and amidation of a C-terminal carboxyl group.

Another type of covalent modification of the ovarian cancer polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence ovarian cancer polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence ovarian cancer polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express ovarian cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to ovarian cancer polypeptides may also be

accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence ovarian cancer polypeptide (for O-linked glycosylation sites). The ovarian cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the ovarian cancer polypeptide at pre-selected bases such that codons are generated that will translate into the desired amino acids.

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Another means of increasing the number of carbohydrate moieties on the ovarian cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. See, e.g., WO 87/05330, and pp. 259-306 in Aplin and Wriston (1981) <u>CRC Crit. Rev.</u> Biochem. CRC Press.

Removal of carbohydrate moieties present on the ovarian cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are applicable. See, e.g., Sojar and Bahl (1987) <u>Arch. Biochem. Biophys.</u> 259:52-57; and Edge, et al. (1981) <u>Anal. Biochem.</u> 118:131-137. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases. See, e.g., Thotakura, et al. (1987) <u>Meth. Enzymol.</u>, 138:350-359.

Another type of covalent modification of ovarian cancer comprises linking the ovarian cancer polypeptide to one of a variety of non-proteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylene. See, e.g., U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192; or 4,179,337.

Ovarian cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules, e.g., comprising an ovarian cancer polypeptide fused to another heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of an ovarian cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the ovarian cancer polypeptide. The presence of such epitope-tagged forms of an ovarian cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the ovarian cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of an ovarian cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of

the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; His6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7, and 9E10 antibodies thereto (Evan, et al. (1985) Mol. Cell. Biol. 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3:547-553). Other tag polypeptides include, e.g., the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth et al. (1990) Proc. Nat'l Acad. Sci. USA 87:6393-6397).

Also included are other ovarian cancer proteins of the ovarian cancer family, and ovarian cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related ovarian cancer proteins from humans or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include the unique areas of the ovarian cancer nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. The conditions for the PCR reaction are well known in the art (e.g., Innis, PCR Protocols, supra).

#### Antibodies to ovarian cancer proteins

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In a preferred embodiment, when the ovarian cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the ovarian cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller ovarian cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are known to the skilled artisan (e.g., Coligan, supra; and Harlow and Lane, supra). Polyclonal antibodies can be raised in a

mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of the figures or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

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The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495-497. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of Tables 1-26 or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (e.g., pp. 59-103 in Goding (1986) Monoclonal Antibodies: Principles and Practice Academic Press). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at

least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid Table 1-26 or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

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In a preferred embodiment, the antibodies to ovarian cancer protein are capable of reducing or eliminating a biological function of an ovarian cancer protein, as is described below. That is, the addition of anti-ovarian cancer protein antibodies (either polyclonal or preferably monoclonal) to ovarian cancer tissue (or cells containing ovarian cancer) may reduce or eliminate the ovarian cancer. Generally, at least a 25% decrease in activity, growth, size or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the ovarian cancer proteins are humanized antibodies (e.g., Xenerex Biosciences; Medarex, Inc.; Abgenix, Inc.; Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')2 or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a nonhuman species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. Humanization can be essentially performed following the method of Winter and co-workers, e.g., by substituting rodent CDRs or CDR sequences for the

corresponding sequences of a human antibody. See, e.g., Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; Presta (1992) Curr. Op. Struct. Biol. 2:593-596; and Verhoeyen, et al. (1988) Science 239:1534-1536). Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species.

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Human antibodies can also be produced using various techniques known in the art, including phage display libraries (see, e.g., Hoogenboom and Winter (1991) J. Mol. Biol. 227:381-388; and Marks, et al. (1991) J. Mol. Biol. 222:581-597) or human monoclonal antibodies (see, e.g., p. 77, Cole, et al. in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; and Boerner, et al. (1991) J. Immunol. 147:86-95). Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. See, e.g., U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016; Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Neuberger (1996) Nature Biotechnology 14:826 commenting on Fishwild, et al. (1996) Nature Biotechnology 14:845-51; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

By immunotherapy is meant treatment of ovarian cancer, e.g., with an antibody raised against ovarian cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the ovarian cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby

inactivating the secreted ovarian cancer protein.

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In another preferred embodiment, the ovarian cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment, bind the extracellular domain of the ovarian cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane ovarian cancer protein. As will be appreciated by one of ordinary skill in the art, the antibody may be a competitive, noncompetitive or uncompetitive inhibitor of protein binding to the extracellular domain of the ovarian cancer protein. The antibody is also an antagonist of the ovarian cancer protein. Further, the antibody prevents activation of the transmembrane ovarian cancer protein. In one aspect, when the antibody prevents the binding of other molecules to the ovarian cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF-α, TNF-β, IL-1, INFγ, and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, ovarian cancer is treated by administering to a patient antibodies directed against the transmembrane ovarian cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be any number of molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of the ovarian cancer protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the ovarian cancer protein. The therapeutic moiety may inhibit enzymatic activity such as protease or collagenase or protein kinase activity associated with ovarian cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to ovarian cancer tissue or cells, results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with ovarian cancer. Cytotoxic agents are numerous and varied and include, but are not limited to,

cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against ovarian cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane ovarian cancer proteins not only serves to increase the local concentration of therapeutic moiety in the ovarian cancer afflicted area, but also serves to reduce deleterious side effects that may be associated with the untargeted therapeutic moiety.

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In another preferred embodiment, the ovarian cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the ovarian cancer protein can be targeted within a cell, e.g., the nucleus, an antibody thereto contains a signal for that target localization, e.g., a nuclear localization signal.

The ovarian cancer antibodies of the invention specifically bind to ovarian cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a  $K_d$  of at least about 0.1 mM, more usually at least about 1  $\mu$ M, preferably at least about 0.1  $\mu$ M or better, and most preferably, 0.01  $\mu$ M or better. Selectivity of binding is also important.

## Detection of ovarian cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the ovarian cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing ovarian cancer) and in ovarian cancer tissue (and in some cases, for varying severities of ovarian cancer that relate to prognosis, as outlined below, or in non-malignant disease are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states,

information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

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"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus ovarian cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is modulated, either up, regulated, resulting in an increased amount of transcript, or down-regulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays. See, e.g., Lockhart (1996) Nature Biotechnology 14:1675-1680. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis, and RNase protection. As outlined above, preferably the change in expression (e.g., up-regulation or down-regulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript, or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the ovarian cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to ovarian cancer genes, e.g., those identified as being important in an ovarian cancer or disease phenotype, can be evaluated in an ovarian disease diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed, or on an individual basis.

In this embodiment, the ovarian cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of ovarian cancer sequences in a particular sample. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity.

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In a preferred embodiment nucleic acids encoding the ovarian cancer protein are detected. Although DNA or RNA encoding the ovarian cancer protein may be detected, of particular interest are methods wherein an mRNA encoding an ovarian cancer protein is detected. Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxygenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding an ovarian cancer protein is detected by binding the digoxygenin with an anti-digoxygenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3indoyl phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The ovarian cancer proteins, antibodies, nucleic acids, modified proteins and cells containing ovarian cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, ovarian cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as prognostic or diagnostic markers of ovarian disease. Detection of these proteins in putative ovarian cancer tissue allows for detection, diagnosis, or prognosis of ovarian disease, and for selection of therapeutic strategy. In one

embodiment, antibodies are used to detect ovarian cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the ovarian cancer protein is detected, e.g., by immunoblotting with antibodies raised against the ovarian cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

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In another preferred method, antibodies to the ovarian cancer protein find use in in situ imaging techniques, e.g., in histology. See, e.g., Asai (ed. 1993) Methods in Cell Biology: Antibodies in Cell Biology (vol. 37) Academic Press. Cells are contacted with from one to many antibodies to the ovarian cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label. In another method the primary antibody to the ovarian cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of ovarian cancer proteins. As will be appreciated by one of ordinary skill in the art, many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing ovarian cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of ovarian cancer proteins. Antibodies can be used to detect an ovarian cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology, and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous ovarian cancer protein.

In a preferred embodiment, in situ hybridization of labeled ovarian cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including ovarian cancer tissue and/or normal tissue, are made. In situ hybridization (see, e.g., Ausubel, supra) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It

is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the ovarian cancer proteins, antibodies, nucleic acids, modified proteins and cells containing ovarian cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to ovarian cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of a plurality of genes being preferred. As above, ovarian cancer probes may be attached to biochips for the detection and quantification of ovarian cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

## Assays for therapeutic compounds

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In a preferred embodiment members of the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The ovarian cancer proteins, antibodies, nucleic acids, modified proteins and cells containing ovarian cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent. See, e.g., Zlokarnik, et al. (1998) Science 279:84-88; and Heid (1996) Genome Res. 6:986-994.

In a preferred embodiment, the ovarian cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified ovarian cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the ovarian cancer phenotype or an identified physiological function of an ovarian cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent. See, e.g., Zlokarnik, supra.

Having identified the differentially expressed genes herein, a variety of assays may be executed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in ovarian cancer, test

compounds can be screened for the ability to modulate gene expression or for binding to the ovarian cancer protein. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing ovarian cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in ovarian cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in ovarian cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

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The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the ovarian cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene expression or protein monitoring of a number of entities, e.g., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the ovarian cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of ovarian cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the expression of one or more ovarian cancer-associated sequences, e.g., a polynucleotide sequence set out inTables 1-26. Generally, in a preferred embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate ovarian cancer, modulate ovarian cancer proteins, bind to an ovarian cancer protein, or interfere with the binding of an ovarian cancer protein and an antibody or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes any molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the ovarian cancer phenotype or the expression of an ovarian cancer sequence,

e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses an ovarian cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induced an ovarian cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, e.g., at zero concentration or below the level of detection.

Drug candidates encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or less than 1500 or less than 1000 or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof. Particularly preferred are peptides.

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In one aspect, a modulator will neutralize the effect of an ovarian cancer protein. By "neutralize" is meant that activity of a protein is inhibited or blocked and the consequent effect on the cell.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to an ovarian cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that

display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (e.g., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks. See, e.g., Gallop, et al. (1994) J. Med. Chem. 37:1233-1251.

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Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175; Furka (1991) Pept. Prot. Res. 37:487-493; and Houghton, et al. (1991) Nature 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT 15 Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Nat'l Acad. Sci. USA 90:6909-913), vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568-570), non-peptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et al. (1992) J. Amer. Chem. Soc. 114:9217-218), analogous organic syntheses 20 of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661-662), oligocarbamates (Cho, et al. (1993) Science 261:1303-305), and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658-xxx). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385-401, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et 25 al.(1996) Nature Biotechnology 14:309-314; and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522; and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, page 33, Baum (Jan. 18, 1993) C&E News; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; 30 morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available.

See, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY; Symphony, Rainin, Woburn, MA; 433A Applied Biosystems, Foster City, CA; 9050 Plus, Millipore, Bedford, MA.

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A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, MA; Orca, Hewlett-Packard, Palo Alto, CA), which mimic the manual synthetic operations performed by a chemist. Any of the above devices are suitable for use with the present invention. The nature and implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J.; Asinex, Moscow, RU; Tripos, Inc., St. Louis, MO; ChemStar, Ltd, Moscow, RU; 3D Pharmaceuticals, Exton, PA; Martek Biosciences, Columbia, MD; etc.).

The assays to identify modulators are amenable to high throughput screening.

Preferred assays thus detect enhancement or inhibition of ovarian cancer gene transcription, inhibition or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

High throughput assays for the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (e.g., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g., Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems typically automate entire procedures, including all sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide

detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

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In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate any nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc., or to purines, etc.

Modulators of ovarian cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids.

For example, digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

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After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an in vitro transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

As will be appreciated by those in the art, these assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702; 5,597,909; 5,545,730; 5,594,117; 5,591,584; 5,571,670; 5,580,731; 5,571,670; 5,591,584; 5,624,802; 5,635,352; 5,594,118; 5,359,100; 5,124,246; and 5,681,697, each of which is hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step

parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

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The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the ovarian cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product.

In addition screens can be done for genes that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress an ovarian cancer expression pattern leading to a normal expression pattern, or to modulate a single ovarian cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated ovarian cancer tissue reveals genes that are not expressed in normal tissue

or ovarian cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for ovarian cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated ovarian cancer tissue sample.

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Thus, in one embodiment, a test compound is administered to a population of ovarian cancer cells, that have an associated ovarian cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (e.g., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once the test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., ovarian cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress the ovarian cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on ovarian cancer activity. By defining such a signature for the ovarian cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "ovarian cancer proteins" or a "ovarian cancer modulatory protein". The ovarian cancer modulatory protein may be a fragment, or alternatively, be the full length protein to the fragment encoded by the nucleic acids of the Tables. Preferably, the ovarian cancer modulatory protein is a fragment. In a preferred embodiment, the ovarian cancer amino acid sequence which is used to determine

sequence identity or similarity is encoded by a nucleic acid of the Tables. In another embodiment, the sequences are naturally occurring allelic variants of a protein encoded by a nucleic acid of the Tables. In another embodiment, the sequences are sequence variants as further described herein.

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Preferably, the ovarian cancer modulatory protein is a fragment of approximately 14 to 24 amino acids long. More preferably the fragment is a soluble fragment. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the fragment has an N-terminal Cys to aid in solubility. In another embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in coupling, e.g., to cysteine. Or, the ovarian cancer proteins are conjugated to an immunogenic agent, e.g., to BSA.

Measurements of ovarian cancer polypeptide activity, or of ovarian cancer or the ovarian cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the ovarian cancer polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of ovarian cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian ovarian cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed in vitro. For example, an ovarian cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the ovarian cancer polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively binds to the ovarian cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNAse protection, dot blotting, are preferred. The level of protein or mRNA is detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or

enzymatically labeled antibodies, and the like, as described herein.

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Alternatively, a reporter gene system can be devised using the ovarian cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or  $\beta$ -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "ovarian cancer proteins." The ovarian cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present.

Alternatively, cells comprising the ovarian cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining an ovarian cancer protein and a candidate compound, and determining the binding of the compound to the ovarian cancer protein. Preferred embodiments utilize the human ovarian cancer protein, although other mammalian proteins, e.g., counterparts, may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative ovarian cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the ovarian cancer protein or the candidate agent is non-diffusably bound to an insoluble support having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be

made of any composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of any convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon<sup>TM</sup>, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition and is non-diffusible. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

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In a preferred embodiment, the ovarian cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the ovarian cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the ovarian cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the ovarian cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one

component can be labeled with different labels, e.g., <sup>125</sup>I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

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In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor is a binding moiety known to bind to the target molecule (e.g., an ovarian cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically 4-40° C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically between 0.1 and 1 hr will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by the test compound. Displacement of the competitor is an indication that the test compound is binding to the ovarian cancer protein and thus is capable of binding to, and potentially modulating, the activity of the ovarian cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the ovarian cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the ovarian cancer protein.

In a preferred embodiment, the methods comprise differential screening to identity agents that are capable of modulating the activity of the ovarian cancer proteins. In this embodiment, the methods comprise combining an ovarian cancer protein and a competitor in a first sample. A second sample comprises a test compound, an ovarian cancer protein, and a

competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the ovarian cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the ovarian cancer protein.

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Alternatively, differential screening is used to identify drug candidates that bind to the native ovarian cancer protein, but cannot bind to modified ovarian cancer proteins. The structure of the ovarian cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of an ovarian cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of an ovarian cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising ovarian cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes an ovarian cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including

chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate ovarian cancer agents are identified.

Compounds with pharmacological activity are able to enhance or interfere with the activity of the ovarian cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting ovarian cancer cell division is provided. The method comprises administration of an ovarian cancer inhibitor. In another embodiment, a method of inhibiting ovarian cancer is provided. The method comprises administration of an ovarian cancer inhibitor. In a further embodiment, methods of treating cells or individuals with ovarian cancer are provided. The method comprises administration of an ovarian cancer inhibitor.

In one embodiment, an ovarian cancer inhibitor is an antibody as discussed above. In another embodiment, the ovarian cancer inhibitor is an antisense or RNAi molecule.

A variety of cell viability, growth, proliferation, and metastasis assays are known to those of skill in the art, as described below.

Soft agar growth or colony formation in suspension

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Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of ovarian cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described in Freshney (1994) <u>Culture of Animal Cells: A Manual of Basic Technique</u> (3d ed.) Wiley-Liss, herein incorporated by reference. See also, the methods section of Garkavtsev, et al. (1996), supra, herein incorporated by reference.

Contact inhibition and density limitation of growth

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Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (<sup>3</sup>H)-thymidine at saturation density can be used to measure density limitation of growth. See, e.g., Freshney (1994), supra. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (<sup>3</sup>H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with an ovarian cancer-associated sequence and are grown for 24 hr at saturation density in non-limiting medium conditions. The percentage of cells labeling with (<sup>3</sup>H)-thymidine is determined autoradiographically. See, e.g., Freshney (1994), supra.

#### 20 Growth factor or serum dependence

Transformed cells typically have a lower serum dependence than their normal counterparts. See, e.g., Temin (1966) <u>J. Nat'l Cancer Inst.</u> 37:167-175; Eagle, et al. (1970) <u>J. Exp. Med.</u> 131:836-879; and Freshney, supra. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

### Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g., Gullino, pp. 178-184 "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) <u>Biological Responses in Cancer Plenum</u>. Similarly,

tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) <u>Sem Cancer Biol.</u> 3:89-96.

Various techniques which measure the release of these factors are described in Freshney (1994), supra. Also, see, Unkeless, et al. (1974) <u>J. Biol. Chem.</u> 249:4295-4305; Strickland and Beers (1976) <u>J. Biol. Chem.</u> 251:5694-5702; Whur, et al. (1980) <u>Br. J. Cancer</u> 42:305-312; Gullino, pp. 178-184 "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) <u>Biological Responses in Cancer</u> Plenum; and Freshney (1985) <u>Anticancer Res.</u> 5:111-130.

### 10 Invasiveness into Matrigel

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The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate ovarian cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Alternatively, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by pre-labeling the cells with <sup>125</sup>I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), supra.

#### Tumor growth in vivo

Effects of ovarian cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the ovarian cancer gene is disrupted or in which an ovarian cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous ovarian cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous ovarian cancer gene with a mutated version of the ovarian cancer gene, or by mutating the endogenous ovarian cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. By breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion. See, e.g., Capecchi, et al. (1989) Science 244:1288-1292. Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual CSH Press; and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) J. Nat'l Cancer Inst. 52:921-930), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) Br. J. Cancer 38:263-272; Selby, et al. (1980) Br. J. Cancer 41:52-61) can be used as a host. Transplantable tumor cells (typically about 106 cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing an ovarian cancer-associated sequences are injected subcutaneously. After a suitable length of time, preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

### Polynucleotide modulators of ovarian cancer

Antisense and RNAi Polynucleotides

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In certain embodiments, the activity of an ovarian cancer-associated protein is down-regulated, or entirely inhibited, by the use of antisense polynucleotide, e.g., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., an ovarian cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturallyoccurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-

sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the ovarian cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized in vitro. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, e.g., be employed to block transcription by binding to the antisense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for ovarian cancer molecules. A preferred antisense molecule is for an ovarian cancer sequences in Tables 1-26, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. An antisense or a sense oligonucleotide can be developed based upon a cDNA sequence encoding a given protein. See, e.g., Stein and Cohen (1988) Cancer Res. 48:2659-2668; and van der Krol, et al. (1988) BioTechniques 6:958-976.

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) <u>Sciencexpress</u> (21March2002); Sharp (1999) <u>Genes Dev.</u> 13:139-141; and Cathew (2001) <u>Curr. Op. Cell Biol.</u> 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) <u>Nature</u> 411:494-498. The mechanism may be used to down-regulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

### Ribozymes

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In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of ovarian cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. Pharmacol. 25: 289-

317 for a general review of the properties of different ribozymes).

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The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparing them are well known to those of skill in the art. See, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Nat'l Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Hum. Gene Ther. 1:39-45; Leavitt, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:699-703; Leavitt, et al. (1994) Hum. Gene Ther. 5:1151-120; and Yamada, et al. (1994) Virology 205:121-126.

Polynucleotide modulators of ovarian cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of ovarian cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating ovarian cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-ovarian cancer antibody that reduces or eliminates the biological activity of an endogenous ovarian cancer protein. Alternatively, the methods comprise administering to a 25 cell or organism a recombinant nucleic acid encoding an ovarian cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the ovarian cancer sequence is down-regulated in ovarian cancer, such state may be reversed by increasing the amount of ovarian cancer gene product in the cell. This can be accomplished, e.g., by over-expressing the endogenous ovarian cancer gene or administering a gene encoding the ovarian cancer sequence, using known gene-therapy techniques, e.g.. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, e.g., when

the ovarian cancer sequence is up-regulated in ovarian cancer, the activity of the endogenous ovarian cancer gene is decreased, e.g., by the administration of an ovarian cancer antisense or RNAi nucleic acid.

In one embodiment, the ovarian cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to ovarian cancer proteins. Similarly, the ovarian cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify ovarian cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to an ovarian cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The ovarian cancer antibodies may be coupled to standard affinity chromatography columns and used to purify ovarian cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the ovarian cancer protein.

#### Methods of identifying variant ovarian cancer-associated sequences

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Without being bound by theory, expression of various ovarian cancer sequences is correlated with ovarian cancer. Accordingly, disorders based on mutant or variant ovarian cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant ovarian cancer genes, e.g., determining all or part of the sequence of at least one endogenous ovarian cancer genes in a cell. This may be accomplished using any number of sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the ovarian cancer genotype of an individual, e.g., determining all or part of the sequence of at least one ovarian cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced ovarian cancer gene to a known ovarian cancer gene, e.g., a wild-type gene.

The sequence of all or part of the ovarian cancer gene can then be compared to the sequence of a known ovarian cancer gene to determine if any differences exist. This can be done using any number of known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the ovarian cancer gene of the patient and the known ovarian cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the ovarian cancer genes are used as probes to determine the number of copies of the ovarian cancer gene in the genome.

In another preferred embodiment, the ovarian cancer genes are used as probes to determine the chromosomal localization of the ovarian cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the ovarian cancer gene locus.

# Administration of pharmaceutical and vaccine compositions

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In one embodiment, a therapeutically effective dose of an ovarian cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques. See, e.g., Ansel, et al. (1999) Pharmaceutical Dosage Forms and Drug Delivery Systems Lippincott; Lieberman (1992) Pharmaceutical Dosage Forms (vols. 1-3) Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding Amer. Pharmaceutical Assn.; and Pickar (1999) Dosage Calculations Thomson. Adjustments for ovarian cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction, and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art. U.S. Patent Application No. 09/687,576, further discloses the use of compositions and methods of diagnosis and treatment in ovarian cancer is hereby expressly incorporated by reference.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the ovarian cancer proteins and modulators thereof of the present invention can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intra-nasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the ovarian cancer

proteins and modulators may be directly applied as a solution or spray.

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The pharmaceutical compositions of the present invention comprise an ovarian cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid, and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules, and lozenges. It is recognized that ovarian cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are well known in the art.

The compositions for administration will commonly comprise an ovarian cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight, and the like in accordance with the particular mode of administration selected and the patient's needs. See, e.g., Remington's Pharmaceutical Science (15th ed., 1980) and Hardman and Limbird (eds. 2001) Goodman and Gillman: The Pharmacological Basis of Therapeutics (10th ed.) McGraw-Hill. Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions are readily available.

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The compositions containing modulators of ovarian cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and/or its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc. Such prophylactic

treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, e.g., in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present ovarian cancer protein-modulating compounds can be administered alone or in combination with additional ovarian cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

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In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in Tables 1-26, such as RNAi, antisense polynucleotides or ribozymes, will be introduced into cells, in vitro or in vivo. The present invention provides methods, reagents, vectors, and cells useful for expression of ovarian cancer-associated polypeptides and nucleic acids using in vitro (cell-free), ex vivo or in vivo (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell. See, e.g., Berger and Kimmel (1987) Guide to Molecular Cloning Techniques from Methods in Enzymology (vol. 152) Academic Press; Ausubel, et al. (eds. 1999 and supplements) Current Protocols Lippincott; and Sambrook, et al. (2001) Molecular Cloning: A Laboratory Manual (3d ed., Vol. 1-3) CSH Press.

In a preferred embodiment, ovarian cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, ovarian cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the ovarian cancer coding regions) can be administered in a gene therapy application. These ovarian cancer genes can include antisense applications, either as gene therapy (e.g., for incorporation into the genome) or as antisense compositions, as will be appreciated by those in the art.

Ovarian cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses. Such vaccine compositions can include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) <u>J. Clin. Invest.</u> 95:341-

349), peptide compositions encapsulated in poly(D,L-lactide-co-glycolide, "PLG") microspheres (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in immune stimulating complexes (ISCOMS; see, e.g., Takahashi, et al. (1990) 5 Nature 344:873-875; Hu, et al. (1998) Clin. Exp. Immunol. 113:235-243), multiple antigen peptide systems (MAPs; see, e.g., Tam (1988) Proc. Nat'l Acad. Sci. USA 85:5409-5413; Tam (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p. 379, in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Chakrabarti, et al. (1986) Nature 320:535-537; Hu, et al. (1986) Nature 320:537-10 540; Kieny, et al. (1986) AIDS Bio/Technology 4:790-795; Top, et al. (1971) J. Infect. Dis. 124:148-154; Chanda, et al. (1990) Virology 175:535-547), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25-35; Eldridge, et al. (1993) Sem. Hematol. 30:16-24; Falo, et al. (1995) Nature Med. 7:649-653), adjuvants (Warren, et 15 al. (1986) Ann. Rev. Immunol. 4:369-388; Gupta, et al. (1993) Vaccine 11:293-306), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585-1589; Rock (1996) Immunol. Today 17:131-137), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745-1749; Robinson, et al. (1993) Vaccine 11:957-960; Shiver, et al., p. 423, in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Cease and Berzofsky (1994) Ann. Rev. Immunol. 12:923-989; and Eldridge, et al. (1993) Sem. Hematol. 30:16-24). Toxin-targeted 20 delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bortadella pertussis, or Mycobacterium tuberculosis derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be

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used as adjuvants.

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Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. See, e.g., Wolff et. al. (1990) Science 247:1465-1468; U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; and WO 98/04720. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivicaine, polymers, peptidemediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode ovarian cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors useful for therapeutic administration or immunization e.g., adeno and adeno-associated virus vectors, retroviral vectors, Salmonella typhi vectors, detoxified anthrax toxin vectors, and the like, will be apparent. See, e.g., Shata, et al. (2000) Mol. Med. Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; and Hipp, et al. (2000) In Vivo 14:571-85.

Methods for the use of genes as DNA vaccines are well known, and include placing an ovarian cancer gene or portion of an ovarian cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in an ovarian cancer patient. The ovarian cancer gene used for DNA vaccines can encode full-length ovarian cancer proteins, but more preferably encodes portions of the ovarian cancer proteins including peptides derived from the ovarian cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from an ovarian cancer gene. For example, ovarian cancer-associated genes or sequence encoding subfragments of an ovarian cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the ovarian cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment ovarian cancer genes find use in generating animal models of ovarian cancer. When the ovarian cancer gene identified is repressed or diminished in cancer tissue, gene therapy technology, e.g., wherein antisense RNA directed to the ovarian cancer gene will also diminish or repress expression of the gene. Animal models of ovarian cancer find use in screening for modulators of an ovarian cancer-associated sequence or modulators of ovarian cancer. Similarly, transgenic animal technology including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the ovarian cancer protein. When desired, tissue-specific expression or knockout of the ovarian cancer protein may be necessary.

It is also possible that the ovarian cancer protein is overexpressed in ovarian cancer. As such, transgenic animals can be generated that overexpress the ovarian cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods find use as animal models of ovarian cancer and are additionally useful in screening for modulators to treat ovarian cancer.

### Kits for Use in Diagnostic and/or Prognostic Applications

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For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In the diagnostic and research applications such kits may include any or all of the following: assay reagents, buffers, ovarian cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, siRNA or antisense polynucleotides, ribozymes, dominant negative ovarian cancer polypeptides or polynucleotides, small molecules inhibitors of ovarian cancer-associated sequences etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing directions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. Any medium

capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of ovarian cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: an ovarian cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing ovarian cancer-associated activity. Optionally, the kit contains biologically active ovarian cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

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#### **EXAMPLES**

# Example 1: Gene Chip Analysis

Molecular profiles of various normal and cancerous tissues were determined and analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

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TABLE 1A lists about 1119 genes up-regulated in ovarian cancer compared to normal adult tissues. These were selected from 59000 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 5.0. The "average" ovarian cancer level was set to the 80th percentile value amongst various non-mailgnant tissues.

TABLE 1A: ABOUT 1119 UP-REGULATED OVARIAN CANCER GENES Pkey: Primekey
Ex. Acon: Exemplar Accession
UG ID: UniGene ID
Title: UniGene title

35 ratio: ratio tumor vs normal tissues

	Pkey	Ex. Acon	UGID	Title	ratio
	423634	AW959908	Hs.1690	heparin-binding growth factor binding protein	65.7
	423017	AW178761	Hs.227948	"serine (or cysteine) proteinase inhibitor, clade 8(ovalbumi	63.6
40	432938	T27013	Hs.3132	steroidogenic acute regulatory protein	58.3
	445810	AW265700	Hs.155660	ESTs	35.9
	431938	AA938471	Hs.115242	developmentally regulated GTP-binding protein 1	32.0
	407112	AA070801	Hs.51615	*ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAM	31.3
	425650	NM 001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen)	30.0
45	402075			predicted exan	27.9
	400301	X03635	Hs.1657	estrogen receptor 1	26.4

PCT/US02/19297

	100000			and field divers	25.3
	402639 421948	L42583	Hs.111758	predicted exon keratin 6A	24.7
	414540	BE379050	113.1111130	"qb:601236655F1 NIH_MGC_44 Homo sapiens cDNA clon	24.6
_	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecule 1)	24.5
5	401575		11 445454	predicted exon	23.6 23.2
	457024 440684	AA397546 Al253123	Hs.119151 Hs.127356	ESTs "ESTs, Highly similar to NEST_HUMAN NESTI [H.sapien	23.2 23.1
	459006	AW298631	Hs.27721	hypothetical protein FLJ20353	22.8
	400964	7.11.250501		predicted exon	22.5
10	402421			predicted exon	20.9
	437329	AAB11977	Hs.291761	ESTs *gb:601283601F1 NIH_MGC_44 Homo saptens cDNA don	20.8 20.7
	414505 411004	BE390440 AW813242		"gb:MR3-ST0191-020200-207-g10 ST0191 Homo sapiens	20.4
	401283	111010212		predicted exon	20.3
15	440633	AI140686	Hs.263320	ESTs	19.9
	445603	H08345	Hs.106234	ESTs	19.7 19.7
	403786 436508	AW604381	Hs.121121	predicted exon ESTs	19.6
	459390	BE385725	16.121121	*ab:601276347F1 NIH_MGC_20 Homo sapiens cDNA clon	19.2
20	421823	N40850	Hs.28625	ESTs	19.0
	417366	BE185289	Hs.1076	small proline-rich protein 1B (comifin)	18.9
	422525	AA758797	Hs.192807	ESTs Human T-cell receptor active alpha-chain mRNA from JM c	18.5 18.3
	458121 430520	S42416 NM_016190	Hs.74647 Hs.242057	chromosome 1 open reading frame 10	18.1
25	450192	AA263143	Hs.24596	RAD51-interacting protein	18.0
	416839	H94900	Hs.17882	ESTs	17.9
	440788	A1806594	Hs.128577	ESTs	17.9 17.7
	451072 402203	AA013451	Hs.117929	ESTs predicted exon	17.7
30	417611	AW993983		*gb:RC1-BN0035-130400-013-a04 BN0035 Homo sapiens	17.3
	438658	Al222068	Hs.123571	ESTs ·	17.3
	403747			predicted exon	17.2
	444958	AW292643	Hs.167047	ESTs predicted exon	17.2 17.1
35	404097 459375	BE251770		*gb:601112470F1 NIH_MGC_16 Homo sapiens cDNA don	16.9
55	443198	AI039813		gb:ox49d06.x1 Soares_total_fetus_Nb2HF8_9w Homo sapi	16.9
	441557	AW452647	Hs.270482	ESTs	16.9
	433871	W02410	Hs.205555	ESTS	16.8 16.7
40	429163 443406	AA884766 A1056238	Hs.143316	gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo sapiens cD ESTs	16.7
40	400613	71000200	110.170010	predicted exon	16.6
	448372	AW445166	Hs.170802	ESTs	16.5
	410929	H47233	Hs.30643	ESTs	16.5 16.1
45	445887 422036	Al263105 AA302647	Hs.145597 Hs.271891	ESTs ·	16.0
73	404767	AA302047	115.27 1051	predicted exan	15.9
	420831	AA280824	Hs.190035	ESTs	15.8
	405196			predicted exon	15.8
50	452947 429538	AW130413 BE182592	Hs.139322	gb:xf50f04.x1 NCI_CGAP_Gas4 Homo saptens cDNA clo small protine-rich protein 3	15.8 15.8
50	435313	A1769400	Hs.189729	ESTs	15.7
	449635	AI989942	Hs.232150	ESTs	15.6
	424098	AF077374	Hs.139322	small proline-rich protein 3	15.4
55	411660 442653	AW855718 BE269247	Hs.170226	"gb:RC1-CT0279-070100-021-a06 CT0279 Homo sapiens c Homo sapiens clone 23579 mRNA sequence	15.4 15.4
	442653	Al076123	115,110220	gb:oy92e04.x1 Soares_fetal_fiver_spleen_1NFLS_S1 Homo	15.4
	458012	AI424899	Hs.188211	ESTs .	15.3
	441018	AI809587	Hs.148782	ESTs	15.1
60	425972	BE391563	Hs.165433	*ESTs, Highly similar to T17342 hypothetical protein DKFZ	15.1 15.1
UU	418092 410909	R45154 AW898161	Hs.106604 Hs.53112	ESTs *ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	15.1
	458234	BE551408	Hs.127196	ESTs	15.0
	434208	T92641	Hs.127648	hypothetical protein PRO2176	15.0
65	403177	4 1400400	11- 400407	predicted exon	15.0 14.9
65	423725 425090	AJ403108 AA350552	Hs.132127	hypothetical protein LOC57822 *gb:EST57886 Infant brain Homo sapiens cONA 5' end, mR	14.7
•	409723	AW885757	Hs.257862	ESTs	14.6
	423735	AA330259		"gb:EST33963 Embryo, 12 week li Homo sapiens cDNA 5"	14.6
70	444266	AJ424984	Hs.125465	ESTs '	14.5 14.4
70	443341 457336	AW631480 AW969657	Hs.8688 Hs.291029	ESTS ESTS	14.4
	440500	AA972165	Hs.150308	ESTs	14.4
	446292	AF081497	Hs.279582	Rh type C glycoprotein	14.3
75	438086	AA336519	Hs.301167	"Homo sapiens cONA: FLJ21545 fis, clone COL06195"	14.3
75	434715	BE005346	Hs.116410	ESTs ESTs	14.2 14.2
	409387 40927 <b>2</b>	AW384900 AB014569	Hs.123526 Hs.52526	KIAA0669 gene product	14.2
	454913	AW841462		gb:RC6-CN0014-080300-012-B09 CN0014 Homo saptens	14.0
00	439846	T63959	Hs.228320	"Homo sapiens cDNA: FLJ23537 fis, clone LNG07690"	14.0
80	409695	AA296961	U- 4000	*gb:EST112514 Adrenal gland tumor Homo sapiens cDNA	13.9 13.9
	422897 404664	AA579784	Hs.4290	ESTs predicted exon	13.9
	458829	AI557388		gb:PT2.1_6_G03.r tumor2 Homo sapiens cDNA 3', mRNA	13.8
	407327	AA487182	Hs.269414		13.8

	455435	AW939445		*gb:QV1-DT0072-310100-056-b07 DT0072 Homo sapiens	13.7
	449327	AI638743	Hs.224672	ESTs	13.7
	411693	AW857271		*gb:CM0-CT0307-210100-158-g09 CT0307 Homo saplens	13.7
5	407463	AJ272034		gb:Homo sapiens mRNA for putative capacitative calcium c	13.6
5	446767 433040	Al380107 H70423	Hs.158954	ESTs ESTs	13.6 13.5
	435209	AW027809	Hs.300511 Hs.187698	*ESTs, Highly similar to cytomegalovirus partial fusion rece	13.5
	441459	A1919142	Hs.214233	ESTs	13.5
	401269			predicted exon	13.4
10	438663	Al199575	Hs.153070	ESTs	13.4
	426698	AA394104	Hs.97489	ESTS	13.4 13.2
	423637 448543	AL137279	Hs.130187 Hs.21380	Homo sapiens mRNA; cDNA DKFZp43401214 (from clon Homo sapiens mRNA; cDNA DKFZp586P1124 (from clon	13.2
	456714	AW897741 AW897265	NS.21300	"ab:CMD-NN0057-150400-335-a04 NN0057 Homo sapiens	13.2
15	458356	AI024855	Hs.131575 .	•	13.2
	431822	AA516049		*gb:ng65d01.s1 NCI_CGAP_Lip2 Homo sapiens cDNA do	13.1
	454822	AW833793		*gb:QV4-TT0008-130100-080-a06 TT0008 Homo sapiens c	13.1
	453358	A1990738	Hs.240066	ESTs	13.1 13.1
20	435542 421286	AA687376 AA806584	Hs.269533 Hs.187895	ESTs ESTs	13.0
20	452799	A1948829	Hs.213786	ESTs	13.0
	444355	BE383686	Hs.191621	ESTs .	13.0
	444271	AW452569	Hs.149804	ESTs	12.9
25	443860	AW856632	11 400400	gb:QV4-SN0024-210400-181-g04 SN0024 Homo sapiens	12.9 12.9
25	428719	AA358193	Hs.193128 Hs.98133	hypothetical projein FLJ10805 ESTs	12.8
	418282 437308	AA215535 AA749417	Hs.292353	ESTs	12.7
	400584	7011 10111	· IDILULUS	predicted exon	12.7
	426306	AA447310	Hs.164059	*Homo sapiens cDNA FLJ13338 fis, clone OVARC100188	12.7
30	448466	Al522109	Hs.171066	ESTs	12.7
	402738	*********	11- 444700	predicted exon	12.7 12.6
	451531 435243	AA018311 AW292886	Hs.114762 Hs.261373	ESTs adenosine A2b receptor pseudogene	12.6
	433243	X65724	Hs.2839	Norrie disease (pseudoglioma)	12.6
35	425108	AI000489	Hs.96967	ESTs	12.5
	422330	D30783	Hs.115263	epiregulin	12.5
	432949	AA570749	Hs.298866	ESTs	12.5
	417009	AA191719	Hs.171872	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 8 (RNA	12.4 12.4
40	456378 432966	AA843387 AA650114	Hs.87279	ESTs *gb:ns92h09.s1 NCI_CGAP_Pr3 Homo saplens cDNA don	12.4
70	440571	AA904461	Hs.130798	ESTs	12.3
	411178	AW820852		"gb:RC2-ST0301-120200-011-f12 ST0301 Homo sapiens c	12.3
	445934	AF131737	Hs.13475	hypothetical prolein	12.3
45	433917	A1809325	Hs.122814	Human DNA sequence from done RP5-1028D15 on chrom	12.2
45	402018	A A 22 E 20 A		predicted exon "gb:EST39787 Epididymus Homo sapiens cDNA 5' end, mR	12.2 12.2
	424101 448533	AA335394 AL119710	Hs.21365	nucleosome assembly protein 1-like 3	12.1
	458154	AWB16379	1 10.2,1000	"gb:QV4-ST0234-181199-035-g01 ST0234 Homo sapiens c	12.1
	440919	AW291274	Hs.262826	ESTs	12.0
50	415747	AA381209	•	gb:EST94257 Activated T-cells I Homo sapiens cDNA 5' e	12.0
	411748	AW859920	Lie CD4CD	*gb:QV1-CT0364-260100-052-g05 CT0364 Homo sapiens	12.0 12.0
	452975 427276	M85521 AA400269	Hs.69469 Hs.49598	dendritic cell protein ESTs	12.0
	454315	AW373564	Hs.251928	nuclear pore complex interacting protein	12.0
55	450786	H86632	Hs.33654	ESTs	12.0
	402578			predicted exon	11.9
	459591	AL037185		gb:DKFZp564A1169_r1 564 (synonym: hfbr2) Homo sapie	11.9 11.9
	433449 429108	AW772282 AA890521	Hs.126035	"gb:hn71b05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA c ESTs	11:8
60	454556	AW807073	115.120000	"gb:MR4-ST0062-031199-018-d06 ST0062 Homo saplens	11.7
•••	443613	Al079356		gb:oz39b09.s1 Soares_NhHMPu_S1 Horno sapiens cDNA c	11.7
	400385	NM_020389	Hs.283104	putative capacitative calcium channel	11.6
	411725	AW858396		gb:CM0-CT0341-181299-130-c06 CT0341 Homo sapiens	11.5
65	455174	AI694575	Hs.147801	ESTs "gb:RC1-HN0015-120400-021-c07 HN0015 Homo sapiens	11.5 11.5
UJ	412402 434205	AW984788 AF119861	Hs.283032	hypothetical protein PRO2015	11.5
	450496	AW449251	Hs.257131	ESTs	11.5
	411149	N68715	Hs.269128	ESTs	11.5
70	414210	BE383592		gb:601297871F1 NIH_MGC_19 Homo sapiens cDNA clon	11.4
70	409994	D86864	Hs.57735	acetyl LDL receptor; SREC	11.3 11.3
	453845	AL157568		gb:DKFZp761F0816_r1 761 (synonym: hamy2) Homo sapi predicted exon	11.3
	404849 442824	BE178065	Hs.1440B1	ESTs .	11.3
	428548	AA430058	Hs.98649	EST	11.3
75	434804	AA649530		*gb:ns44f05.s1 NCI_CGAP_Alv1 Homo sapiens cDNA do	11.3
	430486	BE062109	Hs.241551		11.3
	400174	44710010		predicted exon	11.2 11.2
	424324 447724	AA346316 AW298375	Hs.24477	gb:EST52440 Greater ornentum tumor Homo saptens cDN ESTs	11.2
80	457028	AW449838	Hs.97562	ESTs	11.2
	429900	AA460421	Hs.30875	ESTs	11.2
	452240	AL591147	Hs.61232	ESTs	11.2
	458067	AA393603	Hs.36752	"Homo sapiens cDNA: FLJ22834 fis, clone KAIA4314"	11.1
	402222			predicted exon	11.1

	446745	AW118189	Hs.156400	ESTs	11.1
	453060	AW294092	Hs.21594	ESTs	11.1
	443482	AW188093	Hs.250385	ESTs	11.1
_	436843	AA824588		"gb:oc83d02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA c	11.0
5	416320	H47867	Hs.34024	ESTs	11.0
	435772	AA700019	Hs.132992	*ATP-binding cassette, sub-family G (WHITE), member 5 (	11.0
	451542	AA018365	Hs.32713	ESTs	11.0
	408522	Al541214	Hs.46320	*Small proline-rich protein SPRK [human, odontogenic kera	11.0
10	414712	N88858.comp	Hs.77039	ribosomal protein S3A	10.9
10	411940	AW876686		gb:CM4-PT0031-180200-507-e05 PT0031 Homo sapiens c	10.9
	408733	AW264812	Hs.254290	ESTs	10.9
	452030	AL137578	Hs.27607	Homo sapiens mRNA; cDNA DKFZp564N2464 (from clon	10.9
	458175	AW296024	Hs.150434	ESTs .	10.9
	400612			predicted exon	10.9
15	440159	A1637599	Hs.126127	ESTs	10.8
	429443	AB028967	Hs.202687	potassium voltage-gated channel, Shal-related subfamily, m	10.8
	416319	Al815601	Hs.79197	*CO83 antigen (activated B lymphocytes, Immunoglobulin s	10.8
	405783			predicted exon	10.7
20	405708			predicted exon	10.7
20	433266	AI863224	Hs.288577	"Homo sapiens cDNA FLJ13872 fis, clone THYRO100132	10.6
	456900	AA355442	Hs.169054	ESTs	10.6
	432408	N39127	Hs.76391	"myxovirus (influenza) resistance 1, homolog of murine (int	10.6
	451702	AW665452	Hs.246503	ESTs	10.6
0.5	418179	X51630	Hs.1145	Wilms turnor 1	10.6
25	408987	H85615		gb:yt03f11.r1_Soares retina N2b5HR Homo sapiens cDNA	10.6
	405285			predicted exon	10.5
	419276	BE165909	Hs.134682	"Homo sapiens cDNA: FLJ23161 fis, clone LNG09730"	10.5
	407287	AI678812	Hs.201658	"ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAM	10.5
20	403065			predicted exon	10.5
30	414195	BE263293		gb:601144881F2 NIH_MGC_19 Homo saplens cDNA don	10.4
	454258	A1457286	Hs.143979	"ESTs, Weakly similar to KIAA1276 protein [H.sapiens]"	10.4
	412951	BE018611	Hs.251946	"Homo sapiens cDNA: FLJ23107 ffs, clone LNG07738"	10.4
	428888	AA437010	Hs.266584	ESTs	10.4
25	440834	AA907027	Hs.128606	ESTS	10.4
35	437096	AA744406		"gb:ny51h02.s1 NCI_CGAP_Pr18 Homo saptens cDNA clo	10.4
	400135			predicted exon	10.4
	447849	AJ538147	Hs.164277	ESTs	10.3
	400593			predicted exon	10.3
40	427469	AA403084	Hs.269347	ESTs	10.3
40	402794			predicted exon	10.2
	452743	AW965082	Hs.61455	ESTs	10.2
	448983	AI611654	Hs.224908	ESTs	10.2
	422696	AF242524	Hs.26323	hypothetical nuclear factor SBBI22	10.2
15	428949	AA442153	Hs.104744	"ESTs, Weakly similar to AF208855 1 BM-013 [H.saplens]	10.2
45	409191	AW818390	11. 40.4000	"gb:RC1-ST0278-160200-014-d10 ST0278 Homo sapiens c	10.2
	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	10.2
	406076	AL390179	Hs.137011	Homo sapiens mRNA; cDNA DKFZp547P134 (from clone	10.2
	410626	BE407727	11 445504	"gb:601299771F1 NIH_MGC_21 Homo sapiens cDNA clon	10.1
50	445835	AW290999	Hs.145534	chromosome 21 open reading frame 23	10.1
50	452507	Al904646	11 000000	"gb:QV-BT065-020399-103 BT065 Homo saplens cDNA, m	10.1 10.1
	433297	AV658581	Hs.282633	ESTs	
•	426724	AA383623	Hs.293616	ESTs	10.0
	436659	A1217900	Hs.144464	ESTs	10.0
55	405675	DE444707	11-054405	predicted exon	10.0 10.0
55	413466	BE141737	Hs.254105	"enolase 1, (alpha)"	10.0
	447198	D61523	Hs.283435	ESTs	10.0
	403306	NM_006825	Hs.74368	"transmembrane protein (63kD), endoplasmic reliculum/Go	9.9
	413544	BE147225	11- 420007	*gb:PM2-HT0225-031299-003-f11 HT0225 Homo sapiens	9.9
60	437094	AW103746	Hs.136907	ESTs	9.9
vv	401497	137704	Un genoer	predicted exon	9.9
	416203	H27794	Hs.269055	ESTs	9.9
	426882	AA393108	Hs.97365	ESTs *gb:PM3-LT0031-301299-002-b09 LT0031 Homo sapiens	9.9
	454874	AW836407	U. 270422		9.9
65	405702	Z20656	Hs.278432	"myosin, heavy polypeptide 6, cardiac muscle, alpha (cardio	9.9
05	404952	C14197	Hs.103538	predicted exon ESTs	9.9
	430691 444518	C14187	Hs.146884	ESTs	9.8
	416665	A1160278 H72974	TIS. 140004	gb:yu28a10.s1 Soares fetal liver spleen 1NFLS Homo sapie	9.8
	438691	AA906288	Hs.212184	ESTs	9.8
70		AV-300200	FIS.212104	predicted exon	9.8
, 0	405636 437242	AA747538	Hs.187942	ESTs	9.8
				ESTs	9.8
•	425627 452226	AF019612 AA024898	Hs.297007 Hs.296002	ESTs	9.8
		AM24636 Al123555	Hs.81796	ESTs	9.8
75	418986 441139	AW449009	Hs.126647	ESTs	9.7
15				ESTs	9.7
	427244 423756	AA402400 AA828125	Hs.178045	*gbrod71a09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clo	9.7
	423756		Ur 2044E	Homo sapiens mRNA full length insert cDNA clone EURO	9.6
	457940	AL350159	Hs.30445		9.6
80	443526	AW792804	Hs.134002	ESTs.	9.6
50	440576 419088	AW449775	Hs.126008	smali nuclear ribonucleoprotein polypeptide G	9.6
	419088	AI538323	Hs.77496	"gb:MR1-ST0206-170400-024-g05 ST0206 Homo sapiens	9.6
	454707 446252	AW814989	Hs.150009		9.6
	434374	A1283125 AA631439	ra. (30003	app.np85d02.s1 NCI_CGAP_Thy1 Homo sapiens cDNA cl	9.6
	404014	WW01403		Brankeren Land Tink Land achieve and a	V. 3

	403093			predicted exon	9.6
	454633	AW811380		gb:IL3-ST0143-290999-019-D05 ST0143 Homo sapiens c	9.6
	407291	AA001464		gb:ze45b01.r1 Soares retina N2b4HR Homo sapiens cDNA	9.5
_	455203	AW865450		gb:PM4-SN0020-010400-008-b09 SN0020 Homo sapiens	9.5
5	403647			predicted exon	9.5
	401530	05000754	000005	predicted exon	9.5
	414281	BE269751	Hs.288995	hypothetical protein FLJ20B13	9.5
	411057	AW815098	Hs.27947	"gb:QV4-ST0212-091199-023-f10 ST0212 Homo sapiens c ESTs	9.5 9.5
10	415953 450174	H14425 T82121	Hs.177285	ESTs	9.5 9.5
10	422949	AA319435	113.117200	*gb:EST21657 Adrenal gland tumor Homo sapiens cDNA 5	9.5
	402112	R58624	Hs.2186	eukaryotic translation elongation factor 1 gamma	9.5
	457886	AA742279	Hs.293346	ESTs	9.4
	458145	A1239457	Hs.130794	ESTs	9.4
15	452332	AW014859	Hs.101657	ESTs	9.4
	434950	AW974892		gb:EST386997 MAGE resequences, MAGN Homo sapten	9.3
	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	9.3
	419968	X04430	Hs.93913	"interleukin 6 (interferon, beta 2)"	9.3
20	436211	AK001581	Hs.80961	"polymerase (DNA directed), gamma"	9.3
20	428412	AA428240	Hs.126083	ESTs	9.3
	449441	AI656040	Hs.196532	ESTs	9.3
	458771 458543	AW295151 AA213403	Hs.163612 Hs.257542	ESTs ESTs	9.3 9.3
	414257	A1828500	Hs.21124	"ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	9.3
25	442826	AI018777	Hs.131241	ESTs	9.3
	446740	AI611635	Hs.192605	ESTs ~	9.2
	408938	AA059013	Hs.22607	ESTs	9.2
	434157	AI538316	Hs.158451	ESTs	9.2
20	408774	AW270899	Hs.254569	ESTs .	9.2
30	424268	AA397653	Hs.144339	Human DNA sequence from clone 495010 on chromosome	9.2
	415715	F30364		gb:HSPD20786 HM3 Homo sapiens cDNA clone s400009	9.1
	405277	414007020		predicted exon	9.1
	412167 442771	AW897230 AW409808	Hs.101550	*gb:CM0-NN0057-150400-335-a11 NN0057 Homo sapiens ESTs	9.1 9.1
35	404898	A11403000	155.101000	predicted exon	9.1
55	401230			predicted exon	9.1
	400623			predicted exon	9.1
	418808	AI821836	Hs.10359	ESTs	9.1
40	436396	AI683487	Hs.299112	*Homo sapiens cDNA FLJ11441 fis, clone HEMBA100132	9.1
40	440466	AA885871	Hs.135727	ESTs	9.0
	437568	Al954795	Hs.156135	ESTs	9.0 -
	405382 435673	AF202961	Hs.284200	predicted exon  *Homo sapiens uncharacterized gastric protein ZG12P mRN	9.0 9.0
	405848	A 202301	113.204200	predicted exon	9.0
45	437229	AW976005		gb:EST388114 MAGE resequences, MAGN Homo sapien	9.0
_	417728	AW138437	Hs.24790	KIAA1573 protein	9.0
	454597	AW809648		gb:MR4-ST0124-261099-015-d01 ST0124 Homo sapiens	9.0
	427093	AA398118	Hs.97579	ESTs	9.0
50	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	9.0
30	440556 400163	AW206958	Hs.125968	ESTS	9.0 8.9
	420120	AL049610	Hs.95243	predicted exon transcription elongation factor A (SII)-like 1	8.9
	417549	AA203651	113.33273	gb:zx58f10.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo	8.9
	406163			predicted exon	8.9
55	437918	AI761449	Hs.121629	ESTs	8.9
	449419	R34910	Hs.119172	ESTs	8.9
	434683	AW298724	Hs.202639	ESTs	8.9
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedia C)	8.9
60	454590	AW809762	Hs.222056	"Homo sapiens cDNA FLJ11572 fis, clone HEMBA100337	8.8
OU	454574	AW809109		*gb:MR4-ST0117-070100-027-a04 ST0117 Homo sapiens c	8.8
	441433 416858	AA933809 AW979294	Hs.42746 Hs.85634	ESTs ESTs	8.8 8.8
	421978	AJ243662	Hs.110196	NICE-1 protein	8.8
	451528	AA018297	Hs.35493	ESTs .	8.8
65	408751	N91553	Hs.258343	ESTs	8.7
	401862			predicted exon	8.7
	417344	AW997313		gb:RC2-BN0048-250400-018-f12 BN0048 Homo sapiens	8.7
	454455	AW752710		gb:iL3-CT0219-281099-024-A03 CT0219 Homo saplens c	8.7
70	455592	BE008002		"gb:QV0-BN0147-290400-214-h04 BN0147 Homo saplens	8.7
70	417650	T05870	Hs.100640	ESTs	8.7
	456309 432030	AA225423 AI908400	Hs.143789	*gb:rc24a12r1 NCI_CGAP_Pr1 Homo sapiens cDNA clon ESTs	8.7 8.7
	421492	BE176990	Hs.104916	hypothetical protein FLJ21940	8.7
	402576			predicted exon	8.7
75	426874	N67325	Hs.247132	ESTs	8.7
	403334			predicted exon	8.7
	408562	AI436323	Hs.31141	"Homo sapiens mRNA for KIAA1568 protein, partial cds"	8.7
	439443	AF086261	Hs.127892	ESTS	8.7
80	428600 414539	AW863261	Hs.15036	"ESTs, Highly similar to AF161358 1 HSPC095 [H.sapiens	8.7
50	432527	BE379046 AW975028	Hs.102754	'gb:601236646F1 NIH_MGC_44 Homo sapiens cDNA clon ESTs	8.6 8.6
	403273		110.102107	predicted exon	8.6
	452077	BE144949		"gtr:RC2-HT0187-041099-011-d12 HT0187 Homo sapiens	8.6
	444598	A1288830	Hs.149924	ESTs	8.6
				_	

	40.4000			ml . maanaa	
	434056	AF116649	Hs.283944	"Homo sapiens PR00566 mRNA, complete cds"	8.6
	429643	AA455889	Hs.187548	ESTs	8.6
	432340	AA534222		gb:nj21d02.s1 NCI_CGAP_AA1 Homo sapiens cDNA cion	8.6
_	446142	A1754693	Hs.145968	ESTs	8.6
5	417412	X16896	Hs.82112	"interleukin 1 receptor, type I"	8.6
	416913	AW934714		*gb:RC1-DT0001-031299-011-a11 DT0001 Homo sapiens	8.5
	451318	AA029888	Hs.95071	ESTs	8.5
	405547			predicted exon	8.5
. 0	423843	AA332652		gb:EST36627 Embryo, 8 week I Homo sapiens cDNA 5' en	8.5
10	454145	AA046872	Hs.62798	ESTs	8.4
	401200			predicted exon	8.4
	404166			predicted exon	8.4
	412761	AW995092		*gb:QV0-BN0041-030300-145-a10 BN0041 Homo sapiens	8.4
	412333	AW937485		*gb:QV3-DT0044-221299-045-b09 DT0044 Homo sapiens	8.4
15	455092	BE152428		°gb:CM0-HT0323-151299-126-b04 HT0323 Homo sapiens	8.4
13	419281	H96452	Hs.42189	ESTs	8.4
	446171	AJ374927	115.42 103	gb:ta66c04.x1 Soares_total_fetus_Nb2HF8_9w Homo sapie	8.3
	437362	AL359561	Un 40400		8.3
	402631 -	ALDDS001	Hs.16493 ,	hypothetical protein DKFZp762N2316	
20		W.CC3030	LL- 205424	predicted exon	8.3
20	458573	AV653838	Hs.295131	ESTs	8.3
	439185	AF087976	Hs.233343	ESTs	8.3
	445881	Al263029	Hs.210689	ESTs	8.3
	449737	A1668581	Hs.246316	ESTs	8.3
25	401830	AJ004832	Hs.5038	neuropathy target esterase	8.3
25	421991	NM_014918	Hs.110488	KIAA0990 protein	8.3
	416996	W91892	Hs.59609	ESTs	8.2
	443626	AI540644	Hs.138479	"ESTs, Moderately similar to ALU7_HUMAN ALU SUBF	8.2
	407471	D55644		gb:Human spleen PABL (pseudoautosomal boundary-like se	8.2
20	402664			predicted exon	8.2
30	417682	W69561		gb:zd47a08.r1 Soares_fetal_heart_NbHH19W Homo sapien	8.2
	424983	AI742434	Hs.169911	ESTs	8.2
	434353	AA630863	Hs.131375	"ESTs, Weakly similar to ALUB_HUMAN !!!! ALU CLAS	8.2
	453448	AL036710	Hs.209527	ESTs	8.2
	455121	BE156459		gb:QV0-HT0368-040100-082-606 HT0368 Homo sapiens	8.2
35	404270			predicted exon	8.1
	438297	AW515196	Hs.258238	"ESTs, Moderately similar to ALU1_HUMAN ALU SUBF	8.1
	418122	R42778	Hs.22217	ESTs	8.1
	419929	U90268	Hs.93810	cerebral cavernous malformations 1	8.1
	400925	000200		predicted exon	8.1
40	403350			predicted exon	8.1
. •	426116	AA868729	Hs.144694	ESTs	8.1
	441518	AW161697	Hs.294150	ESTs	8.1
	421888	AA299780	Hs.121036	ESTs	8.1
	402745		113.121000	predicted exon	8.1
45	402071			predicted exon	8.1
73	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated protein homolog	8.0
	430372			ESTs	8.0
	449867	AI206173 AI672379	Hs.211375		8.0
			Hs.73919	"clathrin, light polypeptide (Lcb)"	
50	422174 413382	AL049325	Hs.112493	Homo sapiens mRNA; cDNA DKFZp564D036 (from clone	8.0 8.0
JO .		BE090689	Us 457077	"gb:RC1-BT0720-280300-011-f08 BT0720 Homo sapiens c	
	456502	A1798611	Hs.157277	ESTs	8.0
	405336			predicted exon	8.0
	405917	A1047740	U- 2224C0	predicted exon	8.0
55	436007	AJ247716	Hs.232168	ESTS	8.0
22	439192	AW970536	Hs.105413	ESTs	8.0
	437724	AW444828	Hs.184323	ESTS	8.0
	452755	AW138937	Hs.213436	ESTs	8.0
	401781			predicted exon	7.9
60	406057			predicted exon	7.9
60	406289	AW068311	Hs.82582	"integrin, beta-like 1 (with EGF-like repeat domains)"	7.9
	421459	AI821539	Hs.97249	ESTS	7.9
	448251	BE280486	Hs.84045	"Homo sapiens cDNA FLJ11979 fis, done HEMBB100128	7.9
	429125	AA446854	Hs.271004	ESTs	7.9
C.F	440154	BE077129	Hs.126119	"Homo sapiens cDNA FLJ13273 fis, clone OVARC100101	7.9
65	413233	AW578713	Hs.47534	"ESTs, Weakly similar to ORF YKL201c [S.cerevisiae]"	· 7.9
	438268	AA782163	Hs.293502	ESTs	7.9
	452466	N84635	Hs.29664	Human DNA sequence from clone 682J15 on chromosome 6	7.9
	441194	BE274581		"gb:601120870F1 NIH_MGC_20 Homo sapiens cDNA clon	7.9
70	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	7.9
70	445090	AW205208	Hs.147293	ESTs	7.9
	431292	AA370141	Hs.251453	Human DNA sequence from clone 967N21 on chromosome	7.9
	414266	BE267834		"gb:601124428F1 NIH_MGC_8 Homo sapiens cDNA clone	7.8
	407839	AA045144	Hs.161566	ESTs (2020)	7.8
75	456101	AA159478		gb:zo74d06.s1 Stratagene pancreas (937208) Homo sapiens	7.8
75	455853	BE147225		gb:PM2-HT0225-031299-003-f11 HT0225 Homo sapiens	7.8
	414995	C18200		gb:C18200 Human placenta cDNA (TFujiwara) Homo sapie	7.8
	447247	AW369351	Hs.287955	"Homo sapiens cDNA FLJ13090 fis, clone NT2RP3002142	7.8
	416151	T26661		gb:AB65C7R Infant brain, LLNL array of Dr. M. Soares 1	7.8
00	446435	AW206737	Hs.253582	ESTs	7.8
80	403698			predicted exon	7.8
	424914	AA348410	Hs.119065	ESTs	7.8
	409731	AA125985	Hs.56145	"thymosin, beta, identified in neuroblastoma cells"	7.8
	401604			predicted exon	7.8
	413025	AA805265	Hs.291646	ESTs	7.8

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	405896 454505	AUADOTOCE		predicted exon "gb:IL5-UM0067-240300-050-a01 UM0067 Homo sapiens	7.8 7.7
	448283	AW801365 Al340462	Hs.182979	ribosomal protein L12	7.7
_	434098	AA625499	110.102010	*gb:af69g08.r1 Soares_NhHMPu_S1 Homo saplens cDNA	7.7
5	431673	AW971302	Hs.293233	ESTs	7.7
	421029	AW057782	Hs.293053	ESTS	7.7 7.7
	408391 422529	AW859276 AW015128	Hs.256703	"gb:MR1-CT0352-240200-105-d02 CT0352 Homo sapiens ESTs	7.7
	454389	AW752571	18200100	*gb:IL3-CT0213-170100-055-F02 CT0213 Homo sapiens c	7.7
10	427821	AA470158	Hs.98202	ESTs .	7.7
	434657	AA641876	Hs.191840	ESTs	7.7
	445628 424872	Al344166	Hs.155743	ESTs "gb:EST54302 Fetal heart II Homo sapiens cDNA 5' end, m	7.7 7.7
	439232	AA347923 N48590	Hs.46693	ESTs	7.7
15	441417	AI733297	Hs.144474	ESTs	7.7
_	453596	AA441838	Hs.62905	ESTs	7.7
	430440	X52599	Hs.2561	"nerve growth factor, beta polypeptide"	7.7
	413306 400968	AW303544	Hs.118654	ESTs predicted exon ·	7.7 7.7
20	446726	AW300144	Hs.209209	*Homo sapiens cDNA FLJ11629 fis, clone HEMBA100424	7.7
	427504	AA776743	Hs.191589	ESTs	7.7
	405621			predicted exon	7.6
	414127	AI431863	Hs.135270	ESTS	7.6 7.6
25	409866 446232	AW502152 Al281848	Hs.165547	gb:UI-HF-BR0p-ajr-f-11-0-UI.r1 NIH_MGC_52 Homo sap ESTs	7.6 7.6
20	403568	74201040	110.100011	predicted exoñ	7.6
	451458	A1797558	Hs.270820	ESTs	7.6
	439157	AA912737	Hs.20160	ESTs	7.6
30	401793	A1400204	Un 440442	predicted exon	7.6 7.6
50	429839 445672	Al190291 Al907438	Hs.112143 Hs.282862	ESTs ESTs	7.6
	449444	AW818436	Hs.23590	"solute carrier family 16 (monocarboxylic acid transporters)	7.6
	447499	AW262580	Hs.147674	KIAA1621 protein	7.6
25	.421773	W69233	Hs.112457	ESTs	7.6
35	439706 432189	AW872527 AA527941	Hs.59761	ESTs "gb:nh30c04.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clon	7.5 7.5
	402050	MM32/341		predicted exon	7.5
	429687	AI675749	Hs.211608	nucleoparin 153kD	7.5
40	423193	R07299	Hs.254837	"Homo sapiens cDNA FLJ13502 fis, clone PLACE1004836	7.5
40	416548	H62953	Hs.134169	gb:yr47f06.r1 Soares fetal liver spleen 1NFLS Homo sapien ESTs	7.5 7.5
	443236 435053	A1079496 A1057224	Hs.15443	ESTs	7.4
	437191	NM_006846	Hs.5476	"serine protease inhibitor, Kazal type, 5"	7.4
4.5	451829	AW964081	Hs.247377	ESTs	7.4
45	443151	AI827193	Hs.132714	ESTs	7.4 7.4
	452055 445265	AJ377431 AJ218295	Hs.293772 Hs.144942	ESTs ESTs	7.4
	401032	10210200	10.171012	predicted exon	7.4
<b>50</b>	448184	BE541249	Hs.109697	ESTs	7.4
50	414808	T95945		gb:ye42e02.r1 Soares fetal liver spleen 1NFLS Homo sapien	7.4
	418540 410449	AJ821597 AW748954	Hs.90877 Hs.18192	*ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM Ser/Arg-related nuclear matrix protein (plenty of prolines 1	7.4 7.4
	435568	AA688048	Hs.294080	ESTs	7.4
	459160	Al904723		*gb:CM-BT066-120299-092 BT066 Homo sapiens cDNA,	. 7.4
55	419753	N42531		gb:yy11c12.r1 Soares melanocyte 2NbHM Homo sapiens cD	7.4
	432383 404893	AK000144	Hs.274449	"Homo sapiens cDNA FLJ20137 fis, clone COL07137" predicted exon	7.4 7.4
	425349	AA425234	Hs.79886	ribose 5-phosphale isomerase A (ribose 5-phosphale epimer	7.4
	413864	BE175582		gb:RC5-HT0580-100500-022-C01 HT0580 Homo sapiens	7.3
60	426871	AA393041	Hs.216493	ESTs	7.3
	415613	R20233		gb:yg18h11.r1 Soares infant brain 1NIB Homo sapiens cDN	7.3
	427025 444683	AA397589 Al375101	Hs.97523 Hs.158721	ESTs "ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	7.3 7.3
	447700	AJ420183	Hs.171077	"ESTs, Weakly similar to similar to serine/threonine kinase	7.3
65 ·	412740	AW993984		"gb:RC1-BN0035-130400-013-a05 BN0035 Homo sapiens	7.3
	416642	T96118	Hs.226313	"ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	7.3
	416506 426130	H59879 AA853282	Hs.237306	ESTs gb:NHTBCae04f07r1 Normal Human Trabecular Bone Cell	7.3 7.3
	407392	AB032369		gb:Homo sapiens MIST mRNA, partial cds.*	7.3
70	432365	AK001106	Hs.274419	hypothetical protein FLJ10244	7.3
	451221	Al949701	Hs.210589	ESTs	7.3
	443161	AI038316	He 22240	gb:ox48c08.x1 Soares_total_fetus_Nb2HF8_9w Homo sapi "Homo sapiens cDNA FLJ13496 fis, clone PLACE1004471	7.3 7.3
	418186 439152	BE541042 H65014	Hs.23240	gb:yu66f10.r1 Weizmann Olfactory Epithelium Homo sapie	7.2
75	459534	BE386808	Hs.147905	ESTs	7.2
	443326	BE156494	Hs.188478	ESTs	7.2
	417351	T90278	Hs.15049	ESTs	7.2 7.2
	454182 402298	AW177335		*gb:CM1-CT0129-180899-005-b08 CT0129 Homo sapiens predicted exon	7.2
80	458562	N34128	Hs.145268	ESTs	7.2
	407021	U52077		"gb:Human mariner1 transposase gene, complete consensus	7.2
	449276	AW241510	Hs.252713	ESTs	7.2 7.2
	418251 420788	AA832123 AA937957	Hs.177723 Hs.193367	ESTs ESTs	7.2 7.2
				,· <del>-</del>	

	401881			predicted exon	7.2
	456436	AA251079	Hs.158386	ESTs	7.2
	413425	F20956		*gb:HSPD05390 HM3 Homo sapiens cDNA clone 032-X4-	7.2
5	448966 429340	AW372914 N35938	Hs.287462 Hs.199429	"Homo sapiens cDNA FLJ11875 fis, clone HEMBA100707 Homo sapiens mRNA; cDNA DKFZp434M2216 (from clon	7.2 7.2
3	406053	1600000	113,133723	predicted exon	7.2
	405851			predicted exon	7.2
	431009	BE149762	Hs.248213	"gap junction protein, beta 6 (connexin 30)"	7.2
10	426662 408536	AA879474 AW381532	Hs.122710 Hs.135188	ESTs	7.2 7.1.
10	455013	BE073250	ns. 150 100	"gb:MR0-BT0551-060300-102-e05 BT0551 Homo saptens	7.1
	428910	W03667	Hs.193792	ESTs	7.1
	424634	NM_003613	Hs.151407	"cartilage intermediate layer protein, nucleotide pyrophosph	7.1
15	449794 423410	AW444502 AF058989	Hs.256982 Hs.128231	"ESTs, Highly similar to AF116865 1 hedgehog-interacting "G antigen, family B, 1 (prostate associated)"	7.1 7.1
13	445460	AI797473	Hs.209468	ESTs ·	7.1
	447285	Al371849	Hs.200696	"ATPase, Class VI, type 11C"	7.1
	419750	AL079741	Hs.183114	"Homo sapiens cDNA FLJ14236 fis, clone NT2RP4000515	7.1
20	438986 420757	AF085888 X78592	Hs.269307 Hs.99915	ESTs androgen receptor (dihydrotestosterone receptor, testicular	7.1 7.1
20	432479	AL042844	Hs.275675	katanin p80 (WD40-containing) subunit B 1	7.1
	449733	R74546	Hs.29438	"Homo sapiens cDNA FLJ12094 fis, clone HEMBB100260	7.1
	437846	AA773866	Hs.244569	ESTS	7.1
25	454934 421929	AW846080 AA300543	Hs.247360	gb:MR3-CT0176-081099-002-b09 CT0176 Homo sapiens ESTs	7.1 7.1
20	401780	740000	16.241000	predicted exan	7.0
	448106	A1800470	Hs.171941	ESTs	7.0
	448835	BE277929	Hs.11081	"ESTs, Weakly similar to S57447 HPBRII-7 protein [H.sap	7.0
30	400842 429364	AA451797	Hs.201202	predicted exon *ESTs, Moderately similar to Pro-Pol-dUTPase polyprotein	7.0 7.0
50	454963	AW847647	16.201202	*gb:lL3-CT0213-280100-056-A06 CT0213 Homo sapiens c	7.0
	423891	AK002042	Hs.134795	"Homo sapiens cDNA FLJ11180 fis, clone PLACE1007452	7.0
	407506	U71600	11- 00044	gb:Human zinc finger protein zfp31 (zf31) mRNA, partial	7.0
35	413802 440051	AW964490 BE559980	Hs.32241	ESTs *gb:601345293F1 NIH_MGC_8 Homo sapiens cDNA clone	7.0 7.0
55	446283	AI948801	Hs.171073	ESTs .	7.0
	419236	AA330447	Hs.135159	"Homo sapiens cDNA FLJ11481 fis, clone HEMBA100180	7.0
	405472		11 4010	predicted exon	7.0
40	435024 453969	AI863518 AW090783	Hs.127743 Hs.301731	"ESTs, Weakly similar to V-ATPase G-subunit like protein "Homo saplens cDNA FLJ11738 fis, clone HEMBA100547	7.0 7.0
10	404992	A11030763	112.001701	predicted exon	7.0
	428129	Al244311	Hs.26912	ESTs	7.0
	414315	Z24878		gb:HSB65D052 STRATAGENE Human skeletal muscle cD	7.0
45	400491 459275	H25530 AI808913	Hs.50868 Hs.118321	*solute carrier family 22 (organic cation transporter), memb ESTs	6.9 6.9
	450853	AA479629	Hs.44243	ESTs	6.9
	457460	Al143312	Hs.164004	ESTs	6.9
	434168	A1204525	Hs.116156	ESTS	6.9
50	445153 450028	Al214671 Al912012	Hs.200737	*gb:qm32d02x1 NCI_CGAP_Lu5 Homo sapiens cDNA clo ESTs	6.9 6.9
-	414954	D81402	7151255751	gb:HUM162A03B Human fetal brain (TFujiwara) Homo sa	6.9
	459478	AW195566	Hs.253182	ESTs	6.9
	426269 401050	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (from clon	6.9 6.9
55	447588	Al394154	Hs.279659	predicted exon "ESTs, Wealdy similar to unknown protein [H.sapiens]"	6.9
-	449002	AI620018	Hs.117461	ESTs	6.9
	452759	AW590773	Hs.258996	ESTs	6.9
	443220	R85304	Hs.132032	"Homo sapiens cDNA FLJ11683 fis, clone HEMBA100490	6.9
60	400749 406277			predicted exon predicted exon	6.8 6.8
••	433785	BE044593	Hs.112704	ESTs	6.8
	434129	AI807757	Hs.221041	ESTs	6.8
	453369	BE551550	Hs.232630	ESTs	6.8
65	411722 455152	AW875942 AW858621		*gb:CM1-PT0013-131299-067-b10 PT0013 Homo saptens *gb:CM0-CT0342-021299-115-f04 CT0342 Homo saptens	6.8 6.8
	412670	AA115456		gb:zk89b05.r1 Soares_pregnant_uterus_NbHPU Homo sapi	6.8
	419054	N40340	Hs.191510	"ESTs, Weakly similar to ORF2 [M.musculus]"	6.8
	421316	AA287203	Hs.251397	SMA5	6.8
70	432363 458603	AA534489 AW103046	Hs.6162	gb:nf76g11.s1 NCl_CGAP_Co3 Homo saplens cDNA clone KIAA0771 protein	6.8 6.8
	439527	AW298119	Hs.202536	ESTs	6.8
	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane protein 2	6.8
	439127	AW978465	Hs.292368	ESTs "Venne serious USBC092 mBNA sertial ada"	6.8
75	434890 429413	AF161345 NM_014058	Hs.283930 Hs.201877	"Homo sapiens HSPC082 mRNA, partial cds" DESC1 protein	6.8 6.7
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	6.7
	447252	R90916		gb:yn01e10_r1 Soares adult brain N2b4HB55Y Homo sapien	6.7
	455851	BE146879	11= E004 /	*gb:QV4-HT0222-261099-014-c11 HT0222 Homo sapiens	6.7
80	439509 418858	AF086332 AW961605	Hs.58314 Hs.21145	ESTs "Homo sapiens cDNA: FLJ22489 fis, clone HRC10951"	6.7 6.7
	419323	A1092379	Hs.135275		6.7
	415317	Z43388	Hs.5570	hypothetical protein FLJ10006	6.7
	418654	AA226334	Hs.154291	ESTs	6.7
	407413	AF067801		gb:Homo sapiens HDCGC21P mRNA, complete cds.*	6.7

	439694	AA843915	Hs.54707	ESTs	6.7
	451191	N67900	Hs.118446	ESTs	6.7
	454006 443657	U12775	Hs.37006	agouti (mouse)-signaling protein gb:yf42f10.s1 Soares fetal liver spleen 1NFLS Homo sapien	6.7 6.7
5	455879	R14973 BE153275		gb:PMO-HT0335-180400-008-e11 HT0335 Homo sapiens	6.7
9	451368	BE242152	Hs.288417	protein serine threonine kinase Cik4	6.7
	453509	AL040021		gb:DKFZp434N1812_r1 434 (synonym: htes3) Homo saple	6.7
	420892	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cerevisiae PWP1	6.7
••	423372	AJ246375	Hs.154458	ESTs	6.7
10	450316	W84446	Hs.17850	ESTs	6.7
	447795	AW295151	Hs.163612	ESTs	6.7
	413252	BE074910		*gb:RC5-BT0580-170300-021-F12 BT0580 Homo sapiens	6.7
	405771	A18704044E		predicted exon	6.6 6.5
15	411483 420271	AW848115 AI954365	Hs.42892	*gb:lL3-CT0214-301299-048-C09 CT0214 Homo saplens c ESTs	6.6
13	431948	A1934303 AA917708	Hs.194616	ESTs	6.6
	409629	AW449589	Hs.279724	ESTs	6.6
	458841	W28965	10.2.0.21	gb:54d10 Human retina cDNA randomly primed sublibrary	6.6
	416565	AW000960	Hs.44970	ESTs	6.6
20	409097	AA677927	Hs.144269	ESTs	6.6
	441832	AI018249	Hs.128062	ESTs	6.6
	457285	AI038858	Hs.228780	"ESTs, Highly similar to AF199597 1 A-type potassium cha	6.6
	406504	DE004		predicted exon	6.6
25	414606	BE387771	Un 201072	"gb:601283251F1 NIH_MGC_44 Homo sapiens cDNA don	6.6 6.6
23	452956 410743	AW003578 AA089474	Hs.231872 Hs.272153	ESTs ESTs	6.6
	404599	M1003414	115.272100	predicted exon	6.6
	423575	C18863	Hs.163443	"Homo sapiens cDNA FLJ11576 fis, clone HEMBA100354	6.6
	443027	AI027847	Hs.253550	ESTs	6.6
30	458663	AV658444	Hs.280776	*Homo sapiens cDNA FLJ13684 fis, clone PLACE2000021	6.6
	431277	AA501806	Hs.249965	ESTs	6.6
	445232	BE294357		"gb:601172878F1 NIH_MGC_17 Homo saplens cDNA clon	6.6
	459170	AI905518		*gb:RC-BT091-210199-098 BT091 Homo sapiens cDNA, m	6.6
25	437876	AA770151	Hs.126424	ESTs	6.6
35	406752	A1285598	Hs.217493	annexin A2	6.6 6.6
	401245 446102	AW168067	Hs.252956	predicted exon . ESTs	6.5
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	6.5
	421160	AL080215	Hs.102301	Homo saplens mRNA; cDNA DKFZp586J0323 (from clone	6.5
40	458831	· H71739	Hs.200227	ESTs	6.5
	408914	AW450309		gb:UI-H-BI3-akz-g-08-0-UI.s1 NCI_CGAP_Sub5 Homo sa	6.5
	411018	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo sapiens c	6.5
	436562	H71937	Hs.169756	"complement component 1, s subcomponent"	6.5
15	457620	AA602711		*gb:np03h06.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clon	6.5
45	438647	AA813118	Hs.163230	ESTs	6.5
	439570	T79925	Hs.269165	ESTs	6.5 6.5
	419273 443745	BE271180 AB039670	Hs.293490 Hs.9728	ESTs ALEX1 protein	6.5
	431029	BE392725	Hs.248571	Homo sapiens PAC clone RP5-1163J12 from 7q21.2-q31.1	6.5
50	458695	AV660159	Hs.282284	ESTs	6.5
	410966	AW812088		gb:RC4-ST0173-191099-032-a07 ST0173 Homo sapiens c	6.4
	417135	AA422067	Hs.50547	ESTs	6.4
	416441	BE407197		*gb:601301552F1 NIH_MGC_21 Homo saplens cDNA don	6.4
55	413702	BE170313		*gb:QV4-HT0536-040500-193-g02 HT0536 Homo saplens	6.4
23	452563 4000CC	AI907552	Nº 30E30C	*gb:RC-BT147-120499-044 BT147 Homo sapiens cDNA, m	6.4 6.4
	408956 406349	AK001868	Hs.295306	*ESTs, Highly similar to unnamed protein product (H.sapien predicted exon	6.4
	425420	BE536911	Hs.234545	*ESTs, Weakly similar to AF155135 1 novel retinal pigmen	6.4
	459430	AW662886	110.20 10 10	gb:hi82h11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDN	6.4
60	425733	F13287	Hs.159388	Homo sapiens clone 23578 mRNA sequence	6.4
	458678	Al306162	Hs.170938	"ESTs, Weakly similar to KIAA0705 protein [H.sapiens]"	6.4
	429695	AA835714	Hs.293556	ESTs	6.4
	426872	AA410446	Hs.112011	"ESTs, Weakly similar to unknown [H.sapiens]"	6.4
65	437152	AL050027	Un 422240	gb:Homo sapiens mRNA; cDNA DKFZp566C0324 (from c	6.4 6.4
UJ	440517	AW139632	Hs.132246	ESTs ESTs	6.4
	450877 410664	AI799608; NM_006033	Hs.29178 Hs.65370	"Ilpase, endothelial"	6.4
	405793	1414_000000	115.05570	predicted exon	6.4
	418709	AA227394		gb:zr17c10.r1 Stratagene NT2 neuronal precursor 937230 H	6.4
70	428684	AA431792	Hs.44784	ESTs	6.4
	448516	AW898595		gb:RC1-NN0073-260400-011-g09 NN0073 Homo sapiens	6.4
	400983			predicted exon	6.3
	422365	AF035537	Hs.115521	"REV3 (yeast homolog)-like, catalytic subunit of DNA poly	6.3
75	425612	BE004257		*gb:CMO-BN0103-180300-296-c04 BN0103 Homo sapiens	6.3
75	401521	A1724440	Un tacaer	predicted exon	6.3 6.3
	430290	AI734110 AK000342	Hs.136355 Hs.77646	ESTs Homo sapiens mRNA; cDNA DKFZp761M0223 (from clon	6.3
	414931 437939	AK000342 AW298600	Hs.77646 Hs.141840	"ESTs, Weakly similar to S59501 interferon receptor JFNA	6.3
	457839	AI820539	Hs.267087	"ESTs, Moderately similar to ALU4_HUMAN ALU SUBF	6.3
80	405810			predicted exon	6.3
	443747	AV646352		gb:AV646352 GLC Homo sapiens cDNA done GLCAME	6.3
	427287	NM_014903	Hs.174188	KIAA0938 protein	6.3
	413521	BE145814		gb:MR0-HT0208-101299-202-a04 HT0208 Homo sapiens	6.3
	429090	AW820278	Hs.99066	ESTs	6.3

	451488	H22999	Hs.208846	ESTs	6.3
	455713	BE069891		*gb:QV4-BT0401-201299-064-b01 BT0401 Homo sapiens	6.3
	452161	R43077	Hs.221747	ESTs	6.3
5	428647	AA830050	Hs.124344	ESTs	6.3
3	445063	Al246275	Hs.149196	ESTS	6.3
	456671	AB011142	Hs.114293	KIAA0570 gene product	6.3
	401508	Alamancan	11- 47224	predicted exon	6.3
•	412677 441720	AW029608	Hs.17384	ESTs ESTs	6.3 6.3
10	418051	Al346487 AW192535	Hs.28739 Hs.19479	ESTs	6.3
10	438014	N71183	Hs.121806	"Homo sapiens cDNA FLJ11971 fis, clone HEMBB100120	6.3
	432101	Al918950	Hs.11092	"Homo sapiens cDNA FLJ14290 fis, clone PLACE1006795	6.3
	421032	AW293133	Hs.101340	ESTs	6.3
	436532	AA721522	***************************************	gb:nv54h12r1 NCt_CGAP_Ew1 Homo sapiens cDNA do	6.3
15	431318	AA502700	Hs.293147	ESTs	6.3
	413470	N20934		gb:yx54c11.s1 Soares melanocyte 2NbHM Homo sapiens c	6.3
	402425			predicted exan	6.3
	455993	BE179085		"gb:RCO-HT0613-140300-021-d06 HT0613 Homo sapiens	6.3
20	400160			predicted exon	6.3
20	413795	AL040178	Hs.142003	ESTs	6.2
	405071			predicted exon	6.2
	403741	A10040FF	11- 007520	predicted exon	6.2
	432489 402296	AI804855	Hs.207530	ESTs	6.2 6.2
25	446091	AW022192	Hs.200197	predicted exon ESTs	6.2
23	444788	AI871122	Hs.202821	ESTs "	6.2
	404972		110.202021	predicted exon	6.2
	400227			predicted exon	6.2
	433804	Al936561	Hs.112740	ESTs	6.2
30	448807	Al571940	Hs.7549	ESTs	6.2
	404340			predicted exon	6.2
	424632	AB014523	Hs.151406	KIAA0623 gene product	6.2
	449547	H93543	Hs.117963	ESTs	6.2
25	406945	K01383	Hs.203967	metallothionein 1A (functional)	6.2
35	433663	AF083131	Hs.229535	CATX-15 protein	6.2
	407809	AW082279	Hs.244106	ESTS	6.2
	418342 438007	BE002723 AA133008	Hs.293504 Hs.158675	*ESTs, Moderately similar to ALU1_HUMAN ALU SUBF ribosomal protein L14	6.2 6.2
	410536	N39533	15.130013	gbtyv27d04.s1 Soares fetal liver spleen 1NFLS Homo sapie	6.2
40	448005	AW207437	Hs.170378	ESTs	. 6.2
	414083	AL121282	Hs.257786	ESTs	6.2
	405362		•	predicted exon	6.2
	410102	AW248508	Hs.279727	"Homo sapiens cDNA FLJ14035 fis, clone HEMBA100463	6.2
4.5	457868	AW975133		gb:EST387239 MAGE resequences, MAGN Homo sapien	6.2
45	407395	AF005082		gb:Homo sapiens skin-specific protein (xp33) mRNA, part	6.2
	443603	BE502601	Hs.134289	"ESTs, Weakly similar to KIAA1063 protein [H.sapiens]"	6.2
	430051	AA464611	Hs.52515	transducin (beta)-like 2	6.1
	434569 430481	Al311295 AA479678	Hs.58609 Hs.203269	ESTs "ESTs, Moderately similar to ALU8_HUMAN ALU SUBF	6.1 6.1
50	402859	70741 3010	113.200203	predicted exon	6.1
-	401260			predicted exon	· 6.1
	406544			predicted exon	6.1
	428446	Al024600 .	Hs.98612	ESTs	6.1
	412246	Al160873	Hs.69233	"ESTs, Weakly similar to KIAA1064 protein [H.sapiens]"	6.1
55	400420	AJ277247	Hs.287369	interleukin 22	6.1
	455662	BE065387		"gb:RC1-BT0314-030500-016-d03 BT0314 Homo saplens	6.1
	428613	AB037749	Hs.186928	KIAA1328 protein	6,1
	443267	AW450630	Hs.133851	ESTs	6.1
60	433405	AW157566	Hs.156892	ESTs	6.1
UU	416795	AJ497778 W31254	Hs.7045	"ESTs, Highly similar to AF227948 1 HBV pX associated p GL004 protein	6.1
	435706 450769	AA057418	Hs.33654	ESTs	6.1
	427174	AA398848	Hs.97541	ESTs	6.1
	425389	AW974499	Hs.192183	ESTs .	6.1
65	416675	H73802	Hs.35381	ESTs	6.1
	432749	NM_014438	Hs.278909	Interleukin-1 Superfamily e	6.1
	401809			predicted exon	6.1
	403041			predicted exon	6.0
70	408523	AW833259		"gb:RC2-TT0007-131099-011-c01 TT0007 Homo saplens c	6.0
70	416515	N91716	Hs.194140	ESTs	6.0
	452591	BE173164	Hs.1516	insulin-like growth factor-binding protein 4	6.0
	437146	AA730977	Ue 205700	*gb:nw55f05.s1 NCL_CGAP_Ew1 Homo sapiens cDNA clo	6.0 6.0
	450094 402529	AJ174947	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1164 (from clon predicted exon	6.0
75	430706	NM_003540	Hs.247816	"H4 histone family, member C"	6.0
	459186	Al908287		gb:RC-BT168-020499-035 BT168 Homo sapiens cDNA, m	6.0
	452158	AI699120	Hs.61198	ESTs	6.0
	411237	AW833676		*gb:QV4-TT0008-181199-038-h04 TT0008 Homo sapiens	6.0
00	400441	M15530	Hs.99879	B-cell growth factor 1 (12kD)	6.0
80	439398	AA284267	Hs.221504	ESTs	. 6.0
	440862	H39048	Hs.127432	ESTs	6.0
	415451	H19415	Hs.268720	"ESTs, Moderately similar to ALU1_HUMAN ALU SUBF	6.0
	459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbHPU Homo sapi	6.0
	456072	H54381		gb:yq89a03.s1 Soares fetal liver spleen 1NFLS Homo sapie	6.0

	409954	AW512770	Hs.266457	ESTs	6.0
	443488	A1073495	Hs.133912	*ESTs, Weakly similar to methyl-CpG binding domain-cont	6.0
	430825	AI734186	Hs.185105	ESTs	6.0
5	454466	AA984138	Hs.279895	"Homo sapiens mRNA for KIAA1578 protein, partial cds"	6.0
)	456506	AA278277	Hs.194212	ESTS	6.0
	449228	AJ403107	Hs.148590	*ESTs, Weakly similar to AF208846 1 BM-004 [H.sapiens]	6.0
	457727	AW974687	11- 44040D	gb:EST386776 MAGE resequences, MAGM Homo sapism	6.0
	442440	BE464435	Hs.146180	*ESTs, Weakly similar to non-receptor protein tyrosine kina	5.9
10	455110	BE154505		"gb:PM0-HT0343-281299-003-e06 HT0343 Homo sapiens	5.9
IU	402790	DEGGGGGG		predicted exon	5.9
	409982	BE005839	11- 470000	"gb:RC2-BN0120-250400-012-f03 BN0120 Homo sapiens	5.9
	427635	BE397988	Hs.179982	tumor protein p53-binding protein	5.9
	408948	AW296713	Hs.221441	ESTs	5.9
15	402046 416438	D00000	16-24002	predicted exon ESTs	5.9
13	403083	R89238	Hs.34262		5.9
				predicted exon	5.9
	402481 409867	AW502161		predicted exon gb:UI-HF-BR0p-air-g-12-0-UI.r1 NIH_MGC_52 Homo sap	5.9 5.9
	420362	U79734	Hs.97206	huntingtin interacting protein 1	5.9
20	421375	AA489200	Hs.100595	*ESTs, Moderately similar to ALU1_HUMAN ALU SUBF	5.9
20	437630	AI252782	Hs.153029	ESTs	5.9
	443500	AV646388	Hs.137071	ESTs	5.9
	448995	Al613276	Hs.5662	*guanine nucleotide binding protein (G protein), beta polyp	5.9
	438214	H06076	Hs.26320	TRABID protein	5.9
25	428046	AW812795	Hs.155381	*ESTs, Moderately similar to 138022 hypothetical protein (H	5.9
	431941	AK000106	Hs.272227	"Homo sapiens cDNA FLJ20099 fis, clone COL04544"	5.9
	403356			predicted exon	5.9
	439031	AF075079		gb:Homo sapiens full length insert cDNA YQ80A08	5.9
	430032	AW936136	Hs.99610	ESTs	5.9
30	423457	F08208	Hs.155606	paired mesoderm homeo box 1	5.9
	422158	L10343	Hs.112341	"protease inhibitor 3, skin-derived (SKALP)"	5.9
	406592			predicted exon	5.9
	418636	AW749855		*gb:QV4-BT0534-281299-053-c05 BT0534 Homo sapiens	5.8
	429399	AA452244	Hs.16727	ESTs	5.8
35	408590	AW238162	Hs.253873	ESTs	5.8
-	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psoriasin 1)	5.8
	417421	AL138201	Hs.82120	"nuclear receptor subfamily 4, group A, member 2"	5.8
	401129			predicted exon	5.8
	434745	AW974445	Hs.185155	"ESTs, Weakly similar to HuEMAP [H.sapiens]"	5.8
40	402800			predicted exon	5.8
	436185	AW753380	Hs.49753	"Homo sapiens mRNA for KIAA1561 protein, partial cds"	5.8
	419519	Al198719	Hs.176376	ESTs	5.8
	452542	AW812256		gb:RC0-ST0174-191099-031-a07 ST0174 Homo sapiens c	5.8
4.5	427166	AA431576	Hs.155658	ESTs	5.8
45	416168	H23687		gb:yn72d12.r1 Soares adult brain N2b5HB55Y Homo sapie	5.8
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (from clon	5.8
	421558	AB011125	Hs.105749	KIAA0553 protein	5.8
	458055	AW979121	Hs.131375	"ESTs, Weakly similar to ALUB_HUMAN !!!! ALU CLAS	5.8
50	418345	AJ001696	Hs.241407	"serine (or cysteine) proteinase inhibitor, clade B (ovalbumi	5.8
50	426544	AA492325		gb:ng81b11.s1 NCI_CGAP_Pr6 Homo sapiens cDNA clone	5.8
	433544	AI793211	Hs.165372	*ESTs, Moderately similar to ALU1_HUMAN ALU SUBF	5.8
	442007	AA301116	Hs.142838	"Homo saptens cDNA: FLJ23444 fis, clone HSI01343"	5.8
	443422	R10288	Hs.301529	ESTs	5.8
55	434311	BE543469	Hs.266263	"Homo sapiens cDNA FLJ14115 fis, clone MAMMA10017	5.8
55	424966	AU077312	Hs.153985 Hs.200938	"solute carrier family 7 (cationic amino acid transporter, y+	5.8 5.8
	441744 413101	AA960922 BE065215	NS.200330	ESTs "gb:RC1-BT0314-310300-015-f01 BT0314 Homo sapiens c	5.7
	445687	W80382	Hs.149297	ESTs	5.7
	441369	AA931535	115.143237	gb:oo56a04.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clon	5.7
60	414428	BE296906	Hs.182625	VAMP (vesicle-associated membrane protein)-associated pr	5.7
	431211	M86849	Hs.5566	"gap junction protein, beta 2, 26kD (connexin 26)"	5.7
	411541	W03940	110.0000	gb:za62b02r1 Soares fetal liver spleen 1NFLS Homo sapien	5.7
	448612	AI696363	Hs.171285	ESTs	5.7
	419118	AA234223	Hs.139204	ESTs	5.7
65	406322			predicted exon	5.7
	454690	AW854639		gb:MR1-CT0258-140100-203-d10 CT0258 Homo sapiens	5.7
	450313	AI038989	Hs.24809	hypothetical protein FLJ10826	5.7
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility protein	5.7
	449309	AW589823	Hs.224189	ESTs	5.7
70	408418	AW963897	Hs.44743	KIAA1435 protein	5.7
	416100	H18700	Hs.268799	ESTs	5.7
	437845	AA769578	Hs.90488	ESTs	5.7
	443345	A1052508	Hs.164482	"ESTs, Weakly similar to contains similarity to TPR domain	5.7
7.	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	5.7
75	434557	AW855466	Hs.271866	"ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	5.7
	431688	AA513906		"gb:ng67c08.s1 NCI_CGAP_Lip2 Homo sapiens cDNA do	5.7
	437641	AA811452	Hs.291911	ESTs	5.7
	409319	AW752736	Hs.33565	ESTs	5.7
00	403967	AF030107	Hs.17165	regulator of G-protein signalling 13	5.7
80	445189	AI936450	Hs.147482	ESTs	5.7
	414418	H62943	Hs.154188	ESTs	5.7
	446563	BE326588	Hs.141454	ESTs	5.7
	446075	AW451457	Hs.279179	ESTs	5.7
	428068	AW016437	Hs.233462	ESTs	5.7

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	438425	AW292922	Hs.293170	ESTs	5.7
	415532	R14780	Hs.12826	ESTs	5.7
	441442	AL043282	Hs.131824	ESTs	5.7
5	443380	A1792478	Hs.135377	ESTs	5.7 5.7
,	445527 414376	W39694 BE393856	Hs.83286 Hs.66915	ESTs "ESTs, Weakly similar to 16.7Kd protein [H.sapiens]"	5.7 5.7
	457960	AA771881	Hs.298149	ESTs	5.6
	453293	AA382267	Hs.10653	ESTs	5.6
	452503	AB000509	Hs.29736	TNF receptor-associated factor 5	5.6
10	405227			predicted exon	5.6
	442257	AW503831		gb:UI-HF-BNO-alb-b-05-0-Ul.r1 NIH_MGC_50 Homo sap	5.6
	403403			predicted exon	5.6
	454377	AA076811	11- 000450	gb:7803C12 Chromosome 7 Fetal Brain cDNA Library Hom	5.6
15	438656	H85310	Hs.209456	"ESTs, Weakly similar to NG22 [H.sapiens]" "qb:ol91d05.y5 NCI_CGAP_Kid5 Horno sapiens cDNA clo	• 5.6 5.6
13	419936 437267	AI792788 AW511443	Hs.258110	ESTs	5.6
	430563	AA481269	Hs.178381	ESTs	5.6
	444835	AI 198994	Hs.158479	ESTs	5.6
	444902	AJ132099	Hs.12114	varin 1	5.6
20	451800	AW977435	Hs.31890	ESTs	5.6
	405465			predicted exon	5.6
	403891			predicted exon	5.6
	425557	AI694300	Hs.46730	ESTs	5.6
25	432162	AA584062 A1138635	Hs.272798 Hs.22968	hypothetical protein FLJ20413	5.6 5.6
23	450152 410053	AW579707	Hs.59332	ESTs SESTS	5.6
	421285	NM_000102	Hs.1363	"cytochrome P450, subfamily XVII (steroid 17-alpha-hydro	5.6
	425264	AA353953	Hs.20369	*ESTs, Weakly similar to gonadotropin inducible transcript	5.6
	418844	M62982	Hs.1200	arachidonate 12-lipoxygenase	5.6
30	429616	Al982722	Hs.120845	ESTs	5.6
	423528	AB011137	Hs.129740	KIAA0565 gene product	5.6
	403089	**********		predicted exon	5.6
	414373	AW162907	Hs.75969	proline-rich protein with nuclear targeting signal	5.6
35	403687 417079	U65590	Hs.81134	predicted exon	5.6 5.5
55	432501	BE546532	Hs.287329	interleukin 1 receptor antagonist Fas binding protein 1	5.5
	403691	ULU-1033E	110.201025	predicted exon	5.5
	409545	BE296182		gb:601177324F1 NIH_MGC_17 Homo sapiens cDNA clon	5.5
	435990	AI015862	Hs.131793	ESTs	5.5
40	444409	AJ792140	Hs.49265	ESTs	5.5
	435478	AA682622		gb:zj20f09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo	5.5
	439981	Al348408	Hs.124675	*ESTs, Wealdy similar to unnamed protein product [H.sapie	5.5
	433644	AW342028	Hs.256112	ESTs	5.5
45	441541 400709	AA938663	Hs.199828	ESTs	5.5 5.5
73	400703	AW753085		predicted exon *gb:PM1-CT0247-151299-005-a03 CT0247 Homo sapiens	5.5
	424153	AA451737	Hs.141496	MAGE-like 2	5.5
	452465	AA610211	Hs.34244	ESTs	5.5
	406030			predicted exon	5.5
50	431071	AA491379		gb:aa65f05_r1 NCI_CGAP_GCB1 Homo sapiens cDNA d	5.5
	418086	AA211791	Hs.269666	"Homo sapiens cDNA FLJ13415 fis, clone PLACE1001799	5.5
	453034	BE246010	Hs.184109	ribosomal protein L37a	5.5
	412953 425351	Z45794 Al206234	Hs.238809 Hs.155924	ESTs	5.5 . 5.5
55	406149	AIZUUZJA	FIS. 133324	cAMP responsive element modulator predicted exon	. 5.5 5.5
55	416533	BE244053	Hs.79362	retinoblastoma-like 2 (p130)	5.5
	458378	A1040535	Hs.150524	ESTs	5.5
	401213			predicted exon	5.5
<b>~</b> 0	405904			predicted exon	5.5
60	445132	Z44811		gb:HSC29G031 normalized infant brain cDNA Homo sapie	5.5
	405138	A18/400074	Un OTODAO	predicted exon	5.5 5.5
	442238 416852	AW135374 AF283776	Hs.270949 Hs.80285	ESTs Homo sapiens mRNA: cDNA DKFZp586C1723 (from clon	5.5
	448691	AA481119	Hs.283558	hypothetical protein PRO1855	5.5
65	452242	R50956	Hs.59503	*ESTs, Weakly similar to AF157318 1 AD-017 protein [H.s	5.5
	456994	AA383623	Hs.293616	ESTs	5.5
	440913	Al267491	Hs.160593	ESTs	5.5
	435380	AA679001	Hs.192221	ESTs	5.5
70	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain 12 (meltrin alph	5.5
70	414035	Y00630	Hs.75716	"serine (or cysteine) proteinase inhibitor, clade B (ovalbumi	5.4
	459084 405867	H01699	Hs.27289	CGI-125 protein predicted exon	5.4 5.4
	414093	BE544867		"gb:601078872F1 NIH_MGC_12 Homo saplens cDNA clon	5.4
	447306	Al373163	Hs.170333	ESTs	5.4
75	413083	BE064528		gb:RC4-BT0311-250200-014-h06 BT0311 Homo sapiens	5.4
_	404828			predicted exon	5.4
	402543			predicted exon	5.4
	421988	AW450481	Hs.161333	ESTs	5.4
80	413404	BE503463	Hs.297431	ESTS	5.4
00	459043 404410	Al806444	Hs.208113	"ESTs, Weakly similar to N-WASP [H.sapiens]" predicted exon	5.4 5.4
	430264	AA470519		"gb:nc71f10.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clon	5.4
	431499	NM_001514	Hs.258561	general transcription factor IIB	5.4
	412566	AW962574		gh:EST374647 MAGE resequences, MAGG Homo sapien	5.4
				07	

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				-m.	
	454239	BE176420	Hs.8177	ESTS	5.4 5.4
	458163	AA884304	Hs.131163	ESTS	5.4
	446205	AW172662	Hs.149479	ESTs *gb:EST389810 MAGE resequences, MAGO Homo sapien	5.4
5	455275	AW977806	U- 2220E0	ESTs	5.4
5	415579 423200	AA165232 AA323073	Hs.222069 Hs.289083	ESTs	5.4
	440052	AI633744	Hs.195648	ESTs	5.4
	424717	H03754	Hs.152213	"wingless-type MMTV integration site family, member 5A"	5.4
	420111	AA255652		gb:zs21h11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA do	5.4
10	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	5.4
	414904	AA157881	Hs.143056	ESTs	5.4
	409479	BE163800	Hs.136912	ESTs	5.4
	404727			predicted exon	5.4
	446011	AI623778	Hs.145809	ESTs	5.4
15 -	456083	U46922	Hs.77252	fragile histidine triad gene	5.4
	424834	AK001432	Hs.153408	*Homo sapiens cDNA FLJ10570 fis, clone NT2RP2003117	5.4
	425071	NM_013989	Hs.154424	"deiodinase, iodothyronine, type II"	5.4
	426065	N32049		gb:yw96g08.s1 Soares_placenta_8to9weeks_2NbHP8to9W	5.4
20	415602	F12920	Hs.165575	ESTs	5.4
20	432839	AA579465	Hs.287332	ESTs	5.4
	416879	H98899	Hs.42599	ESTS	5.4 5.4
	456088	BE177320	Hs.156148	"Homo sapiens cDNA: FLJ23082 fis, clone LNG06451"	5.4
	423175 424585	W27595 AA464840	Hs.18653	ESTs qb:zx43h11.r1 Soares_total_fetus_Nb2HF8_9w Homo sapie	5.3
25	452281	T93500	Hs.28792	"Homo sapiens cDNA FLJ11041 fis, clone PLACE1004405	5.3
23	424323	AA338791	Hs.146763	nascent-polypeptide-associated complex alpha polypeptide	5.3
	426701	AI968103	Hs.209461	"Homo sapiens cDNA FLJ12836 fis, clone NT2RP2003206	5.3
	447645	AW897321	Hs.159699	ESTs	5.3
	402974			predicted exon	5.3
30	436607	AW661783	Hs.211061	ESTs	5.3
	428873	AI701609	Hs.98908	ESTs	5.3
	405454			predicted exon	5.3
	431867	AA523660	Hs.191727	ESTs	5.3
25	442768	AL048534	Hs.48458	"ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	5.3
35	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40kD)	5.3
	435098	AF174394	Hs.177461	"Homo sapiens apoptolic-related protein PCAR mRNA, par	5.3
	421284	U62435	Hs.103128	"cholinergic receptor, nicotinic, alpha polypeptide 6"	5.3 5.3
	435711	AF226667	Hs.58553	CTP synthase II	5.3 5.3
40	405292 410123	T16981	Hs.21963	predicted exon ESTs	5.3
40	435435	T89473	Hs.192328	ESTs .	5.3
	417071	N58820	Hs.275133	ESTs	5.3
	438958	H50167	Hs.33113	ESTs	5.3
	457405	AA504860		gb:ab03a10.s1 Stratagene fetal retina 937202 Homo sapiens	5.3
45	413642	BE154837		gb:PM1-HT0345-121199-001-c08 HT0345 Homo sapiens	5.3
	433868	AA612960		gb:nq38g06.s1 NCI_CGAP_Co10 Homo saptens cDNA clo	5.3
	444461	R53734	Hs.25978	ESTs	5.3
	427088	AA398085	Hs.142390	ESTs	5.3
50	451307	AW293207	Hs.211516	ESTs	5.3
50	403831			predicted exon	5.3
	402892	41074000	11- 002004	predicted exon	5.3 5.3
	433420	Al674093 BE080469	Hs.293961	ESTs *gb:QV1-BT0630-280200-086-d06 BT0630 Homo sapiens	5.3
	455759 411379	AI816344	Hs.12554	"ESTs, Weakly similar to Nucleosome Assembly Protein 1-	5.3
55	428483	AI908539	Hs.184592	KIAA0344 gene product	5.3
55	429208	AA447990	Hs.190478	ESTs	5.3
	447572	AI631546	Hs.159732	ESTs	5.3
	434896	AW022054	Hs.136591	ESTs	5.3
	417616	R07728	Hs.268568	ESTs	5.3
60	411805	AW864183		gb:PM0-SN0014-260400-002-d02 SN0014 Homo sapiens	5.3
	419000	T79855	Hs.268592	ESTs	5.3
	413488	BE144017	Hs.184693	"transcription elongation factor B (SIII), polypeptide 1 (15k	5.3
	400975			predicted exon	5.3
65	407453	AJ132087		gb:Homo sapiens mRNA for axonemal dynein heavy chain (	5.3 5.3
03	430757	A1458623	11- 00075	"gb:tk04g09.x1 NCI_CGAP_Lu24 Homo saptens cDNA clo	5.3 5.2
	417793	AW405434	Hs.82575	small nuclear ribonucleoprotein polypeptide B"	5.2
	401877 457122	AB011094 Al026157	Hs.129892 Hs.33728	KIAA0522 protein "ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	5.2
	410706	AI732404	Hs.68846	ESTs	5.2
70	435807	A1033299	Hs.113614	ESTs	5.2
. •	428398	A1249368	Hs.98558	ESTs	5.2
	401088			predicted exon	5.2
	414501	N43991	Hs.171984	ESTs	5.2
75	419083	A1479560	Hs.98613	"Homo sapiens cDNA FLJ12292 fis, clone MAMMA10018	5.2
75	421107	AA283822	Hs.55606	"ESTs, Weakly similar to ZN91_HUMAN ZINC FINGER P	5.2
	411489	AW848346		gb:IL3-CT0214-150200-076-F03 CT0214 Homo sapiens c	5.2
	419249	X14767	Hs.89768	*gamma-aminobutyric acid (GABA) A receptor, beta 1*	5.2
	430082	AW514083	Hs.190135	ESTs	5.2 5.2
80	425698	NM_016112	Hs.159241	polycystic kidney disease 2-like 1	5.2
οU	451686 453867	AA059246 AI020383	Hs.110293	ESTs HSPC037 protein	5.2
	453867 419985	AI929383 H66373	Hs.108196 Hs.15973	"ESTs, Highly similar to bA393J16.3 [H.sapiens]"	5.2
	426650	AA382814	113.13313	gb:EST96097 Testis I Homo sapiens cDNA 5' end, mRNA	5.2
	424115	AA335497	Hs.293965		5.2

	405576			predicted exon	£ 2
	409584	AA076010		gb:zm89f12.s1 Stratagene ovarian cancer (937219) Homo sa	5.2 5.2
	454423	AW603985	Hs.179662	nucleosome assembly protein 1-like 1	5.2
_	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	5.2
5	439155	H81076	Hs.269001	ESTs	5.2
	432267	AK000872	Hs.274227	"Homo sapiens cDNA FLJ10010 fis, clone HEMBA100030	5.2
	459024	AA020799	Hs.179825	RAN binding protein 2-like 1	5.2
	404088			predicted exon predicted exon	5.2
10	403525 445882	A1948717	Hs.225155	"ESTs, Weakly similar to PSF_HUMAN PTB-ASSOCIATE	5.2 5.2
10	448257	AW772070	Hs.253146	ESTS	5.2
	410500	R09442	113,250140	gb:yf26c09.r1 Soares fetal liver spleen 1NFLS Homo sapien	5.2
	456084	AA155859	Hs.79708	ESTs	5.2
	410523	BE143839		*gb:MR0-HT0164-151299-012-d03 HT0164 Homo sapiens	5.2
15	434623	AB023163	Hs.4014	KIAA0946 protein; Huntingtin Interacting protein H	5.2
	454484	AW795196	Hs.215857	ring finger protein 14	5.2
	402131	41000400	11- 470445	predicted exon	5.2
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           459186
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           TABLE 1C:
            Pkey: Unique number corresponding to an Eos probeset
            Ref. Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of
 80
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human chromosome 22" Dunham, et al. (1999) Nature 402:489-495 Strand: Indicates DNA strand from which exons were predicted

Nt\_position: Indicates nucleotide positions of predicted exons

	Okau	Def	Chand	All pacition
	Pkey 400584	Ref 9887612	Strand Minus	NL position 18398-18573
	400593	9887642	Minus	25013-25127
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	400749	7331445	Minus	9162-9293
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1.5	400983	8081198	Plus	107903-108832
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	401260	8076883	Minus	86008-86355
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	402075 402131	8117407 7704961	Plus Minus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076 33114-33209,33496-33678
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                        4567182
                                     Plus
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           406592
70
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TABLE 2A lists about 187 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to be extracellular or cell-surface proteins. These were selected as for Table 1A, except that the ratio was greater than or equal to 2.5, and the predicted protein contained a PFAM domain that is indicative of extracellular localization (e.g., ig, fn3, egf, 7tm domains).

TABLE 2A: ABOUT 187 UP-REGULATED OVARIAN CANCER GENES ENCODING EXTRACELLULAR/CELL SURFACE PROTEINS Pkey: Primekey

Ex. Accn: Exemplar Accession UG ID: UniGene ID

Title: Unigene Title
PFAM domains
ratio: turnor vs. normal tissues

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	Pkey	Ex. Acon No.	UGID	Title	PFAM domain	ratio
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	serpin	63.6
•	431938 425650	AA938471 NM_001944	Hs.115242 Hs.1925	developmentally regulated GTP-bindi desmoglein 3 (pemphigus vulgaris ant	SCP cadherin	32.0 30.0
5	423030 418994	AA296520	Hs.89546	selectin E (endothelial adhesion molec	EGF;lectin_c;sushi	24.5
	452947	AW130413	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	gb:xf50f04.x1 NCI_CGAP_Gas4 Horn	alpha-amylase	15.8
	418092	R45154	Hs.106504	ESTs	pkinase;Activin_recp	15.1
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	Cys_knot	12.6 12.5
10	422330 446745	D30783 AW118189	Hs.115263 Hs.156400	epiregulin ESTs	EGF wra	11.1
10	416319	AI815601	Hs.79197	CD83 antigen (activated B lymphocyt	ka	10.8
	432408	N39127	Hs.76391	myxovirus (influenza) resistance 1, ho	ion_trans;K_tetra	10.6
	405285			predicted exon	AZMAZM_N	10.5
15	405636 403093			predicted exon predicted exon	EGF;ldi_recept_a;ldi_recept_b fn3	9.8 9.6
13	446740	AI611635	Hs.192605	ESTs	RYDR_ITPR	9.2
	405547			predicted exon	ABC_tran;ABC_membrane	8.5
	412333	AW937485		gb:QV3-DT0044-221299-045-b09 DT	7tm_1	8.4
20	404270			predicted exon	SCP	8.1 8.1
20	402745 452755	AW138937	Hs.213436	predicted exon ESTs	EGF;ldi_recept_b;thyroglobufin_1 cystafin	8.0
	421459	AI821539	Hs.97249	ESTs	disintegrin;Reprotysin	7.9
	416151	T26661		gb:AB65C7R Infant brain, LLNL arra	laminin_G;EGF	7.8
25	446232	AI281848	Hs.165547	ESTs	7tm_3	7.6
23	431009 424634	BE149762 NM_003613	Hs.248213 Hs.151407	gap junction protein, beta 6 (connexin cartilage intermediate layer protein, n	connexin ig;tsp_1	7.2 7.1
	400749	000010	110.101701	predicted exon	fn3;kdl_recept_a;kdl_recept_b	6.8
	419054	N40340	Hs.191510	ESTs, Weakly similar to ORF2 [M.m	ig;SPRY	6.8
30	459170	A1905518		gb:RC-BT091-210199-098 BT091 Ho	ABC_tran;ABC_membrane	6.6
30	416441 410664	BE407197 NM_006033	Hs.65370	gb:601301552F1 NIH_MGC_21 Hom lipase, endothelial	SDF Ribosomal_L22	6.4 6.4
	402425	*****	110.00070	predicted exon	ion_trans	6.3
	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_H	Ephrin	6.0
35	403083	11040070	11- 5000	predicted exon	fn3	5.9
33	448995 418345	AJ613276 AJ001696	Hs.5662 Hs.241407	guanine nucleofide binding protein (G serine (or cysteine) proteinase inhibito	SOF serpin	5.9 5.8
	424966	AU077312	Hs.153985	solute carrier family 7 (cationic amino	aa_permeases	5.8
	431211	M86849	Hs.5566	gap junction protein, beta 2, 26kD (co	connexin	5.7
40	430563	AA481269	Hs.178381	ESTs	ABC_tran;ABC_membrane	5.6
40	450152 418844	Al138635 M62982	Hs.22968 Hs.1200	ESTs arachidonate 12-lipoxygenase	ig;pkinase lipoxygenase;PLAT	5.6 5.6
	403089	WALOUL	1.0.1.200	predicted exon	fn3	5.6
	403687			predicted exon	tsp_1;Reprolysin	5.6
45	403891 414035	Y00630	Hs.75716	predicted exon serine (or cysteine) proteinase inhibito	tsp_1;Reprolysin serpin	5.5 5.4
73	421284	U62435	Hs.103128	cholinergic receptor, nicotinic, atpha p	neur_chan	5.3
	435435	T89473	Hs.192328	ESTs	lipase;PLAT	5.3
	457122	AI026157	Hs.33728	ESTs, Weakly similar to ALU1_HUM	lipoxygenase;PLAT	5.2
50	419249 425698	X14767 NM_016112	Hs.89768 Hs.159241	gamma-aminobutyric acid (GABA) A polycystic kidney disease 2-like 1	neur_chan ion_trans	5.2 5.2
50	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	EGF;DSL	5.1
	457948	A1498640	Hs.159354	ESTs	G-alpha;arf	5.1
	435174	AA687378	Hs.194624	ESTs	SPRY	5.0
55	408170 434351	AW204516 AW974991	Hs.31835 Hs.191852	ESTs ESTs, Weakly similar to ALU1_HUM	arfiras arfiras	5.0 4.9
55	430708	U78308	Hs.278485	olfactory receptor, family 1, subfamily	7tm_1	4.8
	422597	BE245909	Hs.118634	ATP-binding cassette, sub-family B (M	ABC_tran;ABC_membrane .	4.8
	405545		11- 470000	predicted exon	ABC_tran;ABC_membrane	4.8
60	426471 409632	M22440 W74001	Hs.170009 Hs.55279	transforming growth factor, alpha serine (or cysteine) proteinase inhibito	EGF sempin	4.7 4.7
00	420206	M91463	Hs.95958	solute carrier family 2 (facilitated gluc	sugar_tr	4.6
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2	Kunitz_BPTI;G-gamma	4.6
	424402	M63108	Hs.1769	luteinizing hormone/choriogonadotrop	7tm_1	4.5 4.5
65	436480 430226	AJ271643 BE245562	Hs.87469 Hs.2551	putative acid-sensing ion channel adrenergic, beta-2-, receptor, surface	ASC 7tm_ <b>1</b>	4.5 4.4
05	436126	AW449757	Hs.163036	ESTs	SNF	4.4
	406812	AF000575	Hs.67846	teukocyte immunoglobulin-like recep	ig	4.4
	409385	AA071267	11- 400404	gb:zm61g01_r1 Stratagene fibroblast (	TIMP	4.3
70	449184 410555	AW296295 U92649	Hs.196491 Hs.64311	ESTs a disintegrin and metalloproteinase do	TNFR_c6 disintegrin;Reprotysin	4.3 4.3
, 0	422389	AF240635	Hs.115897	protocadherin 12	cadherin	4.3
	405281			predicted exon	A2M;A2M_N	4.3
	413548	BE147555	Hs.288541	Homo sapiens mRNA for KIAA1558	EGF;tdi_recept_a;tdl_recept_b	4.3
75	449535 425864	W15267 U56420	Hs.23672 Hs.159903	low density lipoprotein receptor-relate offactory receptor, family 5, subfamily	ldl_recept_a;EGF;ldl_recept_b 7tm_1	4.3 4.3
	410611	AW954134	Hs.20924	KIAA1628 protein	Peptidase_S9	4.2
	430686	NM_001942	Hs.2633	desmoglein 1	cadherin;Cadherin_C_term	4.1
	418693	AI750878	Hs.87409	thrombospondin 1	vwc,TSPN	4.0
80	445924 457148	AI264671 AF091035	Hs.164166 Hs.184627	ESTs KIAA0118 protein	sugar_tr artras	3.9 3.9
-	428568	AC004755	Hs.184922	one cut domain, family member 3	E1-E2_ATPase	3.9
	412170	D16532	Hs.73729	very low density lipoprotein receptor	EGF;tdl_recept_a;tdl_recept_b	3.8
	442566	R37337	Hs.12111	ESTs .	ank;death;RHD;TIG	3.8 3.8
	403763			predicted exon	7tm_1	3.0

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	402074			predicted exon		£2	3.8
	403074 413605	BE152644		gb:CM1-HT0329-250200-128-f09 HT		fn3 alpha-amylase	3.8
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, c		Collagen; COLFI	3.7
_	403661			predicted exon		7tm_3;ANF_receptor	3.7
5	407305	AA715284		gb:nv35f03.r1 NCI_CGAP_Br5 Hom		pkinase;Sema;Plexin_repeat;TIG	3.7
	457353	X65633	Hs.248144	melanocortin 2 receptor (adrenocortic		7tm_1	3.7
	431176	AI026984	Hs.293662	ESTs ESTs		laminin_EGF;laminin_B	3.6 3.6
	436233 431808	A1742878 M30703	Hs.124116 Hs.270833	amphiregulin (schwannoma-derived g		ig EGF	3.6
10	445798	NM_012421	Hs.13321	rearranged L-myc fusion sequence		zf-C2H2	3.6
10	400380	NM_018485	Hs.283079	G protein-coupled receptor C5L2		7tm_1	3.6
	453893	NM_000835	Hs.36451	glutamate receptor, ionotropic, N-met		lig chan	3.5
	409402	AF208234	Hs.695	cystatin B (stefin B)		cystatin	3.5
	421166	AA305407	Hs.102308	potassium inwardly-rectifying channe		IRK	3.5
15	445575	Z25368	Hs.172004	filin		fn3	3.5
	428957	NM_003881	Hs.194679	WNT1 inducible signaling pathway p		tsp_1;vwc;IGFBP	3.5 3.5
	403909 403077	NM_016255	Hs.95260	Homo sapiens mRNA; cDNA OKFZp predicted exon		Na_H_Exchanger fn3	3.5
	455612	BE042896	Hs.274848	ESTs .		ABC_tran;ABC_membrane	3.5
20	424091	AF235097	Hs.139263	calcium channel, voltage-dependent, a		ion_trans	3.5
	403956	W28077	Hs.79389	net (chicken)-like 2		cadherin;Cadherin_C_term	3.4
	457470	AB040973	Hs.272385	G protein-coupled receptor 72		7tm_1	3.4
	401522	N47812	Hs.81360	CGI-35 protein .		disintegrin;Reprolysin	3.4
25	404886	44470000	11. 470004	predicted exon		ion_trans	3.4
25	437692	AA176959	Hs.172004	desmocollin 2		fn3 cadherin	3.4 3.4
	407944 407393	R34008 AB038237	Hs.239727	gb:Homo sapiens mRNA for G protei		7tm 1	3.3
	436936	AL134451	Hs.197478	ESTs		EGF;laminin_G	3.3
	423309	BE006775	Hs.126782	sushi-repeat protein		sushi;HYR	3.3
30	402172	5-25551.75		predicted exon		ig	3.3
	447420	A1378628		gb:tc72g07.x1 Soares_NhHMPu_S1 H ·		ank;pkinase;death	3.3
	438901	AF085834	Hs.29036	ESTs		sushi	3.3
	424362	AL137646	Hs.146001	Homo sapiens mRNA; cDNA DKFZp		trypsin;sushi;CUB	3.3
35	430453	BE387060	Hs.3903	Cdc42 effector protein 4; binder of Rh		fn3 ldl_recept_a;MACPF	3.3 3.3
22	416631 453174	H69466 Al633529	Hs.135238	gb:yr88f07.r1 Soares fetal liver spleen ESTs		7tm_1	3.3
	433848	AF095719	Hs.93764	carboxypeptidase A3		Zr_carbOpept;Propep_M14	3.2
	408546	W49512	Hs.46348	bradykinin receptor B1		7tm_1 .	3.2
	423573	AA328504		gb:EST31993 Embryo, 12 week I Hom		7tm_1 '	3.2
40	458662	AI823410	Hs.169149	karyopherin alpha 1 (importin alpha 5		7tm_3;ANF_receptor	3.2
	433430	AI863735	Hs.186755	ESTs		thyroglobulin_1;IGFBP	3.2
	438850	R33727	Hs.24688	EST		ank;pkinase;death	3.2
	420783	A1659838	Hs.99923	lectin, galactoside-binding, solutile, 7		Gal-bind_lectin	3.2 3.1
45.	409958 430630	U56102 AW269920	Hs.57699 Hs.2621	adhesion glycoprotein cystatin A (stefin A)		ig 7tm_3;ANF_receptor	3.1
73	420737	L08096	Hs.99899	tumor necrosis factor (ligand) superfa		TNF	3.1
	422279	H69644	Hs.114231	C-type lectin-like receptor-2		lectin_c	3.1
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromely		hemopexin;Peptidase_M10	3.1
	412597	AU077051	Hs.74561	alpha-2-macroglobulin		A2M;A2M_N	3.1
50	453420	AJ003459		gb:AJ003459 Selected chromosome 2		IRK	3.1
	404243			predicted exon		zf-C3HC4;SPRY;zf-B_box	3.1
	449987	AW079749	Hs.184719	ESTs, Weakly similar to AF116721 1		ABC_tran;ABC_membrane	3.1 3.0
	422471 400464	AA311027	Hs.271894	ESTs predicted exon		ig Peptidase_S9	3.0
55	458713	BE044496	Hs.282707	ESTs		EGF	3.0
55	421340	F07783	Hs.1369	decay accelerating factor for comptem		sushi	3.0
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5		7tm_1	3.0
	400704			predicted exon		lig_chan;ANF_receptor	3.0
<b>60</b>	416239	AL038450	Hs.48948	ESTs		E1-E2_ATPase;Hydrolase	3.0
60	433664	AW292176	Hs.245834			Ricin_B_lectin	3.0
	423994	X01057	Hs.1724	interleukin 2 receptor, alpha		rm	29 29
	447726	AL137638	Hs.19368	Homo sapiens mRNA; cDNA DKFZp Homo sapiens protocadherin Fat 2 (FA		vwa EGF;cadherin;laminin_G	29
	425483 423513	AF231022 AF035960	Hs.301273 Hs.129719	transglutaminase 5		Transglut_core;Transglutamin_N	2.9
65	401537	74 000000	110.120110	predicted exon		ig;pkinase;LRRNT;LRRCT	2.9
	405790			predicted exon		Sema:Plexin_repeat;TIG	2.9
	422669	H12402	Hs.119122	ribosomal protein L13a		arf;ras;Ribosomal_S17	2.9
	430793	M83181	Hs.247940	5-hydroxytryptamine (serotonin) recep		7tm_1	2.9
70	403411			predicted exon		ABC_tran;ABC_membrane	2.8
70	428188	M98447	Hs.22	transglutaminase 1 (K polypeptide ep		Transglutamin_N;Transglut_core	2.8 2.8
	414482 427223	S57498 BE208189	Hs.76252 Hs.174031	endothelin receptor type A cytochrome c oxidase subunit VIb		7tm_1 COX68	2.8
	404187	DE200109	TIS.174031	predicted exon		ig	2.8
	443537	D13305	Hs.203	chalecystokinin B receptor		7tm_1	2.8
75	428701	NM_013276	Hs.190207	carbohydrate kinase-like		vwa;integrin_A;P2X_receptor	2.7
	411213	AA676939	Hs.69285	neuropilin 1		CUB;MAM;F5_F8_type_C	2.7
	453999	BE328153	Hs.240087	ESTs		kazal	2.7
	401244			predicted exon		waywd;TIL	2.7
90	458930	NM_003612	Hs.24640	sema domain, immunoglobulin domai		Sema	2.7
80	434411	AA632649	Hs.201372			sushi FGF	2.7 2.7
	400421	AF263537	Hs.287370 Hs.22791	fibroblast growth factor 23 transmembrane protein with EGF-like		kazal	2.7
	448999 417350	AF179274 U50928	Hs.82001	polycystic kidney disease 2 (autosoma		ion_trans	2.6
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7		pkinasetig	2.6
				-	106		
					106		

```
401657
                                                   predicted exon
                                                                                                   7tm_1
                                                                                                                                         2.6
                                                                                                   sushi;trypsin;CUB
          456711
432042
                                     Hs 83938
                       AA033699
                                                  ESTs, Moderately similar to MASP-2
                                                                                                                                         Hs 292715
                       AW971345
                                                  ESTs
                                                                                                   sugar_tr
          433138
                                     Hs.59729
                       AB029496
                                                  semaphorin sem2
                                                                                                   io:Sema
  5
                                                                                                   ABC_tran;ABC_membrane
          452530
                       Al905518
                                                  gb:RC-BT091-210199-098 BT091 Ho
          426418
                                     Hs.169825
                                                  collagen, type IV, alpha 5 (Alport syn
                                                                                                   Collagen;C4
                       M90464
                                                  predicted exon
          403796
                                                                                                   cadherin
                                     Hs.268107
                       NM_007351
AW206035
          431728
                                                  multimerin
                                                                                                   EGF;C1q
                                     Hs.192123
          441595
                                                  ESTs
                                                                                                  sugar_tr
EGF;MAM
10
                                                  EGF-like-domain, multiple 6
                       AJ245671
          445537
                                     Hs.12844
          447197
                                                  gb:yh88b01.s1 Soares placenta Nb2H
                                                                                                   SDF
                       R36075
          428765
                       X54150
                                     Hs.193122
                                                  Fc fragment of IgA, receptor for
                                                                                                   ìg
                                                  ESTs, Moderately similar to ALU1_H
                                     Hs.271767
          450245
                       AA007536
                       H5465B
                                     Hs.268942
                                                                                                   E1-E2_ATPase;Hydrolase
          416429
                                                  ESTs
15
                       AJ001417
          417067
                                     Hs.81086
                                                  solute carrier family 22 (extraneurona
                                                                                                  sugar_tr
                       AB039920
                                     Hs.127821
                                                  BWRT protein
                                                                                                   ion_trans
          433182
          403092
                                                  predicted exon
                                                                                                  fn3
                                                                                                  vwc;Collagen;COLFI
          406850
                       AI624300
                                     Hs.172928
                                                  collagen, type I, alpha 1
          ASSESS
                                     Hs.125815
                                                                                                   lipoxygenase;PLAT
                       AW297855
                                                  FSTs
20
                                                  potassium inwardly-rectifying channe
                       NM_013348
                                     Hs.144011
                                                                                                   irk
          456815
          TABLE 2B:
          Pkey: Unique Eos probeset identifier number
          CAT number: Gene cluster number
25
          Accession: Genbank accession numbers
          Pkey
                     CAT Number
          409385
                     112523_1
                                      AA071267 T65940 T64515 AA071334
                                     AW937485 AW937589 AW937658 AW937654 AW937492
BE152644 BE152712 BE152668 BE152659 BE152810 BE152811 BE152816 BE152643 BE152706 BE152656 BE152660 BE152715 BE152662
          412333
                     1289037_1
30
          413605
                     1379792 1
                                     BE152669 BE152661 BE152672 BE152653 BE152716 BE152651 BE152767 BE152677 BE152652 BE152714 BE152708 BE152665 BE152679
                                     BE152771 BE152775 BE152666 BE152768 BE152813 BE152664 BE152676 BE152681 BE152709 BE152667 BE152814 BE152808 BE152711
                                      BE152707 BE152815 BE152678 BE152673 BE152782 BE152671 BE152682 BE152760 BE152769 BE152778 BE152780 BE152762 BE152762
                                     BE152781 BE152774 BE152763 BE152769
35
                                     T26661 Z44135 H23016
BE407197 AA182474 AA180369 BE275628 BE276131
          416151
                     1573926_1
                     159480_1
1605019_1
          416441
          416631
                                      H69466 H93884 N59684
                     229714_1
                                      AA328504 AA327783 AW962370
          423573
          447197
                     711623_1
                                      R35075 Al366546 R36167
40
                                     Al378628 N32350 H85772
Al905518 Al905516 Al905457 Al905515 AW176013 AW176037
          447420
                     721207_1
                     920646 1
          452530
          452947
                     939810_1
                                      AW130413 Al932362
          453420
                     966433_1
          459170
                     920646_1
                                      Al905518 Al905516 Al905457 Al905515 AW176013 AW176037
45
          TABLE 2C:
          Pkey: Unique number corresponding to an Eos probeset
          Ref. Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of
                 human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
50
          Strand: Indicates DNA strand from which exons were predicted
          Nt_position: Indicates nucleofide positions of predicted exons
          Pkey
                                    Strand
                                                Nt_position
           400464
                       9929570
                                                22074-22214
55
           400704
                       8118864
                                    Minus
                                                63110-63241
          400749
                       7331445
                                    Minus
                                                9162-9293
                                                55359-56376
          401244
                       4827300
                                    Minus
                                                186786-187029,190607-190779,198218-198348
          401537
                       7960358
                                    Minus
           401657
                       9100664
                                     Minus
                                                7312-8163
60
           402172
                       8575911
                                     Minus
                                                143378-143671
                                                50224-50395
76516-76690
           402425
                       9796347
                                    Minus
           402745
                       9212200
                                    Minus
                                                143375-143561
           403074
                       8954241
                                     Plus
                       8954241
                                                146923-147222,147326-147628
           403077
                                    Plus
65
           403083
                        8954241
                                     Plus
                                                163070-163351
           403089
                        8954241
                                     Plus
                                                171964-172239
                                                174720-175016,175104-175406,175508-175813
177083-177373,177464-177751
           403092
                        8954241
                                     Plus
                        8954241
           403093
                                     Plus
                        9438635
                                                104247-104420
           403411
                                     Minus
 70
           403661
                                                30268-30482
                        8705027
                                     Minus
           403687
                        7387384
                                     Plus
                                                9009-9534
                                                88280-88463
           403691
                        7387384
                                     Minus
                                                43575-43887
           403763
                                     Minus
                        7229888
                                                75073-77664
           403796
                        8099896
                                     Minus
 75
           404187
                        4481839
                                     Plus
           404243
                        5672609
                                     Plus
                                                74695-75123
                                                3649-3750,4161-4306,5962-6049,6849-6965
                        9828129
                                     Minus
                                                30058-30596
           404886
                        4884062
                                     Plus
                                                34202-34351,35194-35336,45412-45475,45731-45958,47296-47457,49549-49658,49790-49904,50231-50342,53583-53667,54111-
            405281
                        6139075
                                     Minus
 80
                                                55744-55903,57080-57170,61478-61560
118677-118807,119091-119296,121626-121823
124361-124520,124914-125050
           405285
                        6139075
                                     Minus
           405545
                        1054740
                                     Ptus
           405547
                        1054740
                                     Phis
                                                56384-56587
           405636
                        5123990
                                     Plus
```

136364-136509,136579-136699,136805-136941 405790 1203968 Plus

TABLE 3A lists about 1643 genes up-regulated in ovarian cancer compared to normal ovaries. These were selected as for Table 1A, except that the ratio was greater than or equal to 15, and the denominator was the arithmetic mean value for various non-malignant ovary specimens obtained. 5

TABLE 3A: ABOUT 1643 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY Pkey: Primakey
Ex. Accr.: Exemplar Accession
UG ID: UniGene ID
Title: Unigene Title
PFAM domains

10

ratio: tumor vs. normal tissues

	1900: (0)	IOI VS. IIUIIII IIS	2062		
15	Pkey	Ex. Acon No.	UG ID	Title	ratio
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgranulin A)	219.9
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgranulin B)	180.2
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKALP)	165.0
	424799	BE550723	Hs.153179	fatty acid binding protein 5 (psoriasis-associated)	161.5
20	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	150.2
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human, odontogenic k	149.5
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (antileukoprotein	144.9
	430520	NM_016190	Hs.242057	chromosome 1 open reading frame 10	. 136.6 129.5
25	428471 421978	X57348 AJ243662	Hs.184510 Hs.110196	stratifin . NICE-1 protein	108.7
23	437191	NM_006846	Hs.5476	serine protease inhibitor, Kazal type, 5	106.2
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	105.5
	441565	AW953575	Hs.169902	solute carrier family 2 (facilitated glucose transporter),	103.6
	431211	M86849	Hs.5566	gap junction protein, beta 2, 25kD (connexin 26)	102.1
30	419329	AY007220	Hs.288998	S100-type calcium binding protein A14	95.3
	430572	U33114	Hs.245188	tissue inhibitor of metalloproleinase 3 (Sorsby fundus d	87.0
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	86.1
	412636	NM_004415	Hs.74316	desmoptakin (DPI, DPII)	85.0
26	417515	L24203	Hs.82237	ataxia-lelangiectasia group D-associated protein	84.8
35	426295	AW367283	Hs.75839	zinc finger protein 6 (CMPX1)	84.5
	452669	AA216363	Hs.262958	ESTs, Wealty similar to alternatively spliced product u	84.4
	406711	N25514	Hs.77385	myosin, light polypeptide 6, alkali, smooth muscle and n	83.8 81.0
	406712 432680	M31212	Hs.77385	myosin, light polypeptide 6, alkali, smooth muscle and n	81.0
40	416889	T47364 AW250318	Hs.278613 Hs.80395	interferon, alpha-inducible protein 27 mal, T-cell differentiation protein	77.8
40	409453	AI885516	Hs.95612	ESTs	75.3
	424670	W61215	Hs.116651	epithelial V-like antigen 1	67.5
	417130	AW276858	Hs.81256	S100 calcium-binding protein A4 (calcium protein, catv	67.0
	423634	AW959908	Hs.1690	heparin-binding growth factor binding protein	65.7
45	442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, protein-glutamine-g	64.7
	456898	NM_001928	Hs.155597	D component of complement (adipsin)	64.6
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor, clade B (ovalbu	63.6
	447990	BE048821	Hs.20144	small inducible cytokine subfamily A (Cys-Cys), memb	60.7
50	424362	AL137646	Hs.146001	Homo sapiens mRNA; cDNA DKFZp586F0824 (from	60.3
50	414438	A1879277	Hs.76136	thioredoxin	59.9 58.9
	420136 433336	AW801090 AF017986	Hs.195851 Hs.31386	actin, alpha 2, smooth muscle, aorta ESTs, Highly similar to JE0174 frizzled protein-2 [H.sa	58.8
	403741	AP-017-500	16.31000	predicted exon	57.0
	430637	BE160081	Hs.256290	S100 calcium-binding protein A11 (calgizzarin)	56.1
55	424098	AF077374	Hs.139322	small proline-rich protein 3	55.8
	441591	AF055992	Hs.183	Duffy blood group	55.6
	426521	AF161445	· Hs.170219	hypothetical protein	55.5
	406713	U02629	Hs.77385	myosin, light polypeptide 6, alkali, smooth muscle and n	55.3
<b>C</b> O	406725	D51245	Hs.288061	actin, beta	54.1
60	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psoriasin 1)	54.1
	406755	N80129	Hs.94360	metallothionein 1L	54.0
	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	53.3 53.1
	442257 421957	AW503831 AW068637	Hs.109857	gb:UI-HF-BN0-alb-b-05-0-UI.r1 NIH_MGC_50 Homo hypothetical protein DKFZp434H0820	52.3
65	447526	AL048753	Hs.340	small inducible cytokine A2 (monocyte chemotactic pro	51.2
05	406722	H27498	Hs.283305	Homo sepiens SNC73 protein (SNC73) mRNA, comple	51.0
	427223	BE208189	Hs.174031	cytochrome c oxidase subunit VIb	51.0
	414420	AA043424	Hs.76095	immediate early response 3	50.9
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (versican)	50.3
70	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	49.5
	436906	H95990	Hs.181244	major histocompatibility complex, class I, A	49.0
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	49.0
	414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibitor, clade B (ovalbu	48.8
75	432706	NM_013230	Hs.286124	CD24 antigen (small cell lung carcinoma cluster 4 antig	48.8
13	421948		Hs.111758	keratin 6A	48.7 48.5
	414662		Hs.76807 Hs.154424	major histocompatibility complex, class II, DR alpha deiodinase, iodothyronine, type II	48.5
	425071 404767	NM_013989	rts. 104424	predicted exon	48.4
	418327	U70370	Hs.84136	paired-like homeodomain transcription factor 1	48.2
80	436729	BE621807	Hs.3337	transmembrane 4 superfamily member 1	47.7
	414183		Hs.301711	ESTs	47.2
	400163			predicted exon	47.0
	433423	BE407127	Hs.8997	heat shock 70kD protein 1A	46.9
	423457		Hs.155606	paired mesoderm homeo box 1	46.6
				100	

	414085	AA114016	Hs.75746	aldehyde dehydrogenase 6	46.0
	423189	M59371	Hs.171596	EphA2	45.6
	438240	N92638	Hs.124004	ESTs	45.5
					45.3
5	417366	BE185289	Hs.1076	small proline-rich protein 1B (comifin)	
)	412774	AA120865	Hs.23136	ESTs	45.1
	407242	M18728		gb:Human nonspecific crossreacting antigen mRNA, co	44.8
	431292	AA370141	Hs.251453	Human DNA sequence from clone 967N21 on chromos	44.8
	403595			predicted exon	43.5
	417365	D50683	Hs.82028	transforming growth factor, beta receptor (I (70-80kD)	43.4
10					
10	432331	W37862	Hs.274368	Homo sapiens mRNA; cDNA DKFZp586i1524 (from c	43.4
	424479	AF064238	Hs.149098	smoothelin	43.3
	444726	NM_006147	Hs.11801	interferon regulatory factor 6	43.2
	432314	AA533447	Hs.285173	ESTs	43.2
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	43.1
15					
15	441406	Z45957	Hs.7837	Homo sapiens cDNA FLJ10457 fis, clone NT2RP1001	42.7
	412969	AJ373162	Hs.75103	tyrosine 3-monooxygenase/tryptophan 5-monooxygenas	42.6
	423720	AL044191	Hs.23388	Homo sapiens cDNA: FLJ21310 fis, clone COL02160	42.5
	400111			predicted exon	42.4
	407207	TORCE1	Hs.179661		42.4
20		T03651		tubulin, beta polypeptide	
20	417164	AA338283	Hs.81361	heterogeneous nuclear ribonucleoprotein A/B	42.2
	424971	AA479005	Hs.154036	turnor suppressing subtransferable candidate 3	41.9
	439394	AA149250	Hs.56105	ESTs, Weakly similar to WDNM RAT WDNM1 PROT	41.9
	406657	Al678644	Hs.277477	major histocompatibility complex, class I, C	41.8
					41.6
25	451092	AI207256	Hs.13766	Homo sapiens mRNA for FLJ00074 protein, partial cds	
25	412596	AA161219	Hs.799	diphtheria toxin receptor (heparin-binding epidermal gro	41.6
	422103	AA984330	Hs.111676	protein kinase H11; small stress protein-like protein HS	41.5
	428785	Al015953	Hs.125265	ESTs	41.3
	450988	BE618571	Hs.429	ATP synthase, H+ transporting, mitochondrial F0 comp	41.0
	414622	AI752666	Hs.76669		40.8
20		A1732000	ns./0009	nicotinamide N-methyltransferase	
30	405022			predicted exon	40.8
	408221	AA912183	Hs.47447	ESTs	40.8
	446500	U78093	Hs.15154	sushi-repeat-containing protein, X chromosome	40.7
	421416	BE302950	Hs.104125	adenylyl cyclase-essociated protein	40.6
	412247	AF022375	Hs.73793		40.5
25				vascular endothelial growth factor	
35	410541	AA065003	Hs.64179	hypothetical protein	40.5
	406658	Al920965	Hs.77961	major histocompatibility complex, class I, B	40.0
	420225	AW243046	Hs.94789	ESTs	40.0
	406825	Al982529	Hs.84298	CD74 antigen (invariant polypeptide of major histocom	39.4
			Hs.9641		39.4
40	443623	AA345519		complement component 1, q subcomponent, alpha poly	
40	404201	AF059566	Hs.103983	solute carrier family 5 (sodium lodide symporter), mem	39.3
	40513B			predicted exon	39.1
	408733	AW264812	Hs.254290	ESTs	39.0
	414044	BE614194	Hs.75721	profilin 1	38.9
	430152	AB001325	Hs.234642	aquaporin 3	38.8
45					
43	428121	AB006622	Hs.182536	Homo sapiens cDNA: FLJ21370 fis, ctone COL03092	38.8
	434311	BE543469	Hs.266263	Homo sapiens cDNA FLJ14115 fis, clone MAMMA10	38.7
	406140			predicted exon	38.5
	432918	AF077200	Hs.279813	hypothetical protein	38.4
	420107	AL043980	Hs.7886	pellino (Drosophila) homolog 1	38.4
50					
50	427693	BE546832	Hs.180370	cofilin 1 (non-muscle)	38.1
	448835	BE277929	Hs.11081	ESTs, Weakly similar to S57447 HPBRII-7 protein (H.	38.1
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PLACE1010	37.9
	428383	BE616599	Hs.184029	hypothetical protein DKFZp761A052	37.7
	436258	AW867491	Hs.107125	ESTs, Weakly similar to S57447 HPBRII-7 protein (H.	37.7
55					
JJ	420798	W93774	Hs.99936	keratin 10 (epidermolytic hyperkeratosis; keratosis palm	37.7
	400327	M18679	Hs.247942	Human variant 5S rRNA-like gene and ORF, complete	37.6
	401781			predicted exon	37.6
	448257	AW772070	Hs.253146	ESTs	37.3
	428415	AA337211	Hs.184222	Down syndrome critical region gene 1	37.2
60			Hs. 198241		37.2
UU	424206	NM_003734 .		amine oxidase, copper containing 3 (vascular adhesion p	
	406812	AF000575	Hs.67846	leukocyte immunogłobulin-like receptor, subfamily 8 (	37.2
	425882	U83115	Hs.161002	absent in melanoma 1	37.2
	432501	BE546532	Hs.287329	Fas binding protein 1	37.1
	421786	Al188653	Hs.21351	ESTs	37.1
65					37.0
UJ	427981	BE275986	Hs.181311	asparaginyl-tRNA synthetase	
	410143	AA188169	Hs.288819	Homo sapiens cDNA: FLJ21022 fis, clone CAE06383	36.8
	451328	AW853606	Hs.109012	ESTs	36.7
	414135	NM_004419	Hs.2128	dual specificity phosphatase 5	36.7
	414602	AW630088		Homo sapiens mRNA; cDNA DKFZp564B1264 (from	36.7
70		***************************************	Hs.76550		
70	401785	T0000-		predicted exon	36.5
	411469	T09997	Hs.70327	cysteine-rich protein 2	36.2
	419693	AA133749	Hs.92323	FXYD domain-containing ion transport regulator 3	36.1
	417039	AA302180	Hs.80986	ATP synthase, H+ transporting, mitochondrial F0 comp	36.1
	406718	AA505525	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	36.0
75		.4503023	16.105110		
15	402543	******		predicted exon	36.0
	408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molecule (CD31 antig	35.9
	414987	AA524394	Hs.165544	ESTs	35.9
	445810	AW265700	Hs.155660	ESTs '	35.9
	406653	AA574074	Hs.77961	major histocompatibility complex, class I, B	35.7
80			10.11301		35.6
00	407498	U28131		gb:Human HMGI-C chimeric transcript mRNA, partial	
	412524	AA417813	Hs.11177	ESTs	35.5
	401521			predicted exon	35.4
	408948	AW296713	Hs.221441	ESTs	35.1
	405728		Hs.183704	ubiquitin C	34.9
	700120	, 20000	100104	and some a	0.4.0

	440669	Al206964		gb:qr30g06.x1 NCI_CGAP_GC6 Homo sapiens cDNA	34.8
	422658	AF231981	Hs.250175	homolog of yeast long chain polyunsaturated fatty acid	34.8
	452924	AW580939	Hs.97199	complement component C1q receptor	34.7
_	428600	AW863261	Hs.15036	ESTs, Highly similar to AF161358 1 HSPC095 [H.sapi	34.7
5	409828	AW501137		gb:UI-HF-BP0p-ail-e-12-0-Ul.r1 NIH_MGC_51 Homo	34.5
=	459390	BE385725		gb:601276347F1 NIH_MGC_20 Homo sapiens cDNA	34.5
	445055	BE512856	Hs.109051	glycoprolein, synaptic 2	34.3
	411789	AF245505	Hs.72157	Homo sapiens adlican mRNA, complete cds	34.3
			N3.72137		
10	410526	BE407727	11- 00040	gb:601299771F1 NIH_MGC_21 Homo sapiens cDNA	34.2
IU	410706	A1732404	Hs.68846	ESTs	34.2
	419273	BE271180	Hs.293490	ESTs	34.2
	407839	AA045144	Hs.161566	ESTs	34.0
	444286	A1625304	Hs.190312	ESTs	34.0
	449226	AB002365	Hs.23311	KIAA0367 protein	34.0
15	414290	Al568801	Hs.71721	ESTs	33.9
	401245			predicted exon	33.9
	425222	M85430	Hs.155191	vilin 2 (ezrin)	33.8
	409950	R42678	Hs.301669	KIAA0564 protein	33.8
	437201	F29279	Hs.177486		33.7
20				amyloid beta (A4) precursor protein (protease nexin-II,	
20	406566	AF088886	Hs.11590	cathepsin F	33.7
	405071			predicted exon	33.7
	455426	AW937792		gb:QV3-DT0045-140200-082-b07 DT0045 Homo sapi	33.6
	415160	T82802		gb:yd38a04.r1 Soares fetal liver spleen 1NFLS Homo s	33.5 ·
~ ~	424995	Z45023		gb:HSC2FA041 normalized infant brain cDNA Homo s	33.5
25	453870	AW385001	Hs.8042	Homo sapiens cDNA: FLJ23173 fis, clone LNG10019	33.5
	433470	AW960564	Hs.3337	transmembrane 4 superfamily member 1	33.4
	428188	M98447	Hs.22	transglutaminase 1 (K potypeptide epidermal type I, pro	33.3
	417409	BE272506	Hs.82109	syndecan 1	33.3
	425389	AW974499	Hs.192183	ESTs	33.3
30					
30	434658	A1624436	Hs.194488	ESTs	33.2
	456562	AA306049	Hs.102669	DKFZP434O125 protein	33.1
	447111	AI017574	Hs.17409	cysteine-rich protein 1 (Intestinal)	33.0
	432360	BE045243	Hs.274416	NADH dehydrogenase (ubiquinone) 1 alpha subcomple	32.9
~ ~	424125	M31669	Hs.1735	inhibin, beta B (activin AB beta polypeptide)	32.7
35	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	32.7
	429415	NM_002593	Hs.202097	procollagen C-endopeptidase enhancer	32.6
	451541	BE279383	Hs.26557	płakophilin 3	32.6
	424499	N90344	Hs.149435	kinesin family member 58	32.4
	402144			predicted exon	32.4
40	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	32.4
70	400231	10010442	115.1117500		32.3
		VALEDO	Un 00044	predicted exon	
	437712	X04588	Hs.85844	neurotrophic tyrosine kinase, receptor, type 1	32.3
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	32.2
4.0	419659	AB023206	Hs.92186	Leman coiled-coil protein	32.0
45	428582	BE336699	Hs.185055	BENE protein	32.0
	421401	AW410478	Hs.104019	transforming, acidic coiled-coil containing protein 3	. 32.0
	414064	BE245289	Hs.16165	expressed in activated T/LAK lymphocytes	32.0
	431938	AA938471	Hs.115242	developmentally regulated GTP-binding protein 1	32.0
	411930	F06485		gb:HSC19G051 normalized infant brain cDNA Homo s	31.9
50	428150	AW950547	Hs.182684	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)	31.8
-	401887	111100041	113.102007	predicted exon	31.8
	412570	AA033517	Hs.74047		31.7
				electron-transfer-flavoprotein, beta polypeptide	
	422738	X80915	Hs.1573	growth differentiation factor 5 (cartilage-derived morph	31.6
55	453092	X64838	Hs.31638	restin (Reed-Steinberg cell-expressed intermediate filam	31.5
55	413924	AL119964	Hs.75616	KIAA0018 gene product	31.4
	420231	R06866	Hs.19813	ESTs .	31.3
	434715	BE005346	Hs.116410	ESTs	31.3
	422831	R02504		gb:ye86f06.r1 Soares fetal liver spleen 1NFLS Homo sa	31.2
	416854	H40164 ·	Hs.80296	Purkinje cell protein 4	31.2
60	422976	AU076657	Hs.1600	sec61 homolog	31.1
	426356	BE536836		gb:601064837F1 NIH_MGC_10 Homo sapiens cDNA	31.0
	433935	AF112208	Hs.44163	13kDa differentiation-associated protein	30.8
	430040	AW503115	Hs.227823	pM5 protein	30.8
65	406340	AA299679	Hs.180370	cofflin 1 (non-muscle)	30.8
05	426050	AF017307	Hs.166096	E74-like factor 3 (ets domain transcription factor, epith	30.7
	425105	BE280066	Hs.24956	hypothetical protein FLJ22056	30.7
	402066			predicted exon	30.7
	429538	BE182592	Hs.139322	small proline-rich protein 3	30.6
~~	418371	M13560	Hs.84298	CD74 antigen (invariant polypeptide of major histocom	30.4
70	421251	Z28913	Hs.102948	enigma (LIM domain protein)	30.3
	456084	AA155859	Hs.79708	ESTs	30.3
	402023			predicted exon	30.3
	404356			predicted exon .	30.2
	415973	R24707	Hs.260201	ESTs .	30.2
75					
, ,	445983	AJ269107	Hs.132219	ESTs	30.1
	450440	AB024334	Hs.25001	tyrosine 3-monooxygenase/tryptophan 5-monooxygenas	30.1
	458789	AL157468	Hs.20157	Homo sapiens cDNA FLJ20848 fis, clone ADKA01732	30.1
	400842			predicted exon	30.1
00	406828	AA419202	Hs.84298	CD74 antigen (invariant polypeptide of major histocom	30.0
80	423267	AL137416	Hs.126177	Homo sapiens mRNA; cDNA DKFZp434O192 (from c	30.0
	451383	AW239364	Hs.20242	hypothetical protein FLJ12788	30.0
	437042	AK000702	Hs.5420	hypothetical protein FL120695	30.0
	459399	BE407712		gb:601299745F1 NIH_MGC_21 Homo sapiens cDNA	30.0
	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen)	30.0
		001077	10.132		

	416511	NM_006762	Hs.79356	Lysosomal-associated multispanning membrane protein	29.9
	431009	BE149762	Hs.248213	gap junction protein, beta 6 (connexin 30)	29.7
	436651	BE045962	Hs.275998	ESTs	29.6
_	419766	BE243101	Hs.22391	chromosome 20open reading frame 3	29.5
5	420747	BE294407	Hs.99910	phosphofructokinase, platelet	29.5
	436895	AF037335	Hs.5338	carbonic anhydrase XII	29.5
	412765	AK000620	Hs.74571	ADP-ribosylation factor 1	29.4
	419223	X60111	Hs.1244	CD9 artigen (p24)	29.4
10	413796	AW408094	Hs.75545	interleukin 4 receptor	29.4
10	447795	AW295151	Hs.163612	ESTs	29.4
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth factor 8, neurite g	29.4
	415314	N88802	Hs.5422	glycoprotein M6B	29.3
	428411	AW291464	Hs.10338	ESTs	29.3
1.5	430580	AA806105	Hs.140	immunoglobulin heavy constant gamma 3 (Gm marker)	29.3
15	430451	AA836472	Hs.249982	cathepsin B	29.2
	453949	AU077146	Hs.36927	heat shock 105kD	29.2
	413859	AW992356	. Hs.8364	pyruvale dehydrogenase kinase, isoenzyme 4	29.2
	407845	AL036518	Hs.118598	ESTs	29.1
20	453500	AI478427	Hs.43125	ESTs	29.1
20	456054	BE313241		gb:601151545F1 NIH_MGC_19 Homo sapiens cDNA	29.0
	453467	AI535997	Hs.30089	ESTs	29.0
	411794	AL118577	Hs.75658	phosphorylase, glycogen; brain	28.9
	421773	W69233	Hs.112457	ESTs	28.9
25	423621	BE002904		gb:QV4-BN0090-070400-163-c07 BN0090 Homo sapi	28.8
25	408935	BE539706	Hs.285363	ESTs	28.8
	450847	NM_003155	Hs.25590	stanniocalcin 1	28.8
	431243	U46455	Hs.252189	syndecan 4 (amphiglycan, ryudocan)	28.7
	423225	AA852604	Hs.125359	Thy-1 cell surface antigen	28.7
20	433469	F12741		gb:HSC3DG061 normalized infant brain cDNA Homo	28.7
30	405783			predicted exon	28.7
	417308	H60720	Hs.81892	KIAA0101 gene product	28.7
	400749			predicted exon	28.7
	413442	BE140643		gb:RC0-HT0015-310599-016 HT0015 Homo sapiens c	28.6
25	404828			predicted exon	28.6
35	407453	AJ132087		gb:Homo sapiens mRNA for axonemal dynein heavy ch	28.6
	418529	AW005695	Hs.250897	TRK-fused gene (NOTE: non-standard symbol and nam	28.6
	413787	Al352558	Hs.75544	tyrosine 3-monooxygenase/tryptophan 5-monooxygenas	28.5
	450690	AA296696	Hs.25334	FXYD domain-containing ion transport regulator 5	28.5
40	402430			predicted exon	28.4
40	413929	BE501689	Hs.75617	collagen, type IV, alpha 2	28.2
	423803	NM_005709	Hs.132945	PDZ-73 protein	28.2
	406086			predicted exon	28.2
	416585	X54162	Hs.79386	teiomodin 1 (smooth muscle)	28.2
45	417055	N39489	Hs.7258	Homo sapiens cDNA: FLJ22021 fis, done HEP08253	28.1
45	449184	AW296295	Hs.196491	ESTs	28.1
	446542	NM_004281	Hs.15259	BCL2-associated athanogene 3	28.1
	412793	AW997986		gb:RC1-BN0056-230200-021-e11 BN0056 Homo sapie	28.0
	452818	W21909	Hs.8372	ubiquinol-cytochrome c reductase (6.4kD) subunit	28.0
<b>5</b> 0	402869			predicted exon	27.9
50	436810	AA353044	Hs.5321	ARP3 (actin-related protein 3, yeast) homolog	27.9
	402075			predicted exon	27.9
	410480	R97457	Hs.63984	cadherin 13, H-cadherin (heart)	27.8
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell adhesion molecul	27.8
55	439766	AB033492	Hs.301241	Homo sapiens mRNA; cDNA DKFZp586A0424 (from	27.7
55	424482	BE268621	Hs.149155	voltage-dependent anion channel 1	27.6
	420737	F0803e	Hs.99899	tumor necrosis factor (ligand) superfamily, member 7	27.6
	414663	BE396326		gb:601289258F1 NIH_MGC_8 Homo sapiens cDNA c	27.6
	409703	NM_006187	Hs.56009	2-5'oligoadenylate synthetase 3	27.6
60	446108	AL036596	Hs.102773	ESTs	27.5
60	428144	BE269243	Hs.182625	VAMP (vesicle-associated membrane protein)-associate	27.5
	445688	Al248205	Hs.153244	ESTs	27.5
	405411			predicted exon	27.5
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activating enhancer-b	27.5
15	424675	NM_005512	Hs.151641	glycoprotein A repetitions predominant	27.3
65	450455	AL117424	Hs.25035	chloride intracellular channel 4	27.3
	414855	AA156986	Hs.104640	HIV-1 Inducer of short transcripts binding protein	27.2
	433578	BE336886	Hs.3416	adipose differentiation-related protein	27.2
	401994			predicted exon	27.2
70	445033	AV652402	Hs.155145	ESTs	27.2
70	402277			predicted exon	27.1
	428106	BE620016	Hs.182470	PTD010 protein	27.1
	448625	AW970786	Hs.178470	Homo saplens cDNA: FLJ22662 fis, clone HSI08080	27.1
	422587	AI879352	Hs.118625	hexokinase 1	27.0
75	457204	BE264152	Hs.221994	ESTs	27.0
75	444094	Al695764	Hs.202394	ESTs	27.0
	414053	BE391635	Hs.75725	transgelin 2	26.9
	430511	BE018156	Hs.2575	calpain 1, (mu/l) large subunit	26.9
	434039	L32977	Hs.3712	ubiquinol-cytochrome c reductase, Rieske Iron-sulfur po	26.9
00	424939	AK000059	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, partial cds	26.9
80	414539	BE379046		gb:601236646F1 NIH_MGC_44 Homo sapiens cDNA	26.9
	404675			predicted exon	26.8
	401597	AA172106	Hs.110950	Rag C protein	26.8
	401405			predicted exon	26.8
	411541	W03940		gb:za62b02.r1 Soares fetal liver spleen 1NFLS Homo sa	26.8

	440005			cor.	00.7
	412025 414276	AI827451 BE297862	Hs.24143	ESTs gb:601174780F1 NIH_MGC_17 Homo sapiens cDNA	26.7 26.7
	444065	AW449415	Hs.10260	Homo sapiens cDNA FLJ11341 fis, clone PLACE1010	26.7
_	447981	R53772	Hs.8929	hypothetical protein FLJ11362	26.7
5	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein)	26.5
	400982			predicted exon	26.5
	452933 407233	AW391423	Hs.288555 Hs.50964	Homo sapiens cDNA: FLJ22425 fis, clone HRC08685 carcinoembryonic antigen-related cell adhesion molecul	26.5 26.4
	430127	X16354 AA219498	Hs.233952	proteasome (prosome, macropain) subunit, alpha type, 7	26.3
10	448218	Al188489	1.0.2.000	gb:qd09b12.x1 Soares_placenta_8to9weeks_2NbHP8to	26.3
	413511	AI627178	Hs.75412	Arginine-rich protein	26.2
	459511	Al142379		gb:qg64c01.r1 Soares_testis_NHT Homo sapiens cDNA	26.2
	410668	BE379794	Hs.65403	hypothetical protein	26.2
15	458662	Al823410	Hs.169149	karyopherin alpha 1 (importin alpha 5) ESTs	26.2 26.2
13	451219 448939	AA054209 BE267795	Hs.167904 Hs.22595	hypothetical protein FLJ10637	26.2
	400800	Y10262	Hs.46925	eves absent (Drosophila) homolog 3	26.2
	446342	8E298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (from c	26.2
00	421177	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (from	26.1
20	433848	AF095719	Hs.93764	carboxypeptidase A3	26.1 26.1
	448497 415279	BE613269 F04237	Hs.21893 Hs.1447	ESTs, Weakly similar to glycerol 3-phosphate permease glial fibrillary acidic protein	26.0
	419323	A1092379	Hs.135275	ESTs	26.0
	430265	L36033	Hs.237356	stromal cell-derived factor 1	25.9
25	437679	NM_014214	Hs.5753	inositol(myo)::)(or 4)-monophosphatase 2	25.9
	425535	AB007937	Hs.158287	KIAA0468 gene product	25.8
	412923	AA179922	Hs.75056	adaptor-related protein complex 3, delta 1 subunit	25.8 25.8
	447980 419118	Al703397 AA234223	Hs.202355 Hs.139204	ESTs ESTs	25.8 25.8
30 .	421224	AW402154	Hs.125812	ESTs	25.8
<b>50</b> .	414890	BE281095	Hs.77573	uridine phosphorylase	25.8
	447330	BE279949	Hs.18141	ladinin 1	25.7
	405610			predicted exon	25.7
35	447604	AW089933	Hs.293674 Hs.6838	ESTs	25.7 25.7
33	445677 456088	H96577 BE177320	Hs.156148	ras homolog gene family, member E Homo sapiens cDNA: FLJ23082 fis, clone LNG06451	25.7
	417120	N79687	Hs.46616	ESTs	25.6
	405194			predicted exan	25.6
40	410687	U24389	Hs.65436	lysyl oxidase-like 1	25.6
40	421888	AA299780	Hs.121036	ESTs	25.6
	420459	AF016045 N72630	Hs.97905 Hs.33981	ovo (Drosophila) homolog-like 1 Homo sapiens genomic DNA, chromosome 21q, section	25.5 25.5
	416323 446292	AF081497	Hs.279682	Rh type C glycoprotein	- 25.5
	416274	AW160404	Hs.79126	guanine nucleotide binding protein 10	25.5
45	430028	BE564110	Hs.227750	NADH dehydrogenase (ubiquinone) 1 beta subcomplex	25.5
	438450	AI050866	Hs.65853	nodal, mouse, homolog	25.5
	400215	1150054	11- 400405	predicted exon	25.4 25.4
	430014 453582	H59354 AW854339	Hs.182485 Hs.33476	actinin, alpha 4 hypothetical protein FLJ11937	25.4
50	405867	A1100-0003	113.55470	predicted exon	25.4
	459170	Al905518		gb:RC-BT091-210199-098 BT091 Homo sapiens cDNA	25.4
	407944	R34008	Hs.239727	desmocollin 2	25.4
	415748	D90086	Hs.979	pyruvate dehydrogenase (lipoamide) beta	25.3
55	423287 450944	H38340 AA554989	Hs.209061	gb:yp70h07.r1 Soares adult brain N2b4HB55Y Homo s sudD (suppressor of birnD6, Aspergillus nidulans) homo	25.3 25.3
<i>J J</i>	432906	BE265489	Hs.3123	lethal giant larvae (Drosophila) homolog 2	25.3
	400104	00000		predicted exon	25.3
	449019	Al949095	Hs.67776	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFA	25.3
60	406897	M57417		gb:Homo sapiens mucin (mucin) mRNA, partial cds.	25.3
60	402639	4.4040252	15- 000045	predicted exon	25.3
	447147 453379	AA910353 AA035261	Hs.292815 Hs.61753	ESTs ESTs	25.3 25.3
	414217	Al309298	Hs.279898	Homo saplens cDNA: FLJ23165 fis, clone LNG09846	25.3
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	25.3
65	406685	M18728		gb:Human nonspecific crossreacting antigen mRNA, co	25.3
	444747	AW450407	Hs.257291	ESTs, Weakly similar to PSS8_HUMAN PROSTASIN	25.2
	417883	R22519	Hs.23398	ESTS  BAR10 member BAS encessors femily	25.2 25.2
	430235 459001	BE268048 AI761313	Hs.236494 Hs.204605	RAB10, member RAS oncogene family ESTs	25.2 25.2
70	434368	AW519020	Hs.212640	Homo sapiens cDNA FLJ13265 fis, clone OVARC1000	25.2
	415917	Z43912		gb:HSC1OA111 normalized infant brain cDNA Homo	25.2
	444409	AJ792140	Hs.49265	ESTs	25.2
	428578	BE391797	Hs.82148	hypothetical protein	25.1
75	433417	AA587773	Hs.136494	ESTs DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 21	25.1 25.1
, 5	426372 402131	BE304680	Hs.169531	predicted exon	25.1 25.1
	450545	AW135582	Hs.201767	ESTs	25.0
	434162		Hs.116136	ESTs	25.0
00	406571			predicted exon	24.9
80	427600		Hs.179774	proteasome (prosome, macropain) activator subunit 2 (P	24.9
	409402 400135		Hs.695	cystatin B (stefin B) predicted exon	24.9 24.9
	428403		Hs.239894	leucine rich repeat (in FUI) interacting protein 1	24.9
	403223			predicted exon	24.8

	435236	TOSPON	th armon	ECTe Highly cimilar in Any hamanastals at account	24.0
	457439	T03890 AW410408	Hs.157208 Hs.271167	ESTs, Highly similar to Anx homeoprotein [M.musculu L-pipecolic acid oxidase	24.8 24.8
	448667	Z78394	Hs.4896	Homo sapiens cDNA: FLJ22046 fis, clone HEP09276	24.8
_	440605	Z40094	Hs.185698	ESTs	24.8
5	426724	AA383623	Hs.293616	ESTs	24.8
	403359			predicted exon	24.7
	442826	AI018777	Hs.131241	ESTs	24.7
	411503 414540	AW190338 BE379050	Hs.28029	purinergic receptor P2X, ligand-gated ion channel, 4	24.6
10	421595	AB014520	Hs.105958	gb:601236655F1 NiH_MGC_44 Homo sapiens cDNA Homo sapiens cDNA: FLJ22735 fis, clone HUV00180	24.6 24.5
10	438802	AA825976	Hs.136954	ESTs	24.5
	400491	H25530	Hs.50868	solute carrier family 22 (organic cation transporter), me	24.5
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecule 1)	24.5
1.5	426383	BE537380		gb:601064570F1 NIH_MGC_10 Homo sapiens cDNA	24.4
15	418408	AA219321	Hs.173294	ESTs	24.4
	415186	W87575	Hs.269177	ESTs	24.4
	416908 453857	AA333990 AL080235	Hs.80424 Hs.35861	coagulation factor XIII, A1 polypeptide DKFZP586E1621 protein	24.4 24.4
	439706	AW872527	Hs.59761	ESTs	24.4
20	441619	NM_014056	Hs.7917	DKFZP564K247 protein	24.4
	417198	F11533	Hs.81634	ATP synthase, H+ transporting, mitochondrial F0 comp	24.3
	433662	W07162	Hs.150826	CATX-8 protein	24.3
	453986	M13232	Hs.36989	coagulation factor VII (serum prothrombin conversion a	24.3
25	457123	AA770021	Hs.16332	ESTs	24.3 24.3
23	433864 409865	AA931550 AW502208	Hs.192785	ESTs gb:UI-HF-BR0p-atu-e-09-0-UI.r1 NIH_MGC_52 Hom	24.3
	448175	BE296174	Hs.225160	Homo sapiens cDNA FLJ13102 fis, clone NT2RP3002	24.3
	406277			predicted exon	24.3
20	451957	Al796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, done PLACE1006	24.3
30	408802	AL048269	Hs.288544	Homo sapiens cDNA: FLJ20882 fis, clone ADKA0320	24.2
	401757	A1207.400	U- 440CC	predicted exon	24.2
	444751 408647	AI207406 AW245831	Hs.11866	hypothetical protein PRO1197 gb:2822937.5prima NIH_MGC_7 Homo saplens cDNA	24.2 24.2
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fusin)	24.2
35	436913	AA789074	Hs.187478	ESTs	24.2
	434745	AW974445	Hs.185155	ESTs, Wealtly similar to HuEMAP [H.sapiens]	24.2
	451743	AW074266	Hs.23071	ESTs	24.2
	421853	AL117472	Hs.108924	DKFZP586P1422 protein	24.2
40	407926 413973	AW956382 BE279858	Hs.59771 Hs.128417	ESTs Homo sapiens cDNA FLJ14009 fis, clone Y79AA1002	24.1 24.1
••	439078	AF085936	115.120411	gb:Homo sapiens full length insert cDNA clone YR58F	24.1
	401913			predicted exon	24.1
	435138	BE314734		gb:601152976F1 NIH_MGC_19 Homo sapiens cDNA	24.1
45	405311	DE000500		predicted exon	24.0
43	413127 430793	BE066529 M83181	Hs.83484 Hs.247940	SRY (sex determining region Y)-box 4	24.0 24.0
	434445	Al349306	Hs.11782	5-hydroxytryptamine (serotonin) receptor 1A ESTs	24.0
	418166	AI754416	Hs.260024	Cdc42 effector protein 3	24.0
<b>c</b> 0	431971	BE274907	Hs.77385	myosin, light polypeptide 6, alkali, smooth muscle and n	23.9
50	401167			predicted exon	23.9
	454163	AW175997	11- 74200	gb:QV0-BT0078-190899-005-E02 BT0078 Homo sapi	23.9
	403306 410627	NM_006825 AA181339	Hs.74368 Hs.929	transmembrane protein (63kD), endoplasmic reticulum/ myosin, heavy polypeptide 7, cardiac muscle, beta	23.9 23.9
	450796	NM_001988	Hs.25482	envoplakin	23.8
55	442199	BE277633	Hs.286027	etoposide-induced mRNA	23.8
	402699		/	predicted exon	23.8
	426143	BE379836	Hs.167106	proteasome (prosome, macropain) subunit, alpha type, 3	23.8
	437592	NM_003851	Hs.5710	cellular repressor of E1A-stimulated genes	23.8
60	433598 401088	A1762836	Hs.271433	ESTs, Moderately similar to ALU2_HUMAN ALU SU oredicted exon	23.8 23.8
50	445924	Al264671	Hs.164166	ESTs	23.8
	420902	AA742277		gb:ny28e09.s1 NCI_CGAP_GC81 Homo sapiens cDN	23.8
	426369	AF134157	Hs.169487	Kreisler (mouse) maf-related leucine zipper homolog	23.8
65	458698	AW452189	Hs.257528	ESTs	23.7
65	422048	NM_012445 R61610	Hs.288126	spondin 2, extracellular matrix protein ESTs, Wealdy similar to KIAA0918 protein [H.sapiens	23.7 23.6
	413460 401575	ROIDIU	Hs.21527	predicted exon	23.6
	431822	AA516049		gb:ng65d01.s1 NCI_CGAP_Lip2 Homo sapiens cDNA	23.6
	427276	AA400269	Hs.49598	ESTs	23.6
70	417069	AA442192	Hs.81097	cytochrome c oxidase subunit VIII	23.5
	400161	ATIA 004050	11-04-40	predicted exon	23.5
	417190	NM_001359 Al129066	Hs.81548	2,4-dienoyi CoA reductase 1, mitochondrial	23.5
	443667 413544	BE147225	Hs.135457	ESTs gb:PM2-HT0225-031299-003-f11 HT0225 Homo sapie	23.5 23.5
75	400685	J		predicted exon	23.5
-	422090	W05345	Hs.293884	ESTs	23.4
	432517	AF275816	Hs.283096	PR domain containing 9	23.4
	405307	1140300	11- 00000-	predicted exon	23.4
80	416328 427174	H48389 AA398848	Hs.268886	ESTs ESTs	23.4 23.4
50	426148	AA395548 AI751071	Hs.97541 Hs.167135	ESTs Homo sapiens cDNA FLJ10728 fis, clone NT2RP3001	23.4
	452544	AW851888		gb:QV0-CT0225-131099-034-d05 CT0225 Homo sapie	23.3
	404890			predicted exon	23.3
	408725	AA131539	Hs.15669	ESTs	23.3
				110	

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	428352	AA426555	Hs.169333	ESTs	23.3
	425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5-phosphate ep	23.3
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B11 (aldose redu	23.3
5	410962	BE273749	Hs.752	FK506-binding protein 1A (12kD)	23.2
3	411796	AA807197	Hs.6918	ESTs	23.2
	458954	AW379075	Hs.141742	Homo sapiens cDNA FLJ12211 fis, clone MAMMA10	23.2
	408896	A1610447	Hs.48778	niban protein ESTs	23.2 23.2
	457024 414591	AA397546 AI888490	Hs.119151 Hs.55902	ESTs	23.2
10	437846	AA773866	Hs.244569	ESTS	23.2
10	401220	AA773000	113.244303	predicted exon	23.1
	421747	Al816224	Hs.107747	DKFZP566C243 protein	23.1
	452950	AA428123	Hs.7745	17kD fetal brain protein	23.1
	414327	BE408145	Hs.185254	ESTs. Moderately similar to NAC-1 protein (R.norvegic	23.1
15	405256			predicted exon	23.1
	452416	AA026115	Hs.114777	ESTs	23.1
	440684	A1253123	Hs.127356	ESTs, Highly similar to NEST_HUMAN NESTI [H.sap	23.1
	445603	H08345	Hs.106234	ESTs	23.1
20	436306	AA805939	Hs.117927	ESTs	23.1
20	434867	AF159442	Hs. 103382	phospholipid scramblase 3	23.0
	404727	.100.4000	11. 074 464	predicted exon	23.0
	407317	Al204033	Hs.271461	ESTs, Wealty similar to ALU5_HUMAN ALU SUBFA	23.0 23.0
	405580 437898	W81260	Hs.43410	predicted exon ESTs	22.9
25	448781	AW243419	Hs.254048	ESTs .	22.9
LJ	457297	AW968188	Hs.290999	ESTs S	22.9
	405545	A11300100	113.250000	predicted exon	22.9
	431562	A1884334	Hs.11637	ESTs	22.9
	440703	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (from c	22.9
30	439848	AW979249		gb:EST391359 MAGE resequences, MAGP Homo sap	22.9
	418149	AA811473	Hs.291877	ESTs	22.9
	439332	AW842747	Hs.293314	ESTs, Highly similar to unnamed protein product [H.sa	22.8
	401566			predicted exon	22.8
25	425078	NM_002599	Hs.154437	phosphodiesterase 2A, cGMP-stimulated	22.8
35	406684	X16354	Hs.50964	carcinoembryonic antigen-related cell adhesion molecul	22.8
	421651	AW860612	Hs.283586	ESTs	22.8
	421064	Al245432	Hs.101382	tumor necrosis factor, alpha-induced protein 2	22.8 22.8
	441249 457624	AA971585 AA809159	Hs.166250 Hs.287581	ESTs Homo sapiens cDNA FLJ13544 fis, clone PLACE1006	22.8
40	407395	AF005082	115.201301	gb:Homo sapiens skin-specific protein (xp33) mRNA, p	22.8
	459006	AW298631	Hs.27721	hypothetical protein FLJ20353	22.8
	436827	H72187	Hs.5322	guanine nucleotide binding protein (G protein), gamma	22.7
	418174	L20688	Hs.83656	Rho GDP dissociation inhibitor (GDI) beta	22.7
4.5	418307	U70867	Hs.83974	solute carrier family 21 (prostaglandin transporter), mem	. 22.7
45	456035	N54956	Hs.271726	ESTs	22.7
	457867	AA045767	Hs.5300	bladder cancer associated protein	22.7 22.7
	440401 400126	Al126341	Hs.143887	ESTs predicted exon	22.7
	414931	AK000342	Hs.77646	Homo sapiens mRNA; cDNA DKFZp761M0223 (from	22.7
50	406719	AI832962	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	22.6
	439675	W95357	Hs.138860	Rho GTPase activating protein 1	22.6
	456058	N94587	Hs.55063	ESTs	22.6
	441926	Al015051	Hs.130953	ESTs	22.6
55	428423	AU076517	Hs.184276	solute carrier family 9 (sodium/hydrogen exchanger), is	22.6
22	438518	BE561958	Hs.285823	immunoglobulin heavy constant mu	22.6
	420674	NM_000055	Hs.1327	butyrylcholinesterase	22.6 22.5
	422160 412408	AW582898 D51103	Hs.73851	gb:ia07e04.y1 Human Pancreatic Islets Homo sapiens c ATP synthase, H+ transporting, mitochondrial F0 comp	22.5
	400964	031103	113.73031	predicted exon	22.5
60	434360	AW015415	Hs.127780	ESTs	22.5
- •	427977	AW630727	Hs.181307	H3 histone, family 3A	22.4
	450339	A1693281	Hs.54547	ESTs	22.4
	424059	AW451266	Hs.107418	ESTs	22.4
	414626	BE410589		gb:601303308F1 NIH_MGC_21 Homo sapiens cDNA	22.4
65	401991			predicted exon	22.4
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	22.3
	457952	U25750	Hs.210783	Human chromosome 17q21 mRNA clone 1046:1-1	22.3
	422597	BE245909 X99133	Hs.118634	ATP-binding cassette, sub-family B (MDR/TAP), mem lipocalin 2 (oncogene 24p3)	22.3 22.3
70	429504 447306	AI373163	Hs.204238 Hs.170333	ESTs	22.3
. 5	424966	AU077312	Hs.153985	solute carrier family 7 (cationic amino acid transporter,	22.3
	422739	H20106	Hs.119591	adaptor-related protein complex 2, sigma 1 subunit	22.2
	432504	AL121015	Hs.277704	oxygen regulated protein (150kD)	22.2
	423804	AW403448	Hs.1706	interferon-stimulated transcription factor 3, gamma (48k	22.2
75	404683	AI924294	Hs.173259	uncharacterized bone marrow protein BM033	22.2
	441624	AF220191	Hs.179666	uncharacterized hypothalamus protein HSMNP1	22.2
	425751	T19239	Hs.1940	crystallin, alpha B	22.2
	452976	R44214	Hs.101189	ESTS	22.2
80	414642		Uc 7404	gb:zi03h01.r1 Soares_pregnant_uterus_NbHPU Homo	22.2 22.2
UU	437452		Hs.7104 Hs.82124	Homo sapiens mRNA; cDNA DKFZp761P06121 (from laminin, beta 1	22.2
	417426 414774		Hs.77274	plasminogen activator, urokinase	22.1
	424631	AA688021	Hs.179808	ESTs	22.1
	413967	AW204431	Hs.117853	ESTs	22.1

	400174			smdieted avea	22.4
	400174 431837	T79326	Hs.298262	predicted exon ESTs, Wealdy similar to dJ88J8.1 [H.sapiens]	22.1 22.1
	401628	113020	1102250202	predicted exon	22.1
_	418374	AJ011916	Hs.84359	hypothetical protein	22.0
5	429297	X82494	Hs.198862	fibulin 2	22.0
	403508			predicted exon	22.0
	432638	Al017717	Hs.126525	chromosome 21 open reading frame 15	22.0
	407382	AA503620	U- 70227	gbme49b08.s1 NCI_CGAP_Co3 Homo sapiens cDNA	22.0
10	411492	T46848	Hs.70337	immunoglobulin superfamily, member 4	22.0
10	420185 409545	AL044056 BE296182	Hs.158047	ESTs gb:601177324F1 NIH_MGC_17 Homo sapiens cDNA	22.0 22.0
	426662	AA879474	Hs.122710	ESTs	22.0
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	22.0
	443062	N77999	Hs.8963	Homo sapiens mRNA full length insert cONA clone EU	21.9
15	422447	AA310711	Hs.124340	ESTs	21.9
	421574	AJ000152	Hs.105924	defensin, beta 2	21.9
	435302	A1076259	Hs.190337	ESTs .	21.9
	414527	BE241739	Hs.76359	catalase	21.9
20	441436	AW137772	Hs.185980	ESTS	21.9
20	454178	AW177274		gb:CM2-CT0128-230899-005-a02 CT0128 Homo sapie	21.8
	448838 427889	BE614761 AJ400968	Hs.181046	gb:601281335F1 NIH_MGC_39 Homo sapiens cDNA dual specificity phosphatase 3 (vaccinta virus phosphat	21.8 21.8
	441114	AA917466	Hs.126600	ESTs	21.8
	451831	NM_001674	Hs.460	activating transcription factor 3	21.8
25	405600			predicted exon	21.8
	446981	Al652743	Hs.197497	ESTs	21.8
	432839	AA579465	Hs.287332	ESTs	21.8
	405208			predicted exon	21.8
30	435025	T08990	Hs.4742	anchor attachment protein 1 (Gaa1p, yeast) homolog	21.7
20	413976 423515	BE295452 AA327017	Hs.75655 Hs.162204	procollagen-proline, 2-oxoglutarate 4-dioxygenase (pro ESTs	21.7 21.7
	452329	N36626	Hs.29106	milogen-activated protein kinase phosphatase x	21.7
	423050	AA320946	113.23100	gb:EST23529 Adipose tissue, brown Homo sapiens cD	21.7
	413679	BE156765		gb:RC1-HT0370-120100-012-c09 HT0370 Homo sapie	21.7
35	442166	AW845280	Hs.204723	ESTs	21.6
	445585	AI243836	Hs.147066	ESTs	21.6
	406160			predicted exon	21.6
		AA374743	Hs.279920	tyrosine 3-monooxygenase/tryptophan 5-monooxygenas	21.6
40	446598	AW250546	Us 101574	gb:2821774.5prime NIH_MGC_7 Homo sapiens cDNA	21.6
40	434493 429582	AA635305 Al569068	Hs.121574 Hs.22247	ESTs ESTs	21.6 21.6
	403796	A303000	113.22241	predicted exon	21.6
	405028			predicted exon	21.6
	426597	AA382250	Hs.145601	ESTs	21.6
45	437308	AA749417	Hs.292353	ESTs	21.6
	447384	Al377221	Hs.40528	ESTs	21.6
	429060	AW139155	Hs.194995	hypothetical protein DKFZp434O0320	21.6
	437068	AA743643	Hs.291427	ESTs	21.6
50	418509 432999	AB028624 BE294029	Hs.85539 Hs.279903	ATP synthase, H+ transporting, mitochondrial F0 comp	21.5 21.5
50	407663	NM_016429	Hs.37482	Ras homolog enriched in brain 2 COPZ2 for nonclathrin coat protein zeta-COP	21.5
	446627	AI973016	Hs.15725	hypothetical protein SBBI48	21.5
	413605	BE152644		gb:CM1-HT0329-250200-128-f09 HT0329 Homo sapie	21.5
	427286	AW732802	Hs.2132	epidermal growth factor receptor pathway substrate 8	21.5
55	405226			predicted exon	21.4
	402570			predicted exon	21.4
	457960	AA771881	Hs.298149	ESTs	21.4
	400684 425943	MACORC	Un 21001	predicted exon	21.4
60	434240	H46986 AF119912	Hs.31861 Hs.258119	ESTs hypothetical protein PRO3073	21.4 21.4
_ •	448376	A1494332	Hs.196963	ESTs	21.4
	408089	H59799	Hs.42644	thioredoxin-like	21.4
	400304	AF005082	Hs.113261	Homo sapiens skin-specific protein (xp33) mRNA, part	21.4
65	412652	AI801777	Hs.6774	ESTs	21.4
65	428373	Al751656	Hs.183986	poliovirus receptor-related 2 (herpesvirus entry mediato	21.3
	416138	C18946	Hs.79026	myeloid leukemia factor 2	21.3
	425184 411028	BE278288 AW813703	Hs.155048	Lutheran blood group (Auberger b antigen included) gb:RC3-ST0197-130100-014-h09 ST0197 Homo sapien	21.3 21.3
	417438	Z43989	Hs.82141	Human clone 23612 mRNA sequence	21.3
70	417534	NM_004998	Hs.82251	myosin IC	21.3
	427767	AI879283	Hs.180714	cytochrome c oxidase subunit VIa polypeptide 1	21.2
	433300	AA582307		gb:nn49d09.s1 NCI_CGAP_Kid6 Homo sapiens cDNA	21.2
	452061	A1074259	Hs.469	succinate dehydrogenase complex, subunit A, flavoprot	21.2
75	411939	Al365585	Hs.146246	ESTs	21.2
75	435060	AJ422719	Hs.233349	ESTs, Weakly similar to fork head like protein [H.sapie	21.2
	432412 407491	A1470549 S82769	Hs.162201	ESTs gb:GABAA receptor gamma 3 subunit (human, fetal bra	21.2 21.2
	418960	NM_004494	Hs.89525	hepatoma-derived growth factor (high-mobility group p	21.1
	426254	BE018103	Hs.168541	Homo sapiens mRNA full length insert cONA clone EU	21.1
80	458188	AW297226	Hs.137840	ESTs, Moderately similar to SIX1_HUMAN HOMEOB	21.1
	406215			predicted exon	21.1
	425461	AK000602	Hs.157938	hypothetical protein FLJ20595	21.1
	448296	BE622756	Hs.10949	Homo sapiens cDNA FLJ14162 fis, clone NT2RM4002	21.1
	409415	AA579258	Hs.6083	Homo sapiens cDNA: FLJ21028 fis, clone CAE07155	21.1

	408546	W49512	Hs.46348	bradykinin receptor B1	21.1
	450008	H52970	Hs.36688	WAP four-disulfide core domain 1	21.1
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	21.1
-	438901	AF085834	Hs.29036	ESTs	21.1
5	440500	AA972165	Hs.150308	ESTs .	21.1
	413101	BE065215		gb:RC1-BT0314-310300-015-f01 BT0314 Homo sapie	21.1
	447452	BE618258	Hs.102480	ESTs	21.1
	412446	AI768015	Hs.92127	ESTs .	21.1
10	418975	T75496	Hs.296980	ESTs	21.0
10	454961	AW847807		gb:lL3-CT0213-190200-040-E12 CT0213 Homo sapien	21.0
	401072			predicted exon	21.0
	401204	A COZOGEO	15-00247	predicted exon	21.0
	433626	AF078859 R37633	Hs.86347	hypothetical protein	21.0 21.0
15	418047 443380	AJ792478	Hs.4847 Hs.135377	ESTs ESTs	21.0
13	427424	AA402453	Hs.113011	ESTS	21.0
	433412	AV653729	Hs.8185	CGI-44 protein; sulfide dehydrogenase like (yeast)	21.0
	422599	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A) expressed in	20.9
	435656	R93409	Hs.120759	ESTs	20.9
20	413745	AW247252	Hs.75514	nucleoside phosphorylase	20.9
	418874	T60872	115.10014	gb:yb72h11.s1 Stratagene ovary (937217) Homo sapien	20.9
	452574	AF127481	Hs.35093	lymphoid blast crisis oncogene	20.9
	400332	S66407	Hs.248032	PLT4	20.9
	402421			predicted exon	20.9
25	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	20.9
	432038	AA524746	Hs.162110	ESTs	20.8
	423711	AF059194	Hs.131953	v-mai musculoaponeurolic fibrosarcoma (avian) oncoge	20.8
	402297			predicted exon	20.8
	405133			predicted exon	20.8
30	436661	Al125270	Hs.128069	ESTs, Weakly similar to similar to collagen [C.elegans]	20.8
	437836	BE269291	Hs.292458	ESTs	20.8
	437329	AA811977	Hs.291761	ESTs	20.8
	445830	H10451	Hs.42656	Homo sapiens cDNA FLJ12667 fis, clone NT2RM4002	20.8
	406824	AW515961	Hs.84298	CD74 antigen (invariant polypeptide of major histocom	20.7
35	421271	AW170057	Hs.133179	ESTs	20.7
	400256			predicted exon	20.7
	414028	AA782576	Hs.4944	Homo sapiens cDNA FLJ12783 fis, clone NT2RP2001	20.7
	456728		Hs.122967	kelch (Drosophila)-like 2 (Mayven)	20.7
40	417707	AL035786	Hs.82425	actin related protein 2/3 complex, subunit 5 (16 kD)	20.7
40	438713	H16902	Hs.6749	ESTs	20.7
	450306	AL080080	Hs.24766	DKFZP564E1962 protein	20.7
	438898	AI819863	Hs.106243	ESTs	20.7
	403273	55300440		predicted exon	20.7
45	414605	BE390440		gb:601283601F1 NIH_MGC_44 Homo sapiens cDNA	20.7
40	401283			predicted exon	20.7 20.6
	403703 416969	AI815443	Hs.283404	predicted exon	20.6
	442400	AW381148	Hs.3593	organic cation transporter ESTs	20.6
	447563	BE536115	Hs.160983	ESTs	20.5
50	419754	H52299	Hs.75243	bromodomain-containing 2	20.5
50	408204	AA454501	Hs.43666	protein tyrosine phosphatase type IVA, member 3	20.5
	450507	AW295603	Hs.250891	ESTs	20.5
	429612		Hs.252587	pituitary tumor-transforming 1	20.5
	413758	BE162391		gb;PM2-HT0451-090100-002-f04 HT0451 Homo sapie	20.5
55	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	20.5
	400642			predicted exon	20.4
	431582	F07136	Hs.261828	G protein-coupled receptor kinase 7	20.4
	442724	AA355525	Hs.159604	cysteinyl-tRNA synthetase	20.4
	417861	AA334551	Hs.82767	sperm specific antigen 2	20.4
60	402948			predicted exon	20.4
	411004	AW813242		gb:MR3-ST0191-020200-207-g10 ST0191 Homo sapie	20.4
	435478	AA682622		gb:zj20f09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Ho	20.4
	447955	BE544271	Hs.288390	Homo sapiens cDNA: FLJ22795 fis, clone KAIA2543	20.3
CE	433592	NM_004642	Hs.3436	deleted in oral cancer (mouse, homolog) 1	20.3
65	420865	N73241	Hs.100001	solute carrier family 17 (sodium phosphate), member 1	20.3
	449482	AI784266	Hs.28774	ESTs	20.3
	400807	1105100	11. 00044	predicted exon	20.3
	419942	U25138	Hs.93841	potassium large conductance calcium-activated channel	20.3
70	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7 (galectin 7)	20.3
70	402986	BE244588	Hs.6456	chaperonin containing TCP1, subunit 2 (beta) Homo sapiens BAC clone RP11-481J13 from 2	20.3 20.3
	451375 453586	.AI792066 AA248089	Hs.283902 Hs.50841	ESTs, Weakly similar to tuftelin [M.musculus]	20.3
	433090	AA246069 AI720050	Hs.145362	immortalization-upregulated protein	20.3
	425053	AF046024	Hs.154320	ubiquitin-activating enzyme E1C (homologous to yeast	20.3
75	412802		Hs.74602	aquaporin 1 (channel-forming integral protein, 28kD)	20.3
	409738		Hs.56205	insufin induced gene 1	20.3
	428245	AF151048	Hs.183180	hypothetical protein	20.2
	412582	BE270631	Hs.74077	proteasome (prosome, macropain) subunit, alpha type, 6	20.2
	406207	200. 3001		predicted exon	20.2
80	400931			predicted exon	20.2
-	410709	AL122109	Hs.65735	Homo sapiens mRNA; cDNA DKFZp434M1827 (from	20.2
	428438		Hs.2271	endothelin 1	20.2
	446918		Hs.13913	KIAA1577 protein	20.2
	417821	BE245149	Hs.82643	protein tyrosine kinase 9	20.2

	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (prostaglandin G	20.2
	414511	AA148725	Hs.12969	hypothetical protein	20.2
	451546	AF051782	Hs.26584	Homo saplens clone CDABP0038 mRNA sequence	20.1
	441899	Al37258B	Hs.8022	TU3A protein	20.1
5	425811	AL039104		karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	20.1
9			Hs.159557		20.1
	411014	AW816072		gb:MR3-ST0220-070100-021-h07 ST0220 Homo sapie	20.1
	451400	BE160479		gb:QV1-HT0413-210200-081-g05 HT0413 Homo sapi	
	459247	N46243	Hs.110373	ESTs	20.1
10	441633	AW958544	Hs.112242	ESTs	20.1
10	427466	AA523543	Hs.7678	cellular retinoic acid-binding protein 1	20.0
	406893	M22406		gb:Human Intestinal mucin mRNA, partial cds, ctone SM	20.0
	406268			predicted exon	20.0
	403348			predicted exon	20.0
	400970			predicted exon	20.0
15	414045	NM_002951	Hs.75722	ribopherin II	20.0
	427169	AA398823	Hs.97549	EST	20.0
	405586	777030023	10.31043	predicted exon	20.0
		41043200	11- 145520		20.0
	445834	AI913290	Hs.145532	ESTs, Weakly similar to Gag polyprotein [M.musculus	
20	422525	AA758797	Hs.192807	ESTs	20.0
20	425383	D83407	Hs.156007	Down syndrome critical region gene 1-like 1	20.0
	454590	AW809762	Hs.222056	Homo sapiens cDNA FLJ11572 fis, clone HEMBA100	20.0
	411529	AA430348	Hs.288837	Homo sapiens cDNA FLJ12927 fis, clone NT2RP2004	20.0
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	20.0
	403234			predicted exon	19.9
25	427267	AI201185	Hs.119164	ESTs	19.9
	400203			predicted exon	19.9
	449296	AL137257	Hs.23458	Homo sapiens mRNA; cDNA DKFZp434C1613 (from	19.9
	406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac muscle, beta	19.9
	423083	AA321774	Hs.10941	ESTs, Weakly similar to IPP1_HUMAN PROTEIN PH	19.9
20					
30	422112	BE540240	Hs.111783	Lsm1 protein	19.9 19.9
	413282	BE078159		gb:CM0-BT0615-140200-175-e06 BT0615 Homo sapie	
	453702	AA037637	Hs.42128	ESTs	19.9
	403065			predicted exon	19.9
	440633	AI140686	Hs.263320	ESTs	19.9
35	456994	AA383523	Hs.293616	ESTs -	19.9
	458260	R41782	Hs.22279	ESTs	19.9
	452388	BE019696	Hs.29287	retinoblastoma-binding protein 8	19.9
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	19.9
	441989	AA306207	Hs.286241	Homo sapiens cDNA: FLJ22698 fis, done HSI12044	19.9
40	418758	AW959311	Hs.87019	ESTs	19.9
70	406646	M33600	Hs.180255	major histocompatibility complex, class II, DR beta 1	19.8
	433053	BE301909	Hs.279952	glutathione S-transferase subunit 13 homolog	19.8
				N-acylsphingosine amidohydrolase (acid ceramidase)	19.8
	414194	BE175494	Hs.75811		
15	452321	AW844498	Hs.289052	Homo sapiens LENG8 mRNA, variant C, partial sequen	19.8
45	449713	AW027025	Hs.239262	ESTs	19.8
	458827	AW970786	Hs.178470	Homo sapiens cDNA: FLJ22662 fis, done HSI08080	19.8
	414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	19.8
	441730	A1243276	Hs.149017	ESTs	19.8
	420701	N42919	Hs.88630	ESTs, Wealdy similar to AC007228 1 R31665 2 [H.sap	19.8
50	403642			predicted exon	19.8
-	408987	H85615		gb:yt03f11.r1 Soares retina N2b5HR Homo sapiens cD	19.8
	446712	AW204789	Hs.209828	ESTs	19.8
	403286	7.1.120 77 00	110120020	predicted exon	19.8
	434439	AI022360	Hs.190583	ESTs	19.8
55	404067	MUZZJOU	(13.130303	predicted exon	19.7
55		0000000			19.7
	455694	BE067300		gb:PM2-BT0349-161299-001-h10 BT0349 Homo sapie	19.7
	403287	4140050-	11- 400045	predicted exon	
	434633	AJ189587	Hs.120915	ESTS	19.7
60	408199	AA132637	Hs.15396	ESTs	19.7
60	420080	M94065	Hs.94925	dihydroorotate dehydrogenase	19.7
	408852	AW291435	Hs.254961	ESTs	19.7
	403786			predicted exon	19.7
	416839	H94900	Hs.17882	ESTs	19.7
	434385		Hs.259580	ESTs	. 19.7
65	446845	Al343645	Hs.156108	ESTs	19.7
	425612			gb:CM0-BN0103-180300-296-c04 BN0103 Homo sapi	19.7
	402520	DEGOTEO		predicted exon	19.6
		D20507	Uc 0730		19.6
	436098		Hs.9739 Hs.6454	ESTs	19.6
70	438974			chromosome 19 open reading frame 3	
70	447751	AA339541	Hs.24956	hypothetical protein FLJ22056	19.6
	451310		Hs.26213	ESTs, Moderately similar to dJ447F3.3 [H.sapiens]	19.6
	435961	BE293127	Hs.283722	GTT1 protein	19.6
	452937	BE410390	Hs.288940	five-span transmembrane protein M83	19.6
75	404850			predicted exon	19.6
75	438360		Hs.288193	hypothelical protein FLJ10375	19.6
	436508	AW604381	Hs.121121	ESTs	19.6
	430486		Hs.241551	chloride channel, calcium activated, family member 2	19.6
	407824		Hs.9812	ESTs	19.6
	406388			predicted exon	19.6
80	430204		Hs.146137	ESTs, Weakly similar to putative [C.elegans]	19.5
	457560		Hs.163909	ESTs	19.5
	429521			ESTs	19.5
			Hs.50949		19.5
	429758		Hs.246804	ESTs	
	441473	AA934995	Hs.184846	ESTs, Weakly similar to R28830 1 [H.sapiens]	19.5

	444254	4.4330550	11. 74040	achimorros (DNA) II (DNA disease di este confide ) 17	40.5
	411724 450453	AA770559 AA009883	Hs.71618	polymerase (RNA) II (DNA directed) polypeptide L (7. ESTs	19.5 19.5
	419687	A1638859	Hs.50186 Hs.227699	ESTs, Weakly similar to Yhr217cp (S.cerevislae)	19.5
_	442162	AW294966	Hs.150849	ESTs	19.5
5	435056	AW023337	Hs.5422	glycoprotein M6B	19.5
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	19.5
	413825	BE299181	Hs.75564	CD151 antigen	19.4
	422687	AW068823	Hs.119206	insufin-like growth factor binding protein 7	19.4
10	435551	AF212365	Hs.5470	IL-17B receptor	19.4 19.4
10	440069 432277	BE617892 Al669790	Hs.6895 Hs.161825	actin related protein 2/3 complex, subunit 3 (21 kD) - ESTs	19.4
	428044	AA093322	Hs.182225	RNA binding motif protein 3	19.4
	455064	AA256213	Hs.72010	ESTs	19.4
	424897	D63216	Hs.153684	frizzled-related protein	19.4
15	424673	AA345051	Hs.294092	ESTs	19.4
	403852			predicted exon	19.3
	405699			predicted exon	19.3
	433096	AU076803	Hs.282975	carboxylesterase 2 (intestine, liver)	19.3
20	400344 417501	NM_012368 AL041219	Hs.258574 . Hs.82222	olfactory receptor, family 2, subfamily C, member 1 sema domain, immunoglobulin domain (lg), short basic	19.3 19.3
20	400449	ALONIZIS	115.02222	predicted exon	19.3
	453801	AL134751	Hs.23450	mRNA for FLJ00023 protein	19.3
	435849	BE305242	Hs.112442	ESTs, Weakly similar to CLDE_HUMAN CLAUDIN-	19.3
	454181	AW177377		gb:CM4-CT0129-190899-007-e09 CT0129 Homo saple	19.3
25	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(NAD)	19.3
	406326			predicted exon	19.3
	421921	H83363	Hs.109571	translocase of inner mitochondrial membrane 10 (yeast)	19.3
	416700	AW498958	Hs.79572 Hs.224601	cathepsin D (lysosomal aspartyl protease) ESTs	19.2 19.2
30	458857 405501	AI627342	FIS.224001	predicted exon	19.2
50	416601	R08652	Hs.20205	hemoglobin, beta pseudogene 1	19.2
	426600	NM_003378	Hs.171014	VGF nerve growth factor inducible	19.2
	425590	AI954686	Hs.158321	beaded filament structural protein 2, phakinin	19.2
25	428151	AA422028		gb:zv26g06.r1 Soares_NhHMPu_S1 Homo sapiens cDN	19.2
35	426420	BE383808	Hs.169829	KIAA1180 protein	19.2
	414428	BE296906	Hs.182625	VAMP (vesicle-associated membrane protein)-associate	19.2
	404601			predicted exon predicted exon	19.2 19.2
	403861 448363	BE174595	Hs.366	6-pyruvoyitetrahydropterin synthase	19.2
40	406655	M21533	Hs.181244	major histocompatibility complex, class I, A	19.1
	435372	AA809591	Hs.106486	ESTs, Highly similar to CIKG_HUMAN VOLTAGE-G	19.1
	413154	BE067870		gb:RC0-BT0362-021299-031-b06 BT0362 Homo sapie	19.1
	443021	AA368546	Hs.8904	lg superfamily protein	19.1
15	412975	T70956	Hs.75106	clusterin (complement lysis inhibitor, SP-40,40, sulfated	19.1
45	412633	AF001691	Hs.74304	periplakin	19.1
	402071	A1077267	Hs.47094	predicted exon ESTs	19.1 19.1
	410387 423961	Al277367 D13666	Hs.135348	osteoblast specific factor 2 (fasciclin Hike)	19.1
	407032	U73799	110.100010	gb:Human dynactin mRNA, partial cds.	19.0
50	404034			predicted exon	19.0
	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudogene	19.0
	446599	Z97832	Hs.15476	differentially expressed in FDCP (mouse homolog) 6	19.0
	426410	BE298446	Hs.180372	BCL2-like 1	19.0
55	419618	AA528295	Hs.112689	gb:nh26e06.s1 NCI_CGAP_Pr3 Homo sapiens cDNA c ESTs	19.0 19.0
"	457632 417138	AW292151 AA193646	Hs.65771	Homo sapiens chromosome 19, BAC CIT-HSPC_204F	19.0
	417933	X02308	Hs.82962	thymidylate synthetase	19.0
	458808	AW134832	Hs.246295	ESTs	19.0
<b>~</b>	415860	D56051	Hs.78888	diazeparn binding inhibitor (GABA receptor modulator	18.9
60	440919	AW291274	Hs.262826	ESTs	18.9
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	18.9
	401747	414470000		predicted exon	18.9
	454209 417661	AW179083 T84155	Hs.15464	gb:MR4-ST0055-270899-006-A07 ST0065 Homo sapi Homo sapiens cDNA: FLJ21351 fis, clone COL02762	18.8 18.8
65	426499	C14937	Hs.11169	Gene 33/Mig-6	18.8
•••	404240	G		predicted exon	18.8
	439718	AA307634	Hs.6650	vacuolar protein sorting 45B (yeast homolog)	18.8
	401789			predicted exon	18.8
70	456952		Hs.301469	ESTs	18.8
70	439739	Al199391	Hs.124464	ESTs	18.8 18.8
	437974 427490	T74445 Z95152	Hs.5957 Hs.178695	Homo sapiens clone 24416 mRNA sequence mitogen-activated protein kinase 13	18.8
	443482	AW188093	Hs.250385	ESTs	18.8
	411420	BE390652		gb:601286820F1 NIH_MGC_44 Homo sapiens cDNA	18.8
75	435196	F35675	Hs.188128	ESTs, Moderately similar to ALUB_HUMAN [III ALU	18.8
	417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain family 2	18.8
	413531	AL036958	Hs.75416	DAZ associated protein 2	18.7
	428981	BE313077	Hs.93135	ESTs	18.7
80	421598	AW630942	Hs.106061	RD RNA-binding protein	18.7 18.7
30	443907 406754		Hs.9963 Hs.75922	TYRO protein tyrosine kinase binding protein brain protein I3	18.7
	400754	rvvii i LL	0324	predicted exon ·	18.7
	442638	AI088742	Hs.134713	ESTs	18.7
	434169		Hs.179724	ESTs	18.7

	424426	AASSECSE	Un occur	rete.	18.7
	424126 408473	AA335635 BE259039	Hs.96917 Hs.129953	ESTs Ewing sarcoma breakpoint region 1	18.7
	401962	01233033	15.123333	predicted exon	18.7
	447326	AW002252	Hs.201395	ESTs	18.7
5	459053	AI807052	Hs.210361	ESTs	18.7
	403362			predicted exon	18.7
	427697	T18997	Hs.180372	BCL2-like 1	18.7
	402061	H83363	Hs.109571	translocase of inner mitochondrial membrane 10 (yeast)	18.7
10	433785	BE044593	Hs.112704	ESTs	18.7 18.6
10	405423 429259	AA420450	Hs.292911	predicted exon ESTs	18.6
	444071	A1627808	Hs.110524	ESTs .	18.6
	410512	AA085603	Hs.250570	ESTs	18.6
	440376	A1024452	Hs.236816	ESTs	18.6
15	457353	X65633	Hs.248144	melanocortin 2 receptor (adrenocorticotropic hormone)	18.6
	432749	NM_014438	Hs.278909	Interleukin-1 Superfamily e	18.6
	415502	F12920	Hs.165575	ESTs	18.6
	407891	AA486620	Hs.41135	endomucin-2	18.6 18.6
20	455910	Z43712	II. 474004	gb:HSC1JA121 normalized infant brain cDNA Homo s	18.6
20	426716	NM_006379 H93281	Hs.171921 Hs.10710	sema domain, immunoglobulin domain (lg), short basic hypothetical protein FLJ20417	18.6
	444246 428125	AA393071	Hs.182579	leucine aminopeptidase	18.6
	406457	77000011	15.106015	predicted exon	18.5
	446625	Al333070	Hs.156141	ESTs	18.5
25	423334	AK000906	Hs.127273	hypothetical protein FLJ10044	18.5
	423103	AA322029		gb:EST24685 Cerebellum II Homo sapiens cDNA 5' en	18.5
	443549	T89608	Hs.16601	ESTs	18.5
	419299	Al311085	Hs.62406	Homo sapiens cDNA: FLJ22573 fis, done HSI02387	18.5 18.5
30	411942	AW877015	13- 446400	gb:QV2-PT0010-250300-096-f12 PT0010 Homo sapien ESTs, Weakly similar to non-receptor protein tyrosine k	18.5
30	442440 454574	BE464435 AW809109	Hs.146180	gb:MR4-ST0117-070100-027-a04 ST0117 Homo sapie	18.5
	454377	AA076811		gb:7B03C12 Chromosome 7 Fetal Brain cDNA Library	18.5
	422365	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic subunit of DNA p	18.5
	421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (achondroplasia, tha	18.5
35	420603	AB042636	Hs.4775	junctophilin 3	18.4
	401373			predicted exon	18.4
	402292			predicted exon	18.4
	444118	AA458542	Hs.10326	coatomer protein complex, subunit epsilon	18.4
40	408310	AW179023		gb:PM3-ST0036-170899-001-e08 ST0036 Homo sapia	18.4 18.4
40	411236	AW833752	Hs.252574	gb:QV4-TT0008-130100-077-b07 TT0008 Homo sapie ribosomal protein L10a	18.4
	431405 441408	A1470895 A1733249	Hs.126897	ESTs	18.4
	453994	BE180964	Hs.165590	ribosomal protein S13	18.4
	444518	Al160278	Hs.146884	ESTs	18.4
45	402407			predicted exon	18.4
	404270			predicted exon	18.4
	409103	AF251237	Hs.112208	XAGE-1 protein	18.4
	415198	AW009480	Hs.943	natural killer cell transcript 4	18.3
50	430771	BE387244	Hs.2664	flavin containing monooxygenase 4	18.3 18.3
20	432636 433504	AA340864	Hs.278562 Hs.3363	claudin 7 KIAA0214 gene product	18.3
	415606	NM_014874 W70022	113.3500	gb:zd51e10.r1 Soares_fetal_heart_NbHH19W Homo sa	18.3
	401401	8E047878	Hs.99093	Homo sapiens chromosome 19, cosmid R28379	18.3
	420758	AW297536	Hs.33053	ESTs	18.3
55	457520	AA553495	Hs.162264	ESTs .	18.3
	432323	AK001409	Hs.274356	hypothetical protein FLJ10547	18.3
	404750			predicted exon	18.3
	450645	AL117441 .	Hs.25264	DKFZP434N126 protein ESTs	18.3 18.3
60	445160 418461	Al299144 BE242781	Hs.150797 Hs.288037	Homo saplens cDNA FLJ12999 fis, clone NT2RP3000	18.3
50	401809	DLE92101	1 10.200001	predicted exon	18.3
	458121	S42416	Hs.74647	Human T-cell receptor active alpha-chain mRNA from	18.3
	435106	AA100847	Hs.193380	ESTs, Highly similar to AF174600 1 F-box protein Fbx	18.3
	448398	AW444655	Hs.170838	ESTS	18.3
65	428145	BE243327	Hs.182626	chromosome 22 open reading frame 5	18.2
	445302		Hs.12488	hypothetical protein FLJ10675	18.2
	407352		11- 40200	gb:yp76h12.r1 Soares fetal liver spleen 1NFLS Homo s	18.2
	413190		Hs.40368 Hs.113912	adaptor-related protein complex 1, sigma 2 subunit ESTs	18.2 18.2
70	436371 400965		NS.113312	predicted exon	18.2
	433427		Hs.171889	cholinephosphotransferase 1	18.2
	427504		Hs.191589	ESTs	18.2
	426759		Hs.21213	ESTs	18.2
76	423792	AW135866	Hs.245854	ESTs	18.2
75	406826		Hs.84298	CD74 antigen (invariant polypeptide of major histocom	18.1
	406659		Hs.277477	major histocompatibility complex, class I, C	18.1
	437453		Hs.181391	hypothetical protein DKFZp761G2113	18.1 18.1
	409276 449628		Hs.278429 Hs.197713		18.1
80	421043		Hs.89072	ESTs	18.1
	442344		Hs.301212		18.1
	448744		Hs.9469	phosphoinositol 3-phosphate binding protein-1	18.1
	416062	AA724811	Hs.74427	p53-induced protein	18.1
	414500	W24087	Hs.76285	DKFZP564B167 protein	18.1

			•		
		NM_001096	Hs.174140	ATP citrate lyase	18.1
	403964	40040044		predicted exon	18.1
	433217 427902	AB040914 Al809202	Hs.278628 Hs.208343	KIAA1481 protein ESTs, Weakly similar to cerebroside suffotransferase [H	18.1 18.1
5		Al863918	Hs.195078	ESTs Treaty similar to defendance sunot a raise as a pri	18.1
•	430826	U10061	Hs.248019	POU domain, class 4, transcription factor 3	18.1
	414195	BE263293	11022 100 10	gb:601144881F2 NIH_MGC_19 Homo sapiens cDNA	18.1
	416305	AU076628	Hs.79187	coxsackie virus and adenovirus receptor	18.1
	411088	BE247593	Hs.145053	ESTs	18.1
10	419407	AW410377	Hs.41502	Homo sapiens cDNA: FLJ21276 fis, clone COL01829	1B.1
	407938	AA905097	Hs.85050	phospholamban	18.1
	449360	A1540623	Hs.252720	ESTs	18.1
	417286	AA122237	Hs.81874	microsomal glutathione S-transferase 2	18.0
15	405515 439319	AW016401	Hs.233476	predicted exon ESTs	18.0 18.0
15	419387	BE379356	Hs.90107	cell membrane glycoprotein, 110000M(r) (surface antig	18.0
	414015		Hs.75693	prolytcarboxypeptidase (angiotensinase C)	18.0
	447778	BE620592	Hs.71190	ESTs	18.0
	435523	T62849	Hs.11090	high affinity immunoglobulin epsilon receptor beta sub	. 18.0
20	429230		Hs.198274	NADH dehydrogenase (ubiquinone) 1 beta subcomplex	18.0
	457822		Hs.150319	ESTs	18.0
	442424	Al342715	Hs.129569	ESTs, Moderately similar to 834087 hypothetical prote	18.0
	418394	AF132818	Hs.84728	Kruppel-like factor 5 (intestinal)	18.0
25	413477 405277	AI815825	Hs.48756	ESTs, Moderately similar to neuronal-STOP protein [M predicted exon	18.0 18.0
23	450192	AA263143	Hs.24596	RAD51-interacting protein	18.0
	442191	W95186	Hs.8136	endothelial PAS domain protein 1	18.0
	429490	Al971131	Hs.293684	ESTs, Weakly similar to alternatively spliced product u	18.0
	406744	AA554082	Hs.279860	hypothetical protein FLJ20030	17.9
30	425205	NM_005854	Hs.155106	receptor (calcitonin) activity modifying protein 2	17.9
	414387	AL043148	Hs.186257	ESTs	17.9
	411811	AW864370		gb:PM4-SN0016-100500-004-h09 SN0016 Homo saple	17.9
	433882	U90441	Hs.3622	procollagen-proline, 2-oxoglutarate 4-dioxygenase (pro	17.9
35	414333	BE274897		gb:601122959F1 NIH_MGC_20 Homo sapiens cDNA predicted exon	17.9 17.9
55	403747 435542	AA687376	Hs.269533	ESTs	17.9
	403093	771301370	113.203330	predicted exon	17.9
	412088	AI689496	Hs.108932	ESTs	17.9
	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	17.9
40	404763	_		predicted exon	17.9
	454633	AW811380		gb:lL3-ST0143-290999-019-D05 ST0143 Homo sapien	17.9
	440788	A1806594	Hs.128577	ESTs	17.9
	411800	N39342	Hs.5184	TH1 drosophila homolog	17.9
45	441361	BE263308	Hs.7797	TERF1 (TRF1)-interacting nuclear factor 2	17.8
43	422033 405333	AW245805	Hs.110903	claudin 5 (transmembrane protein deleted in velocardiof predicted exon	17.8 17.8
	408297	R17710	Hs.113314	ESTs .	17.8
	403036		18.110014	predicted exon	17.8
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatosis 1)	17.8
50	417091	AA193283	Hs.291990	ESTs	17.8
	440789	AB007857	Hs.7416	KIAA0397 gene product	17.8
	438397	AA806478	Hs.123206	ESTs	17.8
	435948	AA702675	Hs.114135	ESTs	17.8
55	450273 435969	AW296454 W85773	Hs.24743 Hs.191386	hypothetical protein FLJ20171 ESTs	17.8 17.8
55	427031	AA397601	Hs.125147	ESTs	17.8
	454505	AW801365		gb:IL5-UM0067-240300-050-a01 UM0067 Homo sapi	17.8
	403447			predicted exon	17.8
	433297	AV658581	Hs.282633	ESTs	17.8
60	443326	BE156494	Hs.188478	ESTs	17.8
	448283	Al340462	Hs.182979	ribosomal protein L12	17.8
	458067	AA393603	Hs.36752	Homo sapiens cDNA: FLJ22834 fis, clone KAIA4314	17.8
	452359	BE167229	Hs.29206	Homo sapiens clone 24659 mRNA sequence	17.8
65	434098 450911	AA625499 AA011586	Hs.272097	gbtaf69g08.r1 Soares_NhHMPu_S1 Homo sapiens cDN ESTs	17.8 17.7
UJ	410342	R31350	Hs.743	Fc fragment of IgE, high affinity I, receptor for; gamma	17.7
	407082	Z47055	12.710	qb:Human partial cDNA sequence, famesyl pyrophosph	17.7
	415271	X94232	Hs.78335	microtubule-associated protein, RP/EB family, member	17.7
	417413	AA197072	Hs.86092	Human DNA sequence from clone RP11-243J16 on chr	17.7
70	408937	AA210734	Hs.291386	ESTs	17.7
	433459	AA593498	11. 44-46-	gb:nn27b05.s1 NCI_CGAP_Gas1 Homo sapiens cDNA	17.7
	459536	AI254723	Hs.145496	ESTs	17.7
	428500	AI815395	Hs.184641	delta-6 fatty acid desaturase	17.7
75	433463 406537	R41963	Hs.4197	ESTs predicted exon	17.7 17.7
. 5	410003	AA079487		gb:zm97f08.s1 Stratagene colon HT29 (937221) Homo	17.7
	440857	AA907808	Hs.135556	ESTs	17.7
	451072		Hs.117929	ESTs	17.7
00	418693		Hs.87409	thrombospondin 1	17.7
80	443624		Hs.9651	related RAS viral (r-ras) oncogene homolog	17.6
	422626		Hs.118786	metaliothionein 2A	17.6
	410756		Hs.66159	KIAA1399 protein	17.6
	436621 453317		Hs.132929 Hs.41696	ESTs keratin, hair, acidic,1	17.6 17.6
	433317	MM_OOZZII	113.41030	NCIQUI, IGU, GUIUN, I	17.0

	450000			till bemeeken and to 0	
	456828 421486	AF156889	Hs.148427	LIM homeobox protein 3	17.6
	428834	AW408800 AW899713	Hs.104859 Hs.10338	hypothetical protein DKFZp762E1312  · ESTs	17.6 17.6
	451419	R36309	Hs.174369	EST	17.6
5	448413	Al745379	Hs.42911	ESTs .	17.6
	424323	AA338791	Hs.146763	nascent-polypeptide-associated complex alpha polypept	17.6
	423943	AF163570	Hs.135756	polymerase (DNA-directed) kappa	17.6
	439423	BE536678	Hs.147099	ESTs	17.6
1Λ	434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mRNA	17.6
10	408246	N55669	Hs.43946	L13 protein	17.6
	441579 420867	AW468847	Hs.127194 Hs.100002	ESTs HSPC162 protein	17.5 17.5
	453680	NM_014183 AL079647	Hs.14485	ESTs	17.5
	400202	742010041	110.11100	predicted exon	17.5
15	410768	AF038185	Hs.66187	Homo sapians clone 23700 mRNA sequence	17.5
	409932	Al376750	Hs.57600	adaptor-related protein complex 1, sigma 1 subunit	17.5
	425563	AF084199	Hs.299837	ESTs	17.5
	440475	AI807671	Hs.128343	ESTs	17.5
20	452767	AW014195	Hs.61472	ESTs, Weakly similar to unknown [S.cerevisiae]	17.5
20	410570	Al133096	Hs.64593	ATP synthase, H+ transporting, mitochondrial F1F0, su	17.4
	419600	AA448958	Hs.91481	NEU1 protein	17.4
	419588 428975	AI347205 NM_004672	Hs.91375 Hs.194694	Human clone 23614 mRNA sequence mitogen-activated protein kinase kinase kinase 6	17.4 17.4
	448928	Al350260	Hs.5384	Homo sapiens cDNA FLJ11743 fis, clone HEMBA100	17.4
25	403924	74000200	110.0001	predicted exon	17.4
	419889	AA251600		gb:zs10d12.rf NCI_CGAP_GCB1 Homo sapiens cDNA	17.4
	405023	AW408800	Hs.104859	hypothetical protein DKFZp762E1312	17.4
	426065	N32049		gb:yw96g08.s1 Soares_placenta_8to9weeks_2NbHP8to	17.4
20	453199	Al336266	Hs.301854	Homo sapiens PRO0412 mRNA, complete cds	17.4
30	455132	AW857955		gb:PM0-CT0325-151299-002-A12 CT0325 Homo sapi	17.4
	442932	AA457211	Hs.8858	bromodomain adjacent to zinc finger domain, 1A	17.4
	432065	AA401039	Hs.2903	protein phosphatase 4 (formerly X), catalytic subunit	17.3 17.3
	444652 417935	BE513613 R53697	Hs.11538 Hs.170044	actin related protein 2/3 complex, subunit 1A (41 kD) ESTs	17.3
35	430050	AA430993	Hs.227913	APIS-like 1	17.3
55	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn substrate 1	17.3
	425996	W67330	Hs.81256	S100 calcium-binding protein A4 (calcium protein, calv	17.3
	416964	D87467	Hs.80620	guanine nucleotide exchange factor for Rap1; M-Ras-re	17.3
40	437418	AI478954	Hs.59459	ESTs	17.3
40	447255	AI884908	Hs.158607	ESTs	17.3
	402203	*********		predicted exon	17.3
	417611	AW993983	Lie 410070	gb:RC1-BN0035-130400-013-a04 BN0035 Homo sapie	17.3 17.3
	426560 446163	AA381661 AA026880	Hs.119878 Hs.25252	ESTs Homo sapiens cDNA FLJ13603 fis, clone PLACE1010	17.3
45	445017	AI205493	Hs.176860	ESTs	17.3
	438658	Al222068	Hs.123571	ESTs	17.3
	442238	AW135374	Hs.270949	ESTs	17.3
	443195	BE148235	Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone NT2RP3002	17.3
~0	442609	AL020996	Hs.8518	selenoprotein N	17.2
50	416591	AA091976	Hs.79387	proteasome (prosome, macropain) 26S subunit, ATPase	17.2
	403674			predicted exon	17.2
	430514	AA318501	Hs.241587	megakaryocyte-enhanced gene transcript 1 protein	17.2 17.2
	411696 434560	AW857404 R13052	Hs.3964	gb:CM3-CT0313-291199-046-c11 CT0313 Homo saple Homo saplens clone 24877 mRNA sequence	17.2
55	422627	BE336857	Hs.118787	transforming growth factor, beta-induced, 68kD	17.2
55	414364	D38521	Hs.75935	KIAA0077 protein	17.2
	409119	AA531133	Hs.4253	G protein-coupled receptor 44	17.2
	425640	U34051	Hs.299204	ESTs, Highly similar to CD5S_HUMAN CYCLIN-DE	17.2
<b>C</b> O	436044	BE247571	Hs.15627	Nit protein 2	17.2
60	401657			predicted exon	17.2
	449763	AI822112	Hs.118241	ESTS	17.2
	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	17.2 17.2
	449636 444958	AJ656608 AW292643	Hs.281328 Hs.167047	ESTs ESTs	17.2
65	429978	AA249027	Hs.241507	ribosomal protein S6	17.2
-	453043	AW136440	Hs.224277	ESTs	17.2
	458640	AI284935		gb:qk55g09.x1 NCI_CGAP_Co8 Homo sapiens cDNA	17.1
	456329	T41418		gb:ph1h3_19/1TV Outward Alu-primed hncONA librar	17.1
70	414839	X63692	Hs.77462	DNA (cytosine-5-)-methyltransferase 1	17.1
70	403662			predicted exon	17.1
	411651	AW855392		gb:CM3-CT0275-191099-024-e12 CT0275 Homo saple	17.1
	404097 447252	R90916		predicted exon gb:yn01e10.r1 Soares adult brain N2b4HB55Y Homo s	17.1 17.1
	430024	A1808780	Hs.227730	integrin, alpha 6	17.1
75	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob disease, Gerst	17.1
	444558	AW181975	Hs.165892	ESTs	17.1
	420869	X58964	Hs.123638	regulatory factor X, 1 (influences HLA class II expressi	17.1
	448812	H30775	Hs.22140	BM88 antigen	17.0
οΛ	431777	AA570296	Hs.105470	found in inflammatory zone 1	17.0
80	422007	AI739435	Hs.39168	ESTs	17.0
	403051			predicted exon	17.0 17.0
	402427 417408	F17211	Hs.86092	predicted exon  Human DNA sequence from clone RP11-243J16 on chr	17.0
	450598	AF151076	Hs.25199	hypothetical protein	17.0
	.50000				

	421121	AA459028	Hs.86228	TRIAD3 protein	17.0
	458488	AL040565	Hs.209544	ESTs	17.0
	417158	AW965223	Hs.110062	ESTs, Wealty similar to ACR3_HUMAN 30 KD ADIP	17.0
			Hs.6527	G protein-coupled receptor 56	17.0
5	439318	AW837046			
J	428758	AA433988	Hs.98502	Homo sapiens cDNA FLJ14303 fis, clone PLACE2000	17.0
	447572	A1631546	Hs.159732	ESTs .	17.0
	434434	AA633516	Hs.157201	ESTs	17.0
	409994	D86864	Hs.57735	acetyl LDL receptor; SREC	17.0
	408927	AW295650	Hs.255453	ESTs	17.0
1Λ					
10	439093	AA534163	Hs.5476	serine protease inhibitor, Kazal type, 5	17.0
	454466	AA984138	Hs.279895	Homo sapiens mRNA for KIAA1578 protein, partial od	17.0
	426996	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone HEP03447,	17.0
	436659	Al217900	Hs.144464	ESTs	17.0
	422731	AL138411		gb:DKFZp434A1229_r1 434 (synonym: htes3) Homo s	17.0
15			U- 100702		17.0
13	429294	AA095971	Hs.198793	KIAA0750 gens product	
	432847	BE266941	Hs.279554	proteasome (prosome, macropaln) 26S subunit, non-AT	16.9
	416977	AW130242	Hs.293476	ESTs	16.9
	406827	AA971409	Hs.84298	CD74 antigen (invariant polypeptide of major histocom	16.9
	453758	U83527		gb:HSU83527 Human fetal brain (M.Lovett) Homo sap	16.9
20			Un 405422	ESTs	16.9
20	431314	AI732204	Hs.105423		
	423185	BE299590	Hs.125078	ornithine decarboxylase antizyme 1	16.9
	435086	AW975243	Hs.122596	ESTs	16.9
	447383	N24231		gb:yx22a11.r1 Soares melanocyte 2NbHM Homo sapie	16.9
	456251	R13326	Hs.21303	ESTs	16.9
25					16.9
43	456327	H68741	Hs.38774	ESTS	
	450594	N31036		gb:yx51g04.r1 Soares melanocyte 2NbHM Homo saple	16.9
	428177	AA423967	Hs.178113	ESTs, Moderately similar to kinesin like protein 9 (M.m.	16.9
	453250	A1346520	Hs.121619	chromosome 11 open reading frame 15	16.9
	418294	AF061739	Hs.83954	protein associated with PRK1	16.9
30					16.9
JU	446546	BE167687	Hs.156528	ESTs	
	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone COLF6967	16.9
	455993	BE179085		gb:RC0-HT0613-140300-021-d06 HT0613 Homo sapie	16.9
	459375	BE251770		gb:601112470F1 NIH_MGC_16 Homo sapiens cDNA	16.9
	454803	AW860148		gb:RC0-CT0379-290100-032-b10 CT0379 Homo sapie	16.9
35			Hs.259558		16.9
55	445474	Al240014	R5.200000	ESTs	
	443198	A1039813		gb:ox49d06.x1 Soares_total_fetus_Nb2HF8_9w Homo	16.9
	441557	AW452647	Hs.270482	ESTs	16.9
	420206	M91463	Hs.95958	solute carrier family 2 (facilitated glucose transporter),	16.9
	442202	BE272862	Hs.106534	Homo sapiens cDNA: FLJ22625 fis, clone HSI06009	16.9
40			110.100007		16.9
40	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo sapie	
	419355	AA428520	Hs.90061	progesterone binding protein	16.9
	452975	M85521	Hs.69469	dendritic cell protein	16.9
	432525	AI796096	Hs.109414	ESTs	16.8
	453718	AL119317	Hs.120360	phospholipase A2, group VI (cytosolic, calcium-indepe	16.8
45					16.8
43	437270	R18087	Hs.11282	ESTs, Weakly similar to cleft lip and palate transmemb	
	408007	AW135965	Hs.246783	ESTs	16.8
	450954	A1904740	Hs.25691	receptor (calcitonin) activity modifying protein 3	16.8
	402958			predicted exon	16.8
	445656	W22050	Hs.21299	ESTs, Weakly similar to AF151840 1 CGI-82 protein [H	16.8
50					16.8
50	410684	AA088500	Hs.170298	ESTs	
	437669	Al358105	Hs.123164	ESTs, Weakly similar to match to ESTs AA667999 [H.	16.8
	447869	AW139113	Hs.164307	ESTs	16.8
	458025	Al275406		gb:gl63c10.x1 Soares_NhHMPu_S1 Homo sapiens cDN	. 16.8
	445614	AV660763	Hs.110675	apolipoprotein C-IV	16.8
55	454610	AW810224		gb:MR4-ST0125-021199-017-e07 ST0125 Homo sapie	16.8
			11- 00407		
	449303	AK001495	Hs.23467	hypothetical protein FLJ10633	16.8
	422105	A1929700	Hs.111680	endosulfine alpha	16.8
	444788	AI871122	Hs.202821	ESTs	16.8
	414057	AI815559	Hs.75730	signal recognition particle receptor ('docking protain')	16.8
60	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OVARC1000	16.8
00					16.8
	433379	AA586368	Hs.190232	ESTs	
	441552	AA937975		gb:oc08e12.s1 NCI_CGAP_GCB1 Homo sapiens cDN	16.8
	403582			predicted exon	16.8
	433871	W02410	Hs.205555	ESTs	16.8
65	439509		Hs.58314	ESTs	16.8
00	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	16.8
	430129	BE301708	Hs.233955	hypothetical protein FLJ20401	16.8
	401465			predicted exon	16.8
	448913	AA194422	Hs.22564	myosin VI	16.8
70	410261	AF145713	Hs.61490	schwannomin interacting protein 1	16.8
. •				paxilin	16.7
	421199		Hs.102497		
	450489	Al697990	Hs.224375	ESTs	16.7
	410186	AW602528		gb:RCS-BT0562-260100-011-A02 BT0562 Homo sapi	16.7
	447224	BE617125		gb:601441664F1 NIH_MGC_65 Homo sapiens cDNA	16.7
75	403010			predicted exon	16.7
		•			16.7
	404881	40046445	11- 10000	predicted exon	
	445572		Hs.189654	ESTs	16.7
	419440	AB020689	Hs.90419	KIAA0882 protein	16.7
	443406	AI056238	Hs.143316	ESTs	16.7
80	457901		Hs.250497	ESTs, Highly similar to dJ745C22.1 [H.sapiens]	16.7
					16.6
	448364		Hs.16561	HSPC141 protein	
	407239		Hs.67846	leukocyte immunoglobulin-like receptor, subfamily 8 (	16.6
	401847			predicted exon	16.6
	429523	AK000788	Hs.205280	Homo sapiens cDNA FLJ20781 fis, clone COL04235	16.6

	432845	AI989751	Hs.150378	ESTs	16.6
	400246			predicted exon	16.6
	404971			predicted exon	16.6
_	422954	AW998605	Hs.32399	ESTs, Weakly similar to Similar to Ena-VASP like prot	16.6
5	415042	NM_006759	Hs.77837	UDP-glucose pyrophosphorylase 2	16.6
	432201	AI538613	Hs.135657	ESTs	16.6
	456993	AL134577	Hs.200302	ESTs	16.6
	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgranulin A)	16.6
••	444060	AA340277	Hs.10248	Homo sapiens cDNA FLJ20167 fis, clone COL09512	16.6
10	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epithelial)	16.6
	448199	AI953278	Hs.170557	ESTs	16.6
	443422	R10288	Hs.301529	ESTs	16.6
	401117			predicted exon	16.6
	400613			predicted exon	16.6
15	431214	AA294921	Hs.250811	v-rat simian leukemia viral oncogene homolog B (ras re	16.6
	431649	AL133077	Hs.266746	Homo sapiens cDNA: FLJ22615 fis, clone HSi05118	16.5
	421335	X99977	Hs.103505	ARS component B	16.5
	427154	AL137262	Hs.288991	Homo sapiens cDNA: FLJ22523 fis, clone HRC12507	16.5
00	401010			predicted exon	16.5
20	436678	BE512828	Hs.5273	NADH dehydrogenase (ubiquinone) Fe-S protein 3 (30k	16.5
	401589			predicted exon	16.5
	402538			predicted exon	16.5
	430478	NM_014349	Hs.241535	TNF-inducible protein CG12-1	16.5
25	437623	D63880	Hs.5719	chromosome condensation-related SMC-associated pro	16.5
25	401244			predicted exon	16.5
	415167	AA160784	Hs.26410	ESTs	16.5
	438291	BE514605	Hs.289092	Homo sapians cDNA: FLJ22380 fis, clone HRC07453,	16.5
	405183			predicted exon	16.5
20	436480	AJ271643	Hs.87469	putative acid-sensing Ion channel	16.5
30	456691	Al023428	Hs.205696	ESTs	16.5
	418332	R34976	Hs.78293	ESTs	16.5
	446052	AA358760		gb:EST67699 Fetal lung II Homo sapiens cDNA 5' end	16.5
	444859	AW449137	Hs.157487	ESTs	16.5
25	437192	AW975786	Hs.75355	ubiquitin-conjugating enzyme E2N (homologous to yea	16.5
35	400891			predicted exon	16.5
	448372	AW445166	Hs.170802	ESTs	16.5
	425798	AA364002		gb:EST74529 Pineal gland II Homo sapiens cDNA 5' en	16.5
	459253	AL157476	Hs.32913	Homo sapiens mRNA; cDNA DKFZp761C082 (from c	16.5
40	420746	AW195932	Hs.197488	ESTs	16.4
40	414717	BE271039	Hs.77060	proteasome (prosome, macropain) subunit, beta type, 6	16.4
	400727		11- 440054	predicted exon	16.4
	422691	NM_003365	Hs.119251	ubiquinol-cytochrome c reductase core protein I	16.4
	405639	DE000504		predicted exon	16.4
45	414444	BE298594		gb:601119754F1 NIH_MGC_17 Homo saplens cDNA	16.4
43	456146	AL034349	Hs.79005	protein tyrosine phosphatase, receptor type, K	16.4
	414610	BE388044	11- 000400	gb:601283747F1 NIH_MGC_44 Homo sapiens cDNA	16.4
	414267	AL078459	Hs.289109	dimethylarginine dimethylaminohydrolase 1	16.4
	401268			predicted exon	16.4
50	403613	DE000470		predicted exon gb:601150419F1 NIH_MGC_19 Homo sapiens cDNA	16.4 16.4
50	414203	BE262170	Hs.251928		16.4
	454315	AW373564	Hs.8236	nuclear pore complex interacting protein ESTs	16.4
	452114 404638	N22687	NS.0230	predicted exon	16.4
		•		predicted exon	16.3
55	404600 448855	AF070574	Hs.22316	Homo sapiens clone 24819 mRNA sequence	16.3
33	406629	AW277078	Hs.181165	eukaryotic translation elongation factor 1 alpha 1	16.3
	450957	BE515202	Hs.21497	Homo sapiens mRNA for FLJ00042 protein, partial cds	16.3
	449966	H60542	Hs.37848	ESTs	16.3
	402585	1100372	16.01010	predicted exon	16.3
60	436008	AI078428	Hs.58785	ESTs	16.3
•	401492	74070120	12.00.00	predicted exon	16.3
	412288	NM_003005	Hs.73800	selectin P (granule membrane protein 140kD, antigen C	16.3
	405088			predicted exon	16.3
	437345	BE259522	Hs.5556	NADH dehydrogenase (ubiquinone) 1, alpha/beta subco	16.3
65	432280	BE440142	Hs.2943	signal recognition particle 19kD	16.3
-	419596	BE379320	Hs.91448	MKP-1 like protein tyrosine phosphalase	16.3
	428801	AW277121	Hs.254881	ESTs	16.3
	431394	AK000692	Hs.252351	HERV-H LTR-associating 2	16.3
	452998	BE019681	Hs.6019	Homo saniens cDNA: FLJ21288 fis, clone COL01927	16.3
70	439938	Al147392	Hs.124607	ESTs	16.3
	418844	M62982	Hs.1200	arachidonate 12-lipoxygenase	16.3
	.446081	AA972412	Hs.13755	f-box and WD-40 domain protein 2	16.3
	443534	AI076123		gb:oy92e04x1 Soares_fetal_liver_spleen_1NFLS_S1 H	16.3
	459510	AA076706		gb:7801802 Chromosome 7 Fetal Brain cDNA Library	16.3
75	450517	AI523755	Hs.59236	ESTs, Weakly similar to B35049 ankyrin 1, erythrocyte	16.3
	451938	AI354355	Hs.16697	down-regulator of transcription 1, TBP-binding (negativ	16.3
	454478	AW805749		gb:QV1-UM0105-180400-162-f10 UM0105 Homo sap	16.2
	407214	AA412048	Hs.279574	CGI-39 protein; cell death-regulatory protein GRIM19	16.2
~ ~	406580			predicted exon	16.2
80	409452	BE336714	Hs.289271	cytochrome c-1	16.2
	416841	N33878	Hs.249495	heterogeneous nuclear ribonucleoprotein A1	16.2
	458710	AV660856		gb:AV660856 GLC Homo sapiens cDNA clone GLCG	16.2
	450657	AK001579	Hs.25277	hypothetical protein FLJ21065	16.2
	- 404230			predicted exon	16.2

	439471	W69839	Hs.58033	ESTs	16.2
	400848			predicted exon	16.2
	428797	AA496205	Hs.193700	Homo sapiens mRNA; cDNA DKFZp58610324 (from c	16.2
_	416272	AA178882		gb:zp38b09.r1 Stratagene muscle 937209 Homo sapiens	16.2
5	444465	Al206592	Hs.143843	ESTs	16.2
	431257	AF039597		gb:Homo sapiens Ku86 autoanfigen related protein 1 (K	16.2
	447775	BE179318		gb:RC1-HT0615-290300-021-g05 HT0615 Homo sapie	16.2
	403833			predicted exon	16.2
	444140	AV648089	Hs.282383	ESTs	16.2
10	445102	AW168067	Hs.252956	ESTs	16.2
	416475	T70298		gb:yd26g02.s1 Soares fetal liver spleen 1NFLS Homo s	16.2
	430783	AW971248	Hs.291289	ESTs, Wealty similar to ALU1_HUMAN ALU SUBFA	16.2
	414070	AW963783		gb:EST375856 MAGE resequences, MAGH Homo sap	16.2
	444283	Al138971	Hs.154636	ESTs	16.2
15	405599	X92715	Hs.3057	zinc finger protein 74 (Cos52)	16.2
	409427	AW389668		gb:RC2-ST0168-071299-013-f06 ST0168 Homo sapien	16.2
	409417	AA156247	Hs.295908	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFA	16.2
	435380	AA679001	Hs.192221	ESTs	16.2
•	406752	Al285598	Hs.217493	annexin A2	16.2
20	406096	F12200	Hs.5811	chromosome 21 open reading frame 59	16.2
	417551	Al816291	Hs.82273	hypothetical protein	16.2
	441252	AW360901	Hs.183047	ESTs, Weakly similar to unnamed protein product [H.s	16.2
	419608	AL037237	Hs.91586	transmembrane 9 superfamily member 1	16.1
0.5	438894	A1630819	Hs.300431	ESTs ·	16.1
25	451287	AK002158	Hs.26194	hypothetical protein FLJ11296	16.1
	412499	AW956916	Hs.11238	KIAA0622 protein; Drosophila "multiple asters" (Mast	16.1
	433355	AI808235		gb:wf44e01.x1 Soares_NFL_T_GBC_S1 Homo saplen	16.1
	416818	AI986408	Hs.204766	ESTs, Weakly similar to B48013 proline-rich proteogly	16.1
20	438765	AI031888	Hs.132594	ESTs .	16.1
30	424470	BE244261	Hs.5615	nuclear RNA export factor 1	16.1
	416194	H27114	Hs.301212	ESTs	16.1
	446702	R44518	Hs.143496	ESTs	16.1
	414222	AL135173	Hs.878	sorbitol dehydrogenase	16.1
25	443122	AI806656	Hs.209022	ESTs, Weakly similar to Pro-Pol-dUTPase polyprotein	16.1
35	448648	BE614345	Hs.159089	ESTs ,	16.1
	456394	W28506		gb:48f1 Human retina cDNA randomly primed sublibra	16.1
	445887	AI263105	Hs.145597	ESTs	16.1
	412332	AW937661	Hs.288324	Homo sapiens cDNA FLJ13283 fis, done OVARC1001	16.1
40	403912			predicted exon	16.1
40	441446	R66269	Hs.28714	ESTs	16.1
	403153	********		predicted exon	16.0
	444907	AW772596	Hs.148586	ESTs	16.0
	421946	R99629	Hs.109773	hypothetical protein FLJ20625	16.0
15	437513	AW410681	Hs.5648	proteasome (prosome, macropain) 26S subunit, non-AT	16.0
45	407752	AA573581	Hs.13328	ESTS	16.0
	447953	Al804218	Hs.209614	Homo sapiens cDNA: FLJ22343 fis, clone HRC06043	16.0
	425708	AK001342	Hs.14570	Homo sapiens cDNA: FLJ22530 fis, clone HRC12866	16.0
	421449	AA713491	Hs.291501	ESTs	16.0
50	418323	NM_002118	Hs.1162	major histocompatibility complex, class II, DM beta	16.0
50	447787	BE620108	Un 49447E	gb:601483015F1 NIH_MGC_69 Homo sapiens cDNA	16.0 16.0
	422716	Al702835	Hs.124475	ESTs	16.0
	443958	BE241880	Hs.10029	cathepsin C	16.0
	417908	AA207221 AA810131	Hs.123317	gb:zq55h04.s1 Stratagene neuroepithelium (937231) Ho	16.0
55	438542		Hs.149609	ESTS	16.0
55	400288 456825	X06256 H67220	Hs.146406	integrin, alpha 5 (fibronectin receptor, alpha polypeptid ritrilase 1	16.0
		NM_000427	Hs.251680	loricrin	16.0
	431360 414266		NS.251000		16.0
	440571	BE267834 AA904461	Hs.130798	gb:601124428F1 NIH_MGC_8 Homo sapiens cDNA c ESTs	16.0
60	426075	AW513691	Hs.270149		16.0
oo	413488	BE144017	Hs.184693	transcription elongation factor B (SIII), polypeptide 1 (1	16.0
	446767	AJ380107	Hs. 158954	ESTs	16.0
	418008	W56044	Hs.211556	Homo sapiens cDNA: FLJ23378 fis, clone HEP16248	16.0
	404239	1420044	113.211330	predicted exon	16.0
65	458401	AW236939	Hs.172154	ESTs	16.0
05	412955	BE241849	Hs.75082	ras homolog gene family, member G (rho G)	15.9
	423072	Al792946	Hs.123116	solute carrier family 12 (sodium/potassium/chloride tran	15.9
	444954	AW247076	Hs.12163	eukaryotic translation initiation factor 2, subunit 2 (beta	15.9
	449023	Al623261	Hs.248875	ESTs	15.9
70	435729	BE048886	Hs.275017	EST	15.9
. •	438575	BE304709	Hs.146550	myosin, heavy polypeptide 9, non-muscle	15.9
	413047	H02209		gb:yj38c09.r1 Soares placenta Nb2HP Homo sapiens cD	15.9
	425997	AK000086	Hs.165948	hypothetical protein FLJ20079	15.9
	446863	AW614370	Hs.254620	ESTs	15.9
75	448564	AL044962	Hs.21453	Homo sapiens mRNA for inositol 1,4,5-trisphosphate 3	15.9
	455640	BE064059		gb:QV3-BT0296-010300-111-e04 BT0296 Homo sapie	15.9
	404345	AA730407	Hs.159156	protocadherin 11	15.9
	418512	AW498974	Hs.89981	diacylglycerol kinase, zeta (104kD)	15.9
	411551	AW851309		gb:IL3-CT0220-170200-067-C11 CT0220 Homo sapien	15.9
80	446726		Hs.209209	Homo sapiens cDNA FLJ11629 fis, clone HEMBA100	15.9
	410748	BE383816	Hs.136005	ESTs, Highly similar to bG115G20.2 [H.sapiens]	15.9
	449618		Hs.14366	Homo sapiens cDNA FLJ12819 fis, clone NT2RP2002	15.9
	429697		Hs.24605	ESTs	. 15.9
	424012		Hs.137569	turnor protein 63 kDa with strong homology to p53	15.9

	403151			predicted exon	15.8
	452363	A1582743	Hs.94953	ESTs, Highly similar to C1QC_HUMAN COMPLEME	15.8
	425971	AF135024	Hs.165296	kallikrein 13	15.8
_	432826	X75363	Hs.250770	kallikrein 15	15.8
5	431972	Al805145	Hs.191711	ESTs	15.8
	400269 404703	A1004403	U= 00000	predicted exon	15.8 15.8
	449335	AI904493 AW150717	Hs.99890 Hs.296176	polymerase (DNA directed), delta 1, catalytic subunit (1 STAT induced STAT inhibitor 3	15.8
	418443	NM_005239	Hs.85146	v-ets avian erythroblastosis virus E26 oncogene homolo	15.8
10	445773	H73456	Hs.13299	Homo sapiens mRNA; cDNA DKFZp761M0111 (from	15.8
	433782	AF090945		gb:Homo sapiens clone HQ0670	15.8
	406473	4 4 202 204	13- 400025	predicted exon	15.8
	420831 402939	AA280824	Hs.190035	ESTs predicted exon	15.8 15.8
15	405196			predicted exon	15.8
	452947	AW130413		gb:xd50f04.x1 NCI_CGAP_Gas4 Homo sapiens cDNA	15.8
•	414170	AA335996	Hs.3743	matrix metalloproteinase 24 (membrane-inserted)	15.8
	437133	AB018319	Hs.5460	KIAA0776 protein	15.8
20	458356	AI024855	Hs.131575	ESTs	15.8 15.8
20	407857 405687	Al928445	Hs.92254	hypothetical protein FLJ20163 predicted exon	15.8
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molecule (CO31 antig	15.8
	408662	AW247699	Hs.105897	ESTs	15.7
25	448338	Al492857		gb:th72h08.x1 Soares_NhHMPu_S1 Homo sapiens cDN	15.7
25	402694	Alamaraar	U- 025075	predicted exon	15.7
	430224 458792	AW675175 N56666	Hs.235975	hypothetical protein DKFZp434D0412 gb:yw75e02.r1 Soares_placenta_8to9weeks_2NbHP8to	15.7 15.7
	402944	1455555		predicted exon	15.7
	422675	BE018517	Hs.119140	eukaryolic translation initiation factor 5A	15.7
30	408661	AW247625		gb:2820094.5prime NIH_MGC_7 Homo saptens cDNA	15.7
	423238	AA323569	Hs.280482	ESTs	15.7
	421517 429865	AB018352	Hs.105399	KIAA0809 protein	15.7 15.7
	440815	AB023217 AW071945	Hs.225968 Hs.7436	KIAA1000 protein putative acyltransferase	15.7
35	400634	ANOI 1343	113.7 400	predicted exon	15.7
	451034	AL050341	Hs.25846	zinc metalloproteinase, STE24 (yeast, homolog)	15.7
	457571	Al375726	Hs.279918	hypothetical protein	15.7
	450105	BE281124	Hs.288013	similar to yeast BET3 (S. cerevisiae)	15.7
40	407464 439465	AJ276396 AF086285		gb:Homo sapiens mRNA for matrix extracellular phosp gb:Homo sapiens full length insert cDNA clone ZD47B	15.7 15.7
70	451837	T92157	Hs.16970	ESTs	15.7
	435313	Al769400	Hs.189729	ESTs	15.7
	402738			predicted exon	15.7
45	432966	AA650114	11 400000	gb:ns92h09.s1 NCI_CGAP_Pr3 Homo sapiens cDNA c	15.7
43	457666 401269	AW470302	Hs.129663	ESTs predicted exon	15.7 15.7
	427509	M62505	Hs.2161	complement component 5 receptor 1 (C5a ligand)	15.7
	418846	AI821602	Hs.115127	ESTs	15.6
٠.	448891	AI587332	Hs.209115	ESTs	15.6
50	445930	AF055009	Hs.13456	Homo sapiens clone 24747 mRNA sequence	15.6
	421254	AK001724	Hs.102950	coat protein gamma-cop	15.6 15.6
	447073 445438	AW204821 AB014578	Hs.157726 Hs.12707	ESTs KIAA0678 protein	15.6
	432126	AA865239	Hs.55144	ESTs	15.6
55	424091	AF235097	Hs.139263	calcium channel, vollage-dependent, alpha 1F subunit	15.6
	440832	AI057548	Hs.128224	ESTs	15.6
	449228	AJ403107	Hs.148590	ESTs, Wealdy similar to AF208846 1 BM-004 (H.saple	15.6 15.6
	434253 459270	Al393345 Al039604	Hs.116215	ESTs gb:DKFZp434E2211_1 434 (synonym: htes3) Homo s	15.6
60	454425	AW300927	Hs.27192	hypothetical protein dJ1057B20.2	15.6
	412055	AA099907	Hş.271806	ESTs	15.6
	400837			predicted exon	15.6
	458866	BE616694	Hs.288042	Homo sapiens cDNA FLJ14299 fis, done PLACE1010 ESTs	15.6 15.6
65	417124 414376	BE122762 BE393856	Hs.25338 Hs.66915	ESTs, Weakly similar to 16.7Kd protein (H.sapiens)	15.6
05	418636	AW749855	113.00010	gb;QV4-BT0534-281299-053-c05 BT0534 Homo sapie	15.6
	454128	AL031259	Hs.41639	programmed cell death 2	15.6
	441074	AW500001	Hs.4783	Homo saplens cDNA: FLJ22035 fis, clone HEP08838	15.6
70	451742	177609	Hs.117970	ankyrin 2, neuronal	15.6
70	403687 431838	AI097229	Hs.217484	predicted exon ESTs	15.6 15.6
	402855	, 2001 <b>223</b>	1 13.2 17404	predicted exon	15.6
	449635		Hs.232150	ESTs	15.6
75	434392	AW983709	Hs.268051	ESTs	15.6
75	444301	AK000136	Hs.10760	hypothetical protein FLJ20129	15.6
	414973 428374		Hs.183994	gb:C19089 Human placenta cDNA (TFujiwara) Homo protein phosphatase 1, catalytic subunit, alpha isoform	15.5 15.5
	415745		Hs.150790	ESTs	15.5
00	432532		Hs.162246	ESTs	15.5
80	417112	AA193439		gb:zr41b09.s1 Soares_NhHMPu_S1 Homo sapiens cDN	15.5
	418101		Hs.98485	gap junction protein, beta 4 (connexin 30.3)	15.5
	453110 458606		Hs.225160	Homo sapiens cDNA FLJ13102 fis, clone NT2RP3002 gb:AJ239397 Uni-ZAP XR retinal pigment epithelium H	15.5 15.5
	436989		Hs.256155		15.5
				• •	

	407396	AF011757		gb:Homo sapiens RAGE binding protein (P12) mRNA,	15.5
	449684	AI659166	Hs.207144	ESTs	15.5
	454666	AW812994		gb:RC3-ST0186-230300-019-g02 ST0186 Homo sapien	15.5
_	430492	U15197	Hs.300803	Human histo-blood group ABO protein mRNA, partial	15.5
5	439460	AA836220	Hs.13774	ESTs	15.5
_	449231	BE410360		gb:601302340F1 NIH_MGC_21 Homo sapiens cDNA	15.5
	453060	AW294092	Hs.21594	ESTs	15.5
	416961	BE391476	Hs.80617	ribosomal protein S16	15.5
		AA860119		ESTs	
10	439988	AA000119	Hs.255976		15.5
IU	400917	4.404040		predicted exon	15.5
	424585	AA464840		gb:zx43h11.r1 Soares_total_fetus_Nb2HF8_9w Homo	15.5
	431029	BE392725	Hs.248571	Homo sapiens PAC clone RP5-1163J12 from 7q21.2-q3	15.5
	441680	AW444598	Hs.7940	RAP1, GTP-GDP dissociation stimulator 1	15.5
	437830	AB020658	Hs.5867	KIAA0851 protein	15.5
15	409479	BE163800	Hs.136912	ESTs	15.5
	409885	AW503068		gb:UI-HF-BP0p-aje-g-10-0-UI.r1 NIH_MGC_51 Homo	15.4
	459090	AA443323	Hs.107812	ESTs, Wealty similar to SPOP [H.sapiens]	15.4
	429324	AA488101	Hs.199245	inactivation escape 1	15.4
	403766	701100101		predicted exon	15.4
20		1150300	Un 7ECC2		
20	413970	U59309	Hs.75653	fumarate hydratase	15.4
	456674	BE266120	Hs.269358	ESTs	15.4
	417931	W95642	Hs.82961	trefoil factor 3 (intestinal)	15.4
	430125	U46418	Hs.233950	serine protease inhibitor, Kunitz type 1	15.4
25	452154	AW953265	Hs.271277	hypothetical protein from EUROIMAGE 363668	15.4
25	422984	W28614	Hs.75984	chorionic somatomammotropin hormone 2	15.4
	408649	BE242232	Hs.26045	protein tyrosine phosphatase, receptor type, A	15.4
	417497	AW402482	Hs.82212	CO53 antigen	15.4
	404666			predicted exon	15.4
_	456847	Al360456	Hs.37776	ESTs	15.4
30	426995	AA400646	Hs.221988	ESTs	15.4
50	445350	AF052112	Hs.12540	lysophospholipase I	15.4
			Hs.227571		15.4
	450214	BE439763		regulator of G-protein signalling 4	
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	446826	AK000626	Hs.16230	hypothetical protein FLJ20619	15.3
	441211	AW946155	Hs.7750	hypothetical protein AL133206	15.3
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			Un 231008		15.3
	449999	AI679421	Hs.231098 Hs.271663	ESTs, Highly similar to ALU4_HUMAN ALU SUBFA	
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AW809109 AW809112 AW809122 AW809126 AW809128 AW809133 AW809131 AW809113 AW809111 AW809132
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                                          AL039604 AL039497
            459270
                       969232_1
           TABLE 3C:
           Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of
65
                  human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
            Strand: Indicates DNA strand from which exons were predicted
            Nt_position: Indicates nucleotide positions of predicted exons
                                                     Nt position
            Pkev
                        Ref
                                     Strand
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                                                18944-19176
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                     9438381
                                  Pius
          401204
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                                  Minus
           403223
                      7630969
                                                 81529-81692
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                                                 180641-180822
                                                 133809-134099
           403273
                      8018055
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                                                 118369-118872
           403286
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	403348	7239527	Plus	13809-13968
	403359	8570207	Minus	108939-109229
_	403362	8571772	Plus	64099-64260
5	403447	9837821	Minus	159072-159387
	403508	7630898	Plus	5570-5719
	403582	8101186	Plus	18308-18458
	403613	8493504	Plus	81290-81465
4.0	403642	8699671	Plus	7062-7311
10	403662	5823349	Plus	58627-59062,59222-59548
	403674	7321642	Plus	104988-105623,107394-107590
	403587	7387384	Plus	9009-9534
	403695	3046276	Plus	168272-168514
	403703	4966380	Plus	83681-84042
15	403741	7630932	Minus	2833-3468
	403747	7658395	Minus	20493-20621
	403766	7229888	Plus	136283-136830
	403786	8083636	Minus	73028-73217
••	403796	8099896	Minus	75073-77664
20	403833	887461	Plus	13522-13664
	403852	7708872	Minus	124007-124202
	403861	7708966	Plus	58363-58649
	403912	7710730	Minus	72000-72290,72431-72700,72929-73199
~ -	403924	7711688	Minus	89369-89592 <sup>-</sup>
25	403964	7596976	Plus	178174-178300
	404034	8567760	Minus	44635-47010
	404067	3282162	Plus	1415-2071
	404097	7770701	Plus	55512-55781
••	404122	9796270	· Plus	90540-92977
30	404230	7981448	Minus	92934-93093
	404239	5002624	Plus	94841-95095
	404240	5002624	Minus	116132-116407,116653-116922
	404270	9828129	Minus	3649-3750,4161-4306,5962-6049,6849-6965
	404356	7630858	Minus	126433-126623
35	404600	8705107	Plus	118354-118444,118649-118792
	404601	8705107	Plus	128449-128693,129085-129249,130525-130733
	404638	9796751	Minus	99433-99528,100035-100161
	404656	7272179	Minus	18677-18993
40	404675	9797204	Minus	48532-48645,49808-49975,51088-51369,54944-55063
40	404727	8081050	Plus	115534-115747
	404750	7596836	Plus	181879-182198
	404763	7882612	Plus	50981-51392
	404767	7882827	Minus	23244-23759
	404828	6580415	Minus	26291-27253
45	404850	5420148	Minus	35145-35413,40635-41062
	404881	5931510	Minus	36360-36608
	404890	7329390	Plus	101280-101408
	404971	3212939	Minus	74585-75532
	405022	7330304	Plus	217163-217439
50	405028	7533974	Minus	110588-110847,110933-111115
	405071	7708797	Minus	11115-11552
	405088	8072518	Minus	115690-117621
	405133	8516055	Minus	28127-28288
	405138	8576241	Plus	90303-90516
55	405183	7209940	Plus	12335-12653
	405194	7230072	Plus	190465-190645,193346-193610
	405196	7230083	Minus	135716-135851
	405208	7230142	Plus	8068-8214
	405226	7248966	Plus	53547-54128
60	405227	6731245	Minus	22550-22802
	405256	7329310	Plus	. 26070-26309
	405277	3980473	Plus	23471-23572
	405307	3638954	Plus	39195-39429
	405311	3638954	Plus	46313-46496
65	405333	3165399	Plus	149905-150215
	405411	3451356	Minus	17503-17778,18021-18290
	405423	4753276	Plus	6162-6983
	405491	5801645	Plus	81857-82045
	405501	9211311	Minus	49085-49400,49565-49679,50117-50262
70	405515	9454624	Plus	37329-37469
	405545	1054740	Plus	118677-118807,119091-119296,121626-121823
	405580	4512267	Plus	169232-169647
	405586	5002511	Plus	38810-39017 .
~~	405600	5923640	Plus	26662-27225
75	405610	5757553	Minus	71907-72080
	405639	5091650	Plus	211184-211350
	405687	6249668	Minus	54787-54891,55844-55917
	405699	4165331	Plus	100727-100859
	405783	5738434	Minus	27238-27885
80	405867	6758731	Minus	74553-75173
	406086	7107817	Plus	9418-9573
	406124	9149714	Minus	1331-1774
	406130	9161404	Minus	32394-32498
	406140	9168231	Minus	49887-50219
				-

	406160	7144945	Plus	55498-56268
	406207	5923650	Minus	162607-162800
	406215	7342161	Plus	310-432
_	406268	6682695	Minus	6605-7072
5	406277	5686030	Minus	4759-5490
	406326	9212385	Plus	84508-84655
	406388	9256205	Plus	85153-85277
	406457	9755793	Plus	44966-45406
	406473	9795566	Minus	109669-109931
10	406537	7711478	Plus	32904-33017
	406571	7711622	Minus	65634-65912,66116-66596
	406580	7711838	Minus	96654-97640

15 TABLE 4A lists about 131 genes up-regulated in ovarian cancer compared to normal ovaries that are likely to be extracellular or cell-surface proteins. These were selected as for Table 3A, except that the ratio was greater than or equal to 10, and the predicted protein contained a PFAM domain that is indictive of extracellular localization.

TABLE 4A: ABOUT131 UP-REGULATED GENES ENCODING EXTRACELLULAR/CELL SURFACE PROTEINS, OVARIAN CANCER VERSUS NORMAL OVARY Pkey. Primekey
EX. Accr.: Exemplar Accession
UG ID: UniGene ID
Title: Unigene Title
PFAM domains
ratio: furner vs. pormet over:

20

~ -	ratio: tum	or vs. normal ova	ary	•		
25						
	Pkey	Ex. Accn	UGID	Tille	PFAM	ratio
	403077			predicted exon	fn3	- 15.0
	426535	AU077012	Hs.288582	ESTs, Weakly similar to ubiquitous TP	Kunitz_BPTI	14.9
	403089			predicted exon	fn3	14.9
30	457148	AF091035	Hs.184627	KIAA0118 protein	artiras	14.8
-	431176	AI026984	Hs.293662	ESTs	laminin_EGF;laminin_B;	14.8
	434293	NM 004445	Hs.3796	EphB6	fn3;pkinase;EPH_lbd	14.8
	408482	NM_000676	Hs.45743	adenosine A2b receptor	7tm_1	14.6
	428695	A)355647	Hs.189999	purinergic receptor (family A group 5)	7tm_1	14.5
35	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) ho	EGF	14.4
33						
	423732	AF058056	Hs.132183	solute carrier family 16 (monocarboxy	sugar_tr;MCT	14.3
	422125	NM_003459	Hs.111967	solute carrier family 30 (zinc transporte	Cation_efflux	14.2
	407483	NM_012368		(NONE)	7tm_1	14.2
40	446689	AW594695	Hs.167046	ESTs	7tm_1	14.1
40	410184	AW503667	Hs.59545	ring finger protein 15	zf-C3HC4;SPRY;zf-B_box	14.0
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermoly	fn3;vwa	14.0
	405448	Al015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp5	trypsin;sushi;CUB	14.0
	450684	AA872605	Hs.25333	interleukin 1 receptor, type II	ig	14.0
	406692	1.36607		gb:Homo sapiens (clone 22) pregnancy	ig	13.9
45	425549	U64863	Hs.158297	programmed cell death 1	ig	13.8
	452755	AW138937	Hs.213436	ESTs	cystatin	13.8
	427637	AK000816	Hs.179986	flotillin 1	Band_7	13.7
	424591	R55704	Hs.150968	hypocretin (orexin) receptor 1	7tm_1	13.7
	405024			predicted exon	TGF-beta;TGFb_propeptide	13.7
50	405285			predicted exon	A2M:A2M N	13.7
	412116	AW402166	Hs.784	Epstein-Barr virus induced gene 2 (lym	7tm_1	13.7
	420256	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascu	cadherin;Cadherin_C_term	13.6
	420511	AF052692	Hs.98485	gap junction protein, beta 4 (connexin 3	connexin	13.5
	448638	R17122	Hs.21639	nuclear protein, marker for differentiat	ig	13.4
55	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	EGF;DSL '	13.4
55	439285	AL133916	Hs.298998	ESTs	ig;pkinase;LRRNT;LRRCT	13.4
	424283	AA338246	Hs.301678	ESTs	E1-E2 ATPase:Hydrolase	13.3
•						13.3
	436233	Al742878	Hs.124116	ESTs	lg land	13.2
60	443859	NM_013409	Hs.9914	follistatin	kazal	
UU	410016	AA297977	Hs.57907	small inducible cytokine subfamily A (	IL8	13.2
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologo	IL8	13.2
	400242			predicted exon	Ephrin .	13.0
	429057	AF156557	Hs.194816	stomatin-like protein 1	Band_7;SCP2	12.9
15	438294	AI693753	Hs.143004	ESTs	E1-E2_ATPase;Hydrolase	12.9
65	458493	AV649408	Hs.282418	ESTs	RYDR_ITPR	12.8
	444181	AB033063	Hs.10491	KIAA1237 protein	fn3;ig;PH;RhoGEF	12.8
	422357	AF016272	Hs.115418	cadherin 16, KSP-cadherin .	cadherin	12.7
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	serpin	12.7
	407000	U12139		gb:Human alpha1(XI) collagen (COL1	TSPN;Collagen;COLFI	12.6
70	417064	W02903	Hs.15440	ESTs	lectin_c	12.6
	439389	AA318940	Hs.56004	ESTs	hemopexin;Peptidase_M10	12.6
	407786	AA687538	Hs.38972	tetraspan 1	transmembrane4	12.5
	410498	AA355749		gb:EST64459 Jurkat T-cells VI Homo	aa_permeases	12.5
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	vwd	12.5
75	422330	D30783	Hs.115263	epiregulin	EGF	12.5
	402425			predicted exon	ion_trans	12.4
	414875	H42679	Hs.77522	major histocompatibility complex, clas	lg la	12.2
	424239	M67439	Hs.143526	dopamine receptor D5	7tm. 1	12.2
	442622	NM_000435	Hs.8546	Notch (Drosophila) homolog 3	EGF;ank;notch	12.2
80	405368		10.0070	predicted exon	7tm_1	12.2
50	402406			predicted exon	Gal-bind_lectin	12.1
	426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteoge	TGF-beta;TGFb_propeptide	12.1
	426314	U82979	Hs.67846	leukocyte immunoglobulin-like recepto	ig	12.0
	416441	BE407197	r15.07 040	ab:601301552F1 NIH_MGC_21 Homo	SDF	12.0
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439710 47550\_1 AF086543 W96291 W96225 443296 56539\_2 AI765286 AW297086 BE568658 TABLE 4C 5 Pkey: Unique number corresponding to an Eos probeset Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495 Strand: Indicates DNA strand from which exons were predicted Nt\_position: Indicates nucleotide positions of predicted exons 10 Strand Nt\_position 400464 9929670 22074-22214 Plus 400834 8705192 Plus 121963-122288 402114 8318586 Plus 71578-71715 15 402172 143378-143671 8575911 Minus 10872-11123,12932-13048 402406 3970929 Plus 402425 9796347 Minus 50224-50395 146923-147222,147326-147628 403077 8954241 Plus 403089 8954241 Phrs 171964-172239 20 403691 88280-88463 7387384 Minus 405024 88500-88697 7107727 Plus 55744-55903,57080-57170,61478-61560 405285 6139075 Minus 405368 2104517 46055-47188 Plus 25 TABLE 5A lists about 685 genes down-regulated in ovarian cancer compared to normal ovaries. These were selected as for Table 3A, except that the numerator and denominator were switched, and the ratio was greater than or equal to 3.0 (i.e. 3-fold down-regulated in tumor vs. normal ovary). TABLE 5A: 685 DOWN-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY 30 Pkey: Primekey Ex. Accn: Exemplar Accession UG ID: UniGene ID Title: UniGene Title ratio: ration normal ovary vs tumor 35 ratio LIGID Pkey Ex. Acon Tifle 421013 mutated in colorectal cancers M62397 Hs.1345 ESTs, Weakly similar to Z141\_HUMAN ZINC FINGE 12.8 439360 AA448488 Hs.55346 D16815 Hs.37288 nuclear receptor subfamily 1, group 0, member 2 12.6 407644 40 424851 AA676441 Hs.119059 11.6 gb:RC1-CT0249-170200-025-h04 CT0249 Homo sapie 11.5 455056 AW853057 Hs.99886 complement component 4-binding protein, beta 11.3 420727 H75701 451617 C01056 Hs.168000 **ESTs** 10.0 predicted exon 9.9 401308 45 440987 AA911705 Hs.130229 9.7 9.7 409725 T40760 Hs.90459 **EST** Hs.78776 9.7 415752 BE314524 putative transmembrane protein 9.6 437690 AA804362 Hs.180544 **ESTs** 437787 AI908263 Hs.291625 9.5 50 459054 AW798466 Hs.82396 2',5'-oligoadenylate synthelase 1 9.2 9.2 435330 R16769 Hs.185689 **ESTs** 9.1 436642 AA724430 Hs.127960 **ESTs** gb:DKFZp762E152\_r1 762 (synonym: hmel2) Homo sa 453752 AL120800 451683 Al808964 Hs.207673 ESTs 55 401464 AF039241 Hs.9028 histone deacetylase 5 9.0 gb:UI-H-BW0-zip-g-09-0-UI.s1 NCI\_CGAP\_Sub6 Hom gb:601062418F1 NIH\_MGC\_10 Homo sapiens cDNA 435812 AW298067 8.7 8.7 410758 BF535988 AA115097 Hs.261313 412637 **ESTs** 419166 AA234638 Hs.293584 **ESTs** 8.3 60 8.1 423739 AA398155 Hs.97600 8.1 413813 M96956 Hs.75561 teratocarcinoma-derived growth factor 1 gb:yg45c03.r1 Soares infant brain 1NIB Homo sapiens 8.0 R14625 416211 7.9 443131 AI033833 Hs.132689 T10115 Hs.92423 KIAA1566 protein 7.9 415866 65 7.9 7.8 7.7 410130 AI912097 Hs.163208 ESTs, Weakly similar to FAFY\_HUMAN PROBABLE 439426 Al131502 Hs.143135 ESTs, Moderately similar to neurogenic basic-helix-loop 408141 U69205 Hs.45152 Hs.14463 7.6 419015 T79262 **FSTs** 441573 BE563966 Hs.6529 **ESTs** 70 AA236867 419386 Hs.143868 7.5 430562 D78260 Hs.285097 7.5 7.4 7.4 7.4 7.4 7.3 7.3 gb:od17e02.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA 434738 AA836265 403283 predicted exon ESTs 415861 Z43123 Hs.144513

7.3

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gb:RC2-BN0033-180200-015-g06 BN0033 Homo sapie

ESTs, Weakly similar to neuronal thread protein AD7c-gb:PM3-HT0344-071299-003-c08 HT0344 Homo sapie

gb:601117374F1 NIH\_MGC\_16 Homo sapiens cDNA

gb:ob88g05.s1 NCI\_CGAP\_GCB1 Homo sapiens cDN

gb:RC0-CT0201-270999-011-03 CT0201 Homo sacien

ESTs, Weakly similar to similar to O-sialoglycoprotein

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412732

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AW993300

AW118681

N57659

BE154650

BE258835

AA805639

AW302885

AW752363

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Hs.117183

Hs 201217

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ESTs

**FSTs** 

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	400942 407596	R86913		predicted exon gb:yq30f05.r1 Soares fetal liver spleen 1NFLS Homo sa	6.9 6.9
	422046	AI638562		gb:ts50a10.x1 NCI_CGAP_Ut1 Homo sapiens cDNA c	6.9
_	441284	AA927676	Hs.196542	ESTs	6.9
5	446224	AW450551	Hs.13308	ESTs	6.9
	424943	AU077260	Hs.153924	death-associated protein kinase 1	6.9
	453967	AW009077	Hs.232947	ESTs	6.9
	448683	AA167642	Hs.14632	ESTs	6.8
10	431877	AA521204	'Hs.105507	ESTs ab: 0\02 170028 270200 108 412 1 70038 Home again	6.8 6.8
10	411337 410596	AW837349 AA374186		gb:QV2-LT0038-270300-108-d12 LT0038 Homo sapie gb:EST86290 HSC172 cells I Homo sapiens cDNA 5' e	6.8
	417762	AA205976		gb:zq48a10.r1 Stratagene hNT neuron (937233) Homo	6.7
	406364			predicted exon	6.7
	452238	F01811	Hs.187931	ESTs, Moderately similar to S22703 voltage-gated pota	6.7
15	415288	R15794	Hs.141027	ESTs, Wealty similar to ALU1_HUMAN ALU SUBFA	6.7
	407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cds.	6.7
	439126	AF085984		gb:Homo sapiens full length insert cDNA clone YT99F	6.6
	452453	AI902519	15-400045	gb:QV-BT009-101198-051 BT009 Homo sapiens cDNA	6.6
20	431800 426380	AW452768 AJ291267	Hs.162045 Hs.149990	ESTs ESTs, Weakly similar to unnamed protein product [H.sa	6.5 6.5
20	449529	AI990559	Hs.232033	ESTs	6.4
	437755	AW204256	Hs.291887	ESTs	6.4
	448307	A1480289	Hs.211026	ESTs	6.4
25	439586	AA922936	Hs.110039	ESTs	6.4
25	420051	N35696	Hs.44745	ESTs	6.4
	425806 433923	Al522299 Al823453	Hs.173369	ESTs ESTs	6.4 6.4
	408159	H63977	Hs.146625 Hs.118526	ESTs .	6.3
	434844	AF157116	Hs.301355	hypothetical protein LOC56757	6.3
30	430197	AA468888	Hs.187697	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFA	6.3
-	440332	Al218517	Hs.188051	ESTs	6.3
	450061	A1797034	Hs.201115	ESTs	6.3
	454994	AW850176		gb:IL3-CT0219-271099-022-H04 CT0219 Homo sapien	6.3
35	402105	WECKEZ	11- 402400	predicted exon	6.3
33	409090 405752	W56067	Hs.103105	ESTs predicted exon	6.2 6.2
	408074	R20723	Hs.124764	ESTs ESTs	6.2
	459200	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	6.1
	416310	T81421	Hs.221396	ESTs	6.1
40	421976	AL138443	Hs.23450	mRNA for FLJ00023 protein	6.1
	429755	NM_001364	Hs.215839	discs, large (Drosophila) homolog 2 (chapsyn-110)	6.0
	448732	BE614063	11- 002255	gb:601503993F1 NIH_MGC_71 Homo sapiens cDNA	6.0
	453909	AW004045 AA493884	Hs.203355 Hs.218008	ESTS Verse content of NA: El 121440 for close COL04399	6.0 6.0
45	431178 449671	AW959755	Hs.288896	Homo sapiens cDNA: FLJ21440 fis, clone COL04389 Homo sapiens cDNA FLJ12977 fis, clone NT2RP20062	6.0
	421349	W01715	Hs.102958	ESTs, Weakly similar to Lpg6p [S.cerevisiae]	6.0
	453282	AK000043	Hs.32922	hypothetical protein FLJ20036	5.9
	420618	AA278781	Hs.280698	ESTs	5.9
50	412480	BE142364		gb:CM0-HT0143-270999-062-d12 HT0143 Homo sapi	5.9
50	449858	AW205979	Hs.196065	ESTs	5.9
	429884 416453	AL049925 H56968	Hs.225984 Hs.114593	DKFZP547G0910 protein ESTs	5.9 5.9
	459497	AA825742	Hs.87517	ESTs	5.9
	433773	AA759293	Hs.112692	ESTs	5.9
55	458942	AA009647	Hs.8850	a disintegrin and metalloproteinase domain 12 (metrin a	5.9
	436054	A1076262	Hs.119813	ESTs	5.9
	410495	N95428		gb:zb80d09.s1 Soares_senescent_fibroblasts_NbHSF H	5.8
	403277	A114011E	Un 225120	predicted exon	5.8 5.8
60	444302 439834	Al140115 Al754576	Hs.225130 Hs.124523	ESTs ESTs	5.8
	404020	. 4. 0 101 0		predicted exon	5.8
	454338	AW381251	Hs.1050	pleckstrin homology, Sec7 and colled/coll domains 1(cy	5.7
	430922	AW373747	Hs.183337	ESTs	5.7
65	420289	N55394	Hs.96398	8-oxoguanine DNA glycosylase	5.7
65	428498	AA429575	Hs.243032	ESTS	· 5.7
	445597 411543	H65649 AW851248		gb:yr72d10.r1 Soares fetal liver spleen 1NFLS Homo sa gb:lL3-CT0220-160200-066-F01 CT0220 Homo sapien	5.7 5.7
	408354	AI382803	Hs.159235	ESTs	5.7
	444431	AW513324	Hs.42280	ESTs	5.7
70	406605			predicted exon	5.7
	405541	AF039241	Hs.9028	histone deacetylase 5	5.6
	458090	AI282149	Hs.56213	ESTs, Highly similar to FXD3_HUMAN FORKHEAD	5.6 5.6
	454529 445832	Z45439 Al261545	Hs.270425	ESTs gb:qz30a07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA	5.6 5.6
75	441223	AI475067	Hs.132499	ESTs	5.6
	432552	AI537170	Hs.173725	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFA	5.6
	443650	AI698330	Hs.151444	ESTs	5.6
	403714			predicted exon	5.6
80	444165	AL137443	Hs.10441	hypothetical protein FLJ11236	5.6
ov	458914	BE327696 AA278807	Hs.280922	ESTs ESTs	5.6 5.5
	420620 458228	AA278807 AA934995	Hs.173343 Hs.184846	ESTs, Wealdy similar to R28830 1 [H.sapiens]	5.5
	448067	R68568	Hs.183373	src homology 3 domain-containing protein HIP-55	5.5
	427000	AI187420	Hs.145221	ESTs	5.5

	452351	AA025647		gb:ze85d01.r1 Soares_fetal_heart_NbHH19W Homo sa	5.5
	459359	N99545		gb:za40a05.r1 Soares fetal liver spleen 1NFLS Homo sa	5.5
	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.5
5	450938	AW753734	Hs.277215	ESTS	5.5
5	431888 459418	H99557 W96550	Hs.2864 Hs.26418	early endosome antigen 1, 162kD ESTs	5.4 5.4
	416718	R83017	Hs.204828	ESTs	5.4
	413236	H16442	Hs.127376	KIAA0266 gene product	5.4
	439063	AF085922	Hs.113968	ESTs	5.4
10	446361	Al291234	Hs.282241	ESTs	5.4
	458253	AW296952	Hs.196802	ESTs	5.4
	433682	AA642418	Hs.17381	ESTs	5.4
	455790	BE090690		gb:RC1-BT0720-280300-011-g02 BT0720 Homo sapie	5.4
1.5	445755	AW294870	Hs.223672	ESTs	5.3
15	436513	AJ278110	Hs.125507	DEAD-box protein	. 5.3
	416671	N94087	Hs.26073	ESTs, Moderately similar to HG14_HUMAN NONHIS	5.3
	440231	AW015420	Hs.163323	ESTs	5.3
	429866	AA460104	Hs.99540	ESTs	5.3
20	437779	AA345232	Hs.21227	ESTs	5.3 5.3
20	424029 425614	AB014594 Al334963	Hs.137579 Hs.156256	KIAA0594 gene product ESTs	5.3
	430653	AW902062	Hs.30280	ESTs	5.3 5.2
	408855	T83061	Hs.279604	desmin	5.2
	410454	AW749041	183213004	gb:RC3-BT0319-100100-012-c05 BT0319 Homo sapie	5.2
25	438116	AI904105	Hs.122016	FSTe	5.2
	409138	W73159	Hs.58290	ESTs	5.2
	423047	NM_005323	Hs.123064	H1 histone family, member T (testis-specific)	5.2
	440212	AW300959	Hs.126216	ESTs, Wealty similar to good similarity to E. coll hypo	5.2
20	404108			predicted exon	5.2
30	456253	T12198		gb:A588F Heart Homo sapiens cDNA clone A588, mRN	5.2
	409365	AA702376	Hs.226440	Homo sapiens done 24881 mRNA sequence	5.1
	444013	T08531	Hs.44404	hypothetical protein PRO1488	5.1
	454071	AI041793	Hs.42502	ESTs	5.1
35	419761	M17373	Hs.93177	interferon, beta 1, fibroblast	5.1
33	451250	AA491275	Hs.236940	Homo sapiens cDNA FLJ12542 fis, clone NT2RM4000	5.1
	405290	AW796342		predicted exon	5.1 5.1
	454487 444131	AV1796342 AI806600	Hs.207119	gb:PM2-UM0027-230200-002-h02 UM0027 Homo sap	5.1
	441679	BE502267	Hs.65996	EST, Weakly similar to intrinsic factor-B12 receptor pr ESTs	5.1
40	450077	AA523752	Hs.120855	ESTs	5.1
	421209	AJ010230	Hs.102576	ret finger protein-like 1 antisense	5.1
	445140	Al650599	Hs.197913	ESTs	5.1
	421126	M74587	Hs.102122	insulin-like growth factor binding protein 1	5.1
	447037	Al357568	Hs.157612	ESTs	5.1
45	407168	R45175		gb:yg40f01.s1 Soares infant brain 1NIB Horno sapiens	5.0
	436196	AK001084		gb:Homo sapiens cDNA FLJ10222 fis, clone HEMBB1	5.0
	442772	AW503680	Hs.300513	ESTs, Weakly similar to T15B7.2 [C.elegans]	5.0
	444138	AI701572	Hs.151153	ESTs	5.0
50	458589	AV654623	Hs.288141	Homo sapiens cDNA FLJ13016 fis, clone NT2RP30006	5.0
50	451640 441318	AA195601 Al078234	Hs.26771 Hs.176130	Human DNA sequence from clone 747H23 on chromos ESTs	5.0 5.0
	407490	S79281	U2:1/0190	gb:pancreatic ribonuclease [human, mRNA Recombinan	4.9
	438224	AA933999		gb:on91f04.s1 Soares_NFL_T_GBC_S1 Homo sapiens	4.9
	451638	AW798466	Hs.82396	2,5-oligoadenylate synthetase 1	4.9
55	457356	AA489621	Hs.191670	ESTs	4.9
	430679	R44428	Hs.22801	ESTs	4.9
	445747	AI820863	Hs.145328	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFA	4.9
	409036	T88693	Hs.226410	ESTS	4.9
<b>C</b> O	433382	T64293	Hs.291453	ESTs	4.9
60	401287			predicted exon	4.9
	424188	AW954552	Hs.142634	zinc finger protein	4.9
	404858	*********	11 00004	predicted exon	4.9
	410152	AW593104	Hs.23681	ESTs .	4.9 4.9
65	444997	AI204451	Hs.146196	ESTS	4.8
05	431075 429033	BE267477 NM_007374	Hs.194756	gb:601189542F2 NIH_MGC_7 Homo sapiens cDNA cl sine oculls homeobox (Drosophila) homolog 6	4.8
	414337	BE386606	113.134730	gb:601273980F1 NIH_MGC_20 Homo sapiens cDNA	4.8
	410336	BE391510	Hs.18498	Homo sapiens cDNA FLJ12277 fis, clone MAMMA10	4.8
	445283	AW515763	Hs.246872	ESTs	4.8
70	434792	AA649253	Hs.132458	ESTs	4.8
-	433403	AF040247		gb:Homo sapiens erythroid differentiation-related factor	. 4.8
	454940	AW846202		gb:QV0-CT0179-011299-061-f10 CT0179 Homo sapie	4.8
	455534	AW991925		gb:PM3-BN0011-130100-002-b07 BN0011 Homo sapi	4.8
75	416437	N48990	Hs.37204	ESTs	4.8
75	433767	AA609245	11- 000	gb:af13a11.s1 Soares_testis_NHT Homo sapiens cDNA	4.8
	434977	AI734233	Hs.226142	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFA	4.8
	416192 459218	NM_005036 AA812633	Hs.998	peroxisome proliferative activated receptor, alpha ESTs	4.8 4.8
	402109	rru (2033	Hs.10845	predicted exon	4.8
80	444490	Al151080	Hs.146830	ESTs	4.8
	432632	AW973801	Hs.134656	ESTs	4.8
	438683	AA813982	Hs.291842	ESTs	4.8
	404044			predicted exon	4.8
	449862	AI672277	Hs.199475	ESTs	4.8

	419002	T78625	Hs.268594	ESTs	4.7
	4255B2	AL157686	Hs.293737	ESTs	4.7
	416086	H18252	Hs.227263	ESTs	4.7
5	441133 446323	AA918191 AI288274	Hs.194457 Hs.149868	ESTs ESTs	4.7 . 4.7
,	440347	AI205274 AI125590	Hs.142864	ESTs	4.7
	439481	AF086294	Hs.125844	ESTs	4.6
	456388	W28557	10.120041	gb:48d8 Human retina cDNA randomly primed sublibra	4.6
	441864	R34177	Hs.181315	ESTs, Moderately similar to ALU4_HUMAN ALU SU	4.6
10	445910	R93483	Hs.260273	ESTs	4.6
	403531			predicted exon	4.6
	429773	AI332482	Hs.218791	proteoglycan 4, (megakaryocyte stimulating factor, artic	4.6
	422563	BE299342	Hs.19348	Homo sapiens cDNA FLJ13119 fis, clone NT2RP30026	4.6
	422890	Z43784	Hs.78713	solute carrier family 25 (mitochondrial carrier; phospha	4.6
15	453663	AL048807	Hs.180714	cytochrome c oxidase subunit VIa polypeptide 1	4.6
	447839	N72050	Hs.164144	ESTs	4.5
	415612	F12893	Hs.13301	ESTs	4.5
	433371	T25451		gb:PTHI188 HTCDL1 Homo saplens cDNA 5/3' simila	4.5
20	410667	AW936099		gb:QV0-DT0020-210100-095-d04 DT0020 Homo sapie	4.5
20	410890	AW809575		gb:MR4-ST0121-060200-002-a12 ST0121 Homo sapie	4.5 4.5
	404451 441705	AI087052	Hs.55993	predicted exon ESTs	4.5 4.5
	439597	W79579	Hs.58552	ESTs	4.5
	407825	NM_006152	Hs.40202	lymphoid-restricted membrane protein	4.5
25	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Drosophila) ho	4,5
	456278	BE300369	Hs.42643	ESTs, Weakly similar to KIAA1016 protein [H.sapiens	4.5
	424719	H90452		gb:yv01c03.r1 Soares fetal liver spleen 1NFLS Homo sa	4.5
	439542	AW297571	Hs.17646	ESTs	4.5
	444433	AV649844	Hs.282436	ESTs	. 4.5
30	438831	BE263273	Hs.301128	ESTs	4.5
	410065	AW812744		gb:RC3-ST0186-181099-012-c09 ST0186 Homo saplen	4.5
	453895	AA039843	Hs.61948	ESTs	4.5
	458250	AI807339	Hs.152174	ESTs, Weakly similar to Z140_HUMAN ZINC FINGE	4.5
25	423403	AA325483		gb:EST28475 Cerebellum II Homo sapiens cDNA 5' en	4.5
35	454679	AW813110		gb:CM4-ST0189-051099-021-f05 ST0189 Homo sapien	4.5
	445368	Al221631	Hs.166788	ESTs	4.5
	401004	A E007EC7	Lie 4 chenn	predicted exon	4.5
	425837 420497	AF007567 AW206285	Hs.159609 Hs.253548	insulin receptor substrate 4 ESTs	4.5 4.5
40	449438	AA927317	Hs.176719	ESTs	4.5 4.5
40	429409	Al694817	Hs.155980	ESTs	4.5
	447959	Al452784	Hs.270270	ESTs	4.4
	407340	AA810168	Hs.232119	ESTs	4.4
	424326	NM_014479	Hs.145296	disintegrin protease	4.4
45	443479	AF027219	Hs.9443	zinc finger protein 202	4.4
	443246	T75157	Hs.285516	ESTs, Weakly similar to hypothetical protein [H.sapien	4.4
	414475	BE302955	Hs.119598	ribosomal protein L3	4.4
	432075	AW972934		gb:EST385030 MAGE resequences, MAGM Homo sap	4.4
50	417906	R24769	Hs.23725	ESTs	4.4
50	406518	W28077	Hs.79389	nel (chicken)-like 2	4.4
	441460	Al962478	Hs.226804	ESTs, Moderately similar to ALUC_HUMAN !!!! ALU	4.4
	450549	T49427 AA380828	Hs.181244	major histocompatibility complex, class I, A gb:EST93827 Activated T-cells VII Homo saplens cDN	4.4 4.4
	426528 430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo sapi	4.4
55	408479	BE047329	Hs.144483	ESTs	4.3
-	448636	Al557139	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PLACE10090	4.3
	411280	N50617		gb:yy89h02.r1 Soares_multiple_sclerosis_2NbHMSP H	- 4.3
	440790	AW593050	Hs.128580	ESTs	4.3
	458301	AF003834		gb:AF003834 Clontech HI1149x Homo sapiens cDNA	4.3 -
60	442277	AW448914	Hs.202391	ESTs	4.3
	449463	AI657038	Hs.196109	ESTs	4.3
	433426	H69125	Hs.133525	ESTs	4.3
	410782	AW504860	Hs.288836	Homo sapiens cDNA FLJ12673 fis, clone NT2RM4002	4.3
65	423040	AA320749	Hs.209464	KIAA1604 protein	4.3
03	432430	AW079984	Hs.262480	ESTs	4.3
	432072	N62937	Hs.269109	ESTs Homo sapiens mRNA; cDNA DKFZp566D224 (from c	4.3 4.3
	452213 403635	AL110237	Hs.28425	predicted exon	4.3
	441919	A1553802	Hs.128121	ESTs	4.3
70	416717	H79559	Hs.297726	ESTs	4.3
	430995	NM_005092	Hs.248197	tumor necrosis factor (tigand) superfamily, member 18	4.2
	429269	AA449013	Hs.99203	ESTs	4.2
	415840	R15955	Hs.21758	ESTs	4.2
7.5	451300	AA017066	Hs.237686	EST	4.2
75	445366	Al221511	Hs.298662	ESTs	4.2
	424194	BE245833	Hs.169854	hypothetical protein SP192	4.2
	459105	NM_014517	Hs.28423	upstream binding protein 1 (LBP-1a)	4.2
	455387	BE069037	11- 074 400	gb:QV3-BT0379-161299-040-e12 BT0379 Homo sapie	4.2
80	410507	AA355288	Hs.271408	ESTS	4.2
OU	453823 450966	AL137967 AA017245	He 32704	gb:DKFZp761D2315_r1 761 (synonym: hamy2) Homo	4.2 4.2
	432694	AW991585	Hs.32794 Hs.276755	ESTs ESTs, Weakly similar to F53B1.2 (C.elegans)	4.2
	455108	AW856866		gb:RC0-CT0299-291199-031-G02 CT0299 Homo sapie	4.2
	443609	AV650231	Hs.282941	ESTs	4.2

	427469	AA403084	Hs.269347	ESTs	4.2
	417178	N51636	1 to 50704	gb:yy87b01.s1 Soares_multiple_sclerosis_2NbHMSP H	4.2
	439751 431982	AA196090 AW419296	Hs.50794	Homo sapiens mRNA full length insert cDNA clone EU ESTs	4.2 4.1
5	442641		Hs.105754	ESTs	
,	422128	AI890955 AW881145	Hs.262983	gb:QV0-OT0033-010400-182-a07 OT0033 Homo sapie	4.1 4.1
	449156	AF103907	Hs.171353	prostate cancer antigen 3	4.1
	419668	AI033098	Hs.132777	ESTs	4.1
	418236	AW994005	Hs.172572	hypothetical protein FLJ20093	4.1
10	432663	AI984317	Hs.122589	ESTs	4.1
	448313	BE622486	Hs.121688	Homo sapiens cDNA FLJ13463 fis, clone PLACE10034	4.1
	411279	AW884776		gb:QV4-OT0057-010300-121-d01 OT0057 Homo sapie	4.1
	440652	AJ216751	Hs.143977	ESTs	4.1
	416608	R11499	Hs.189716	ESTs	4.1
15	420405	AA743396	Hs.189023	ESTs	4.1
	405717			predicted exon	4.1
	435267	N23797	Hs.110114	ESTs ·	4.1
	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr virus) recepto	4.1
20	403560	AJ929721	Hs.5120	dynein, cytoplasmic, light polypeptide	4.1
20	449162	AI632740	Hs.10476	ESTs	4.1
	459157	AI904385		gb:CM-BT054-080399-054 BT054 Homo sapiens cDN	4.1
	432474	AA584042		gb:nn65e09.s1 NCI_CGAP_Lzr1 Homo sapiens cDNA	4.1
	455388	AW936234	Un 120000	gb:QV0-DT0020-090200-106-g05 DT0020 Homo saple	4.0 4.0
25	426456 438597	AA580748 AA811662	Hs.130658 Hs.171497	ESTs	4.0
23	437934	AW880871	Hs.77496	small nuclear ribonucleoprotein polypeptide G	4.0
	459385	BE380047	110.77750	gb:601159362F2 NIH_MGC_53 Homo sapiens cDNA	4.0
	436404	AW968556	'Hs.137240	Homo sapiens mRNA for partial 3 UTR, sequence 2	4.0
	457740	AW500458		gb:UI-HF-BNO-akb-d-07-0-UI.r1 NIH_MGC_50 Homo	, 4.0
30	437385	AA757055	Hs.164060	ESTs	4.0
_	444530	AV650124	Hs.282435	ESTs	4.0
	408066	AA046914		gb:zf47h10.r1 Soares refina N2b4HR Homo sapiens cD	4.0
	411256	AW834039		gb:QV0-TT0010-091199-053-e09 TT0010 Homo sapie	4.0
0.5	433582	BE548749	Hs.148016	ESTs	4.0
35	438637	BE500941	Hs.126730	ESTs, Weakly similar to KIAA1214 protein [H.sapiens	4.0
	414571	BE410746	Hs.22868	protein tyrosine phosphatase, non-receptor type 11	4.0
	446190	A1279299	Hs.256564	ESTs	4.0
	443542	A1927065	Hs.146040	ESTs	4.0
40	430444	AW296421	Hs.121035	ESTs	4.0 4.0
40	454573 409846	BE146471 AW501748		gb:QV0-HT0216-011199-043-c09 HT0216 Homo sapie gb:UI-HF-BR0p-ajm-b-12-0-UI.r1 NIH_MGC_52 Hom	4.0
	. 456141	AI751357	Hs.288741	Homo saplens cDNA: FLJ22256 fis, done HRC02860	4.0
	456140	AA169515	Hs.6006	ESTs	4.0
	441685	A1459261	Hs.144481	ESTs	4.0
45	416677	T83470	110.111101	gb:yd46g06.r1 Soares fetal liver spleen 1NFLS Homo s	4.0
	401740			predicted exon	4.0
	420122	AA255714	Hs.284153	Fanconi anemia, complementation group A	4.0
	442594	AW272467	Hs.254655	Untitled	3.9
	426294	AA374185		gb:EST86289 HSC172 cells I Homo sapiens cDNA 5' e	3.9
50	411922	AW876260		gb:PM4-PT0019-131299-006-E04 PT0019 Homo saple	3.9
	452320	AA042873	Hs.160412	ESTs ,	3.9
	431644	AW972822	Hs.169248	cytochrome c .	3.9
	409892	AW956113		gb:EST368183 MAGE resequences, MAGD Homo sap	3.9
55	418132	T92670	Hs.117421	ESTs	3.9
55	414372 400196	AA143654		gb:zo65a02.r1 Stratagene pancreas (937208) Homo sap	3.9 3.9
	416900	M59964	Hs.1048	predicted exon KIT ligand	3.9
	445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled/coil domains, bind	3.9
	435957	· N39015	Hs.190368	ESTs	3.9
60	442299	AW467791	Hs.155561	ESTs	3.9
	419499	AA808136	Hs.177698	ESTs	3.9
	438403	AA806607	Hs.292206		3.9
	449386	AA001308	Hs.193213	ESTs	3.9
~=	443283	BE568610		gb:601342622F1 NIH_MGC_53 Homo sapiens cDNA	3.9
65	405481			predicted exon	3.9
	453530	AW021633		gb:df26c02.y1 Morton Felal Cochlea Homo sapiens cDN	3.9
	415558	AA885143	Hs.125719	ESTs	3.9
	416874	H98752	Hs.42568	ESTS	3.9
70	454885 419896	AW836922 Z99362		gb:QV1-LT0036-150200-074-h06 LT0036 Homo sapie gb:HSZ99362 DKFZphamy1 Homo sapiens cDNA clon	3.9 3.9
70	440962	Al989961	Hs.233477	ESTs, Moderately similar to A Chain A, Secypa Compl	3.9
	419401	AW804663	110.235411	gb:QV4-UM0094-160300-135-d06 UM0094 Homo sap	3.9
	406562	71100-1000		predicted exon	3.8
	405690	BE409855	Hs.808	heterogeneous nuclear ribonucleoprotein F	3.8
75	435282	AA677428	Hs.189731	ESTs .	3.8
	402451			predicted exon	3.8
	451577	N69101	Hs.32703	ESTs	3.8
	457141	AA521410	Hs.41371	ESTs	3.8
00	407817	H92553	Hs.40400	ESTs	3.8
80	412613	AA653507	Hs.285711	Homo sapiens cDNA FLJ13089 fis, clone NT2RP30021	3.8
	418355	L42563	Hs.1165	ATPase, H+/K+ transporting, nongastric, alpha polypep	3.8
	446357	AW161533	Hs.300866	ESTs	3.8
	407448	AJ001865		gb:Homo Sapiens mRNA, partial cDNA sequence for h	3.8
	456383	Al148037		gb:qg61e01_1 Soares_testis_NHT Homo saptens cDNA	3.8

	444651	W58469	Hs.103120	ESTs	3.8
	455067	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo sapie	3.8
	442657	BE502631	Hs.130645	ESTs	3.8
_	429142	AA835639	Hs.104972	ESTs	3.8
5	429274	A1379772	Hs.99206	ESTs	3.8
	437774	AW978199	Hs.291648	ESTs	3.8
	427737	AA435988	Hs.178066	ESTs, Weakly similar to AF068289 5 HDCME31P [H.s	3.8
	405671	05400000		predicted exon	3.8
10	413627	BE182082	Hs.246973	ESTs	3.8
10	438858	R37529	Hs.269924	ESTs	3.8
	416612	H70565		gb:yr97c04.r1 Soares fetal liver spleen 1NFLS Homo sa	3.8
	423045	AW967472	Hs.301511	ESTs, Highly similar to KPT2_HUMAN SERINE/THR	3.8
	453361	AA035197	Hs.107375	ESTs	3.7
1.5	437243	AA747549	Hs.259122	ESTs	3.7
15	437987	AW450202	Hs.122963	ESTs	3.7
	408781	BE148621	Hs.254602	ESTs	3.7
	455895	BE154837		gb:PM1-HT0345-121199-001-c08 HT0345 Homo sapie	3.7
	431492	AW612343		gb:hg97c10.x1 NCI_CGAP_Kid11 Homo sapiens cDN	3.7
20	413247	AW963969		gb:EST376042 MAGE resequences, MAGH Homo sap	3.7
20	422866	NM_002410	Hs.121502	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-g	3.7
	431828	AA572994		gb:nm33f12.s1 NCI_CGAP_Lip2 Homo saplens cDNA	3.7
	438872	R64197	Hs.23589	ESTs	3.7
	438673	AJB24717	Hs.123443	ESTs	3.7
25	416624	H69044		gb:yr77h05.s1 Soares fetal liver spleen 1NFLS Homo sa	3.7
25	401963			predicted exon	3.7
	402867			predicted exon	3.7
	408315	AW179148		gb:MR4-ST0067-200899-002-B07 ST0067 Homo sapie	3.7
	418320	D86981	Hs.84084	amyloid beta precursor protein (cytoplasmic tail)-bindin	3.7
20	447199	Al939421	Hs.160900	ESTs	3.7
30	422590	AA312758	Hs.193945	Homo sapiens cDNA FLJ13962 fis, clone Y79AA10012	3.7
	451996	AW514021	Hs.245510	ESTs	3.7
	412463	AW953444	Hs.78672	taminin, alpha 4	3.7
	440928	AL046575	Hs.130198	ESTs	3.7
25	441951	W31002	Hs.128195	ESTs	3.7
35	440705	AA904244	Hs.153205	ESTs	3.7
	434231	AF119901	Hs.250568	hypothelical protein PRO2831	3.7
	411039	AL135674	Hs.163348	ESTs	3.7
	413137	BE066915		gb:PM0-BT0340-231199-001-b07 BT0340 Homo saple	3.7
40	417970	AA309234	Hs.57760	Homo sapiens cDNA: FLJ23119 fis, clone LNG07978	3.7
40	439786	AV652707	Hs.33756	Homo sapiens mRNA full length insert cDNA clone EU	3.7
	459595	AL040421		gb:DKFZp434B0714_r1 434 (synonym: htes3) Homo s	3.7
	443601	Al078554	Hs.15682	ESTs	3.7
	404041			predicted exon	3.6
15	406122			predicted exon	3.6
45	404582			predicted exon	3.6
	455786	BE090077		gb:RC6-BT0710-300300-021-F02 BT0710 Homo saple	3.6
	411899	AA370573		gb:EST82238 Prostate gland I Homo sapiens cDNA 5' e	3.6
	426758	AL036430	Hs.197772	ESTs	3.6
50	421776	AW301994	Hs.108183	candidate tumor suppressor p33 ING1 homolog	3.6
50	430169	AA468531	Hs.189047	ESTs	3.6
	407695	AI808007	Hs.66450	ESTs	3.6
	454564	AW807573	.1 404040	gb:MR1-ST0088-021299-004-g01 ST0088 Homo sapie	3.6
	425902	X52509	Hs.161640	tyrosine aminotransferase	3.6
55	439328	W07411	Hs.118212	ESTs, Moderately similar to ALU3_HUMAN ALU SU	3.6
55	429066	AA868555	Hs.178222	ESTs	3.6
	428690	AI948490	Hs.98765	ESTs	3.6
	437302	AA837146	Hs.180275	ESTs	3.6
	443973	AI580083	Hs.176154	ESTs	3.6
60	453993	AW615224	Hs.252839	ESTs	3.6
60	413623	AA825721	Hs.246973	ESTs	3.6
	409196	NM_001874	Hs.169765	carboxypeptidase M	3.6
	424916	AW867440	Hs.23096	ESTs	3.6
	424769	H06469	Hs.142653	ret finger protein	3.6
C 5	400080			predicted exon .	3.6
65	421521	A1638760	Hs.161795	ESTs	3.6
	405549			predicted exon	3.6
	446114	AI275715	Hs.145926	ESTS	3.6
	441392	AW451831	Hs.222119	ESTs, Weakly similar to K1CQ_HUMAN KERATIN, T	3.6
70	424025	AI701852	Hs.301296	ESTS	3.5
70	448527	A1525606		gb:PT1.3_03_G05.r tumor1 Homo sapiens cDNA 5', mR	3.5
	437063	AA351109	Hs.5437	Tax1 (human T-cell leukemia virus type I) binding prot	3.5
	449880	A1673006	Hs.231948	ESTs, Weakly similar to ALUB_HUMAN !!!! ALU CL	3.5
	449311	Al657014		gb:tt49a12x1 NCI_CGAP_GC6 Homo sapiens cDNA c	3.5
75	442999	AW662889	Hs.132395	ESTs	3.5
75	416238	W90448		gb:zh78c08.s1 Soares_fetal_liver_spleen_1NFLS_S1 H	3.5
	423209	8E278528	Hs.106823	H.sapiens gene from PAC 42616, similar to syntaxin 7	3.5
	409854	AW501833		gb:UI-HF-BR0p-ajo-d-01-0-UI.r1 NIH_MGC_52 Hom	3.5
	414941	C14865	Hs.182159	ESTs	3.5
QΛ	456337	AW751661	Hs.65919	ESTS	3.5
80	415296	F05086		gb:HSC01A011 normalized infant brain cDNA Homo s	3.5
	423338	AB007961	Hs.127338	KIAAD492 protein	3.5
	415618	F12954		gb:HSC3GG091 normalized infant brain cDNA Homo s	3.5
	405583	45043546	11 0000	predicted exon	3.5
	435601	AF217509	Hs.283077	centrosomal P4.1-associated protein; uncharacterized bo	3.5

	450867	AA011454	Hs.245122	ESTs	3.5
	431339	AA506294	Hs.257266	ESTs	3.5
	441969	AI733386	Hs.129194	ESTs, Wealtly similar to ALU1_HUMAN ALU SUBFA	3.5
_	431343	AW970603	Hs.300941	Homo sapiens cDNA FLJ11661 fis, clone HEMBA100	3.5
5	434317	A1674095	Hs.116323	ESTs	3.5
	414741	R51321	Hs.25780	Homo sapiens cDNA FLJ12252 fis, clone MAMMA10	3.5
	439707	AW297702	Hs.102915	ESTs	3.5
	443178	AI531241	Hs.47312	ESTs	3.5
	400397	AJ270770	Hs.154485	transcription factor 7-like 2 (T-cell specific, HMG-box)	3.5
10	455887	BE154173		gb:PM1-HT0340-201299-004-f12 HT0340 Homo sapie	3.5
	434362	W27081	Hs.295446	ESTs	3.5
	409211	AA078835	1.00.000110	gb:zm94h04.s1 Stratagene colon HT29 (937221) Homo	3.5
	414390	BE281040		gb:601156234F1 NIH_MGC_21 Homo sapiens cDNA	3.5
	457142	AI924353	Hs.290969	EST	3.5
15	423006	U29700	Hs.123014	anti-Mullerian hormone receptor, type II	3.5
LJ	453363	Al989776	Hs.232623	ESTs	3.5
	418913	BE046745	T5.20202J		3.4
	440016		Lb 127057	gb:hn39b06.x1 NCI_CGAP_RDF2 Homo sapiens cDN ESTs	3.4
		AW118114	Hs.137057	predicted exon	3.4
20	405096	AUTC00470	11- 440020	F	3.4
20	435072	AW592176	Hs.116932	ESTs	3.4
	438535	1.09078	11. 402470	gb:Homo sapiens mRNA fragment	3.4
	424001	W67883	Hs.137476	KIAA1051 protein	
	428361	NM_015905	Hs.183858	transcriptional intermediary factor 1	3.4
25	410587	AA370706	Hs.11252	ESTs, Weakly similar to Weak similarity with the Ysy6	3.4
25	454543	AW806895		gb:QV4-ST0023-160400-172-c06 ST0023 Homo sapien	3.4
	419515	S81944	Hs.90791	gamma-aminobutyric acid (GABA) A receptor, alpha 6	3.4
	410280	AA083558	Hs.261286	ESTs	3.4
	· 425714	AW96327B		gb:EST375351 MAGE resequences, MAGH Homo sap	3.4
20	416895	AW961600		gb:EST373672 MAGE resequences, MAGG Homo sap	3.4
30	427935	AW503687	Hs.119424	ESTs, Weakly similar to unnamed protein product [H.sa	3.4
	411673	BE064863		gb:RC1-BT0313-110300-015-f06 BT0313 Homo sapien	3.4
	453339	AW992599	Hs.252797	ESTs	3.4
	424696	BE439547	Hs.151903	Homo sapiens clone 24706 mRNA sequence	3.4
	436242	AK002187		gb:Homo sapiens cDNA FLJ11325 fis, clone PLACE10	3.4
35	442837	AI022082	Hs.50492	ESTs	3.4
	452807	AA028933	Hs.162434	ESTs	3.4
	418110	R43523	Hs.217754	Homo sapiens cDNA: FLJ22202 fis, clone HRC01333	3.4
	433936	AI208072	Hs.123459	ESTs	3.4
	458177	AJ744995	Hs.267072	ESTs, Moderately similar to ALU4_HUMAN ALU SU	3.4
40	401896			predicted exon	3.4
	406237			predicted exon	3.4
	457688	AL110157	Hs.3843	Homo sapiens mRNA; cDNA DKFZp586F2224 (from	3.4
	456914	AW363582	Hs.75323	prohibitin	. 3.4
	421916	R34441	Hs.101007	Homo sapiens cDNA: FLJ23546 fis, clone LNG08361	3.4
45	419321	N48146	Hs.269069	ESTs	3.4
1.5	447876	AV654978	Hs.19904	cystathionase (cystathionine gamma-lyase)	3.4
	406197	A1004310	113.13304	predicted exon	3.4
	443005	AJ027184	Hs.200918	ESTs	3.4
	450078	Al681743	113.200310	gb:bx38g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA	3.4
50	431301	AA502384	Hs.151529	ESTs	3.4
50	430202	T85775	110.101020	gb:yd60g02.r1 Soares fetal liver spleen 1NFLS Homo s	3.4
	428559	H24338	Hs.27041	ESTs	3.4
	455731	BE072188	113.27041	gb:QV4-BT0536-211299-055-b09 BT0536 Homo sapie	3.4
•	420735	AW297440	Hs.88653	ESTs	3.4
55	430881	NM_000809	Hs.248112	gamma-aminobutyric acid (GABA) A receptor, alpha 4	3.3
55	405836	*****	. 13.270112	predicted exon	3.3
	449178	A1633748	Hs.197597	ESTs	3.3
	453265	U61232	Hs.32675	tubulin-specific chaperone e	3.3
	430700				. 3.3
60		AA768902	Hs.247812 Hs.129212	H2A histone family, member K, pseudogene	3.3
UU.	424496 446963	AI733451 AI862668	Hs.176333	ESTS ESTS	3.3
					3.3
	422879	A1241409	Hs.188092	ESTs ESTs	3.3 3.3
	419831	AW448930	Hs.5415		
65	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_1NFLS_S1 H	3.3
03	406255	114500000		predicted exon	3.3
	412319	, AW936903		gb:RC1-DT0029-030200-012-d02 DT0029 Homo sapie	3.3
	401350			predicted exon	3.3
	439098	AF085955	Ile negene	gb:Homo sapiens full length insert cDNA clone YR86G	3.3
70	450589	AI701505	Hs.202526	ESTs	3.3
70	430749	AJ242956	Hs.25960	v-myc avlan myelocylomatosis viral related oncogene, n	3.3
	430689	AI695595	Hs.293219	ESTS	3.3
	454753	AW819212	11- 20040	gb:CM1-ST0283-071299-061-c07 ST0283 Homo sapie	3.3
	444479	AA194980	Hs.30818	Homo sapiens cDNA FLJ13681 fis, clone PLACE20000	3.3
75	413516	BE145907		gb:MR0-HT0208-221299-204-e12 HT0208 Homo sapie	3.3
75	425541	AA359119		gb:EST68172 Fetal lung II Homo sapiens cDNA 5' end,	3.3
	457107	AA418245	Hs.185796	ESTs, Weakly similar to b3418.1 [H.sapiens]	3.3
	421480	NM_016158	Hs.104671	erythrocyte transmembrane protein	3.3
	444289	BE267060	Hs.76391	myxovirus (influenza) resistance 1, homolog of murine	3.3
0.0	417725	R25257	Hs.21503	ESTs	3.3
80	453631	AL046418		gb:DKFZp434N247_r1 434 (synonym: htes3) Homo sa	3.3
	450692	H50603	Hs.94037	hypothetical protein FLJ23053	3.3
	413357	W47611		gb:zc35e06.r1 Soares_senescent_fibroblasts_NbHSF H	3.3
	415327	H22769	Hs.1861	membrane protein, palmitoylated 1 (55kD)	3.3
	457569	AW970021	Hs.291120	. ESTs, Weakly similar to ALU8_HUMAN ALU SUBFA	• 3.3
				4.44	

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	448601	R61666	Hs.293690	ESTs	3.3
	436526	AW993633	Hs.287681	Homo sapiens cDNA: FLJ21685 fis, clone COL09372	3.3
	440589	BE397763	Hs.194478	Homo saplens mRNA; cDNA DKFZp434O1572 (from	3.3
-	418768	T39310	Hs.1139	cold shock domain protein A	3.3
5	426768	AW303337	Hs.270411	ESTs	3.3
	400394	AF040257	Hs.283818	Homo saptens TNF receptor homolog mRNA, partial cd	3.3
	433565	AA599763	Hs.112520	ESTs	3.3
	424093	AA335025	11 00-00	gb:EST39621 Epididymus Homo sapiens cDNA 5' end,	3.3
10	449552	AA001742	Hs.83722	ESTs	3.3 3.3
10	431892	AA521315	Hs.194424	ESTs	3.3
	405512	A10C4747	11- 000000	predicted exon	3.3
	446990	AI354717	Hs.223908	ESTs ESTs, Weakly similar to ALU7_HUMAN ALU SUBFA	3.2
	457729	A1821863 AL157545	Hs.293467 Hs.42179	bromodomain and PHD finger containing, 3	3.2
15	417333 456420	AU 401361	Hs.91773	protein phosphatase 2 (formerly 2A), catalytic subunit,	3.2
13	403497	AW401301	ns.91713	predicted exon	3.2
	427145	R52635	Hs.25935	ESTs	3.2
	406454	IWEND	113.20300	predicted exon	3.2
	441033	BE562555		gb:601335867F1 NIH_MGC_44 Homo sapiens cDNA	3.2
20	408444	AW661839	Hs.253204	ESTs	3.2
20	434739	AA804487	Hs.144130	ESTs	3.2
	437060	AA745591	Hs.292063	ESTs	3.2
	423092	BE274837	Hs.123637	putative homeodomain transcription factor	3.2
	424695	U58331	Hs.151899	sarcoglycan, delta (35kD dystrophin-associated glycopr	3.2
25	443362	AI053464	Hs.166505	ESTs ~	3.2
	437500	AL390150		gb:Homo sapiens mRNA; cDNA DKFZp547L156 (from	3.2
	425458	H89317	Hs.182889	ESTs	3.2
	439171	AA831133	Hs.294128	ESTs	3.2
	407647	AW860158		gb:RC0-CT0379-290100-032-b04 CT0379 Homo saple	3.2
30	435608	AW183971	Hs.250896	ESTs	3.2
	426743	AA383833	Hs.245022	ESTs	3.2
	457525	AW973800		gb:EST385901 MAGE resequences, MAGM Homo sap	3.2
	413800	Al129238	Hs.192235	ESTs	3.2
~ -	414193	BE260069		gb:601150964F1 NIH_MGC_19 Homo sapiens cDNA	3.2
35	455565	BE000537		gb:RC3-BN0072-240200-011-d07 BN0072 Homo sapie	3.2
	410061	T91029	Hs.15069	ESTs	3.2
	450666	T99968	Hs.18799	ESTs	3.2
	458529	AV652120	Hs.213232	ESTs .	3.2
40	424751	AA769482	Hs.296320	ESTs	3.2
40	442225	AI306597	Hs.129192	ESTS	3.2
	410990	AW812929		gb:RC3-ST0186-250200-018-c05 ST0186 Homo saplen	3.2
	435644	AA700867	Hs.269659	ESTs	3.2
	405347	41000440	11 400000	predicted exon	3.2 3.2
45	441202	AI632143	Hs.135853	ESTs	3.2 3.2
40	446694	AV659942	Hs.258132	ESTs	3.2
	454652 418985	AW812088 Al042330	Hs.87128	gb:RC4-ST0173-191099-032-a07 ST0173 Homo sapien ESTs, Weakly similar to similar to YBS4 YEAST [C.el	3.2
	430118	AI377255	Hs.183287	ESTs	3.2
	430691	C14187	Hs. 103538	EST <sub>6</sub>	3.2
50	416313	H47205	Hs.194109	ESTs, Weakly similar to ALUB_HUMAN !!!! ALU CL	3.2
50	446122	AJ362790	Hs.181801	ESTs	3.2
	453725	W28543		gb:48c5 Human retina cDNA randomly primed sublibra	3.2
	453954	AW118336	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding protein 1	3.2
	428166	AA423849	Hs.79530	M5-14 protein	3.2
55	447506	R78778	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone CAS05917	3.2
	401871			predicted exon	3.2
	442160	Al337127	Hs.156325	ESTs	3.2
	404708			predicted exon	3.1
	412588	AW993055	Hs.44024	ESTs	3.1
60	431976	AA719001	Hs.291065	ESTs	3.1
	408884	AW891024	Hs.281172	ESTs	3.1
	433811	AW975015	Hs.123138	ESTs	3.1
	431691	AI208511	Hs.292510	ESTs	3.1
65	418719	AW975590	Hs.161707	ESTs	3.1
65	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721 67 PRO1777 (H	3.1
	435699	AI911488	Hs.213724	ESTs	3.1
	459344	AW499533	Hs.257976	ESTs	3.1
	431729	AW004714	Hs.162033	ESTs	3.1
70	436771	AW975687	Hs.292979	ESTS	3.1 3.1
70	434480	AW956268	Hs.59395	Homo sapiens clone IMAGE:112574 mRNA sequence	3.1
	459547	AI400579	Hs.225186	EST Homo sapiens cDNA: FLJ21120 fis, clone CAS05691	3.1
	427962 403743	AA946582	Hs.133546	oredicted exon	3.1
	413560	BE148411		gb:MR0-HT0241-131299-002-f04 HT0241 Homo sapie	3.1
75	454372	H96643	Hs.283565	FOS-like antigen-1	3.1
, ,	454572	AA421642	Hs.24309	hypothetical protein FLJ11106	3.1
	428839	AI767756	Hs.82302	ESTs	3.1
	407110	AA018042	Hs.95078	ESTs	3.1
	436133	T77531	Hs.191124	ESTs	3.1
80	418872	R94785	Hs.270263	ESTs	3.1
	404418			predicted exon	3.1
	446877	A1559472	Hs.270720	ESTs	3.1
	429053	AA443967	Hs.194114	ESTs	3.1
	425189	H16622		. gb:ym26c07_r1 Soares infant brain 1NIB Homo sapiens	3.1
				4.44	

```
predicted exon
           404134
                                    Hs.126895
           441404
                      A1638880
                                                    ESTs
                                                    predicted exon
           400076
                                                    ESTs, Weakly similar to KIAA0443 [H.sapiens]
                                                                                                                          3.1
           411876
                      AW961336
                                    Hs.69705
  5
                                                                                                                          3.1
3.1
                      AA013349
                                     Hs.60602
           451048
           447021
                      Al356564
                                    Hs.161406
                                                    ESTs
                                                                                                                           3.0
                                                    predicted exon
ESTs
           404083
           415833
                      H05175
                                    Hs.107510
                                                                                                                           3.0
                                                    predicted exon
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                TABLE 5C:
               Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of
35
                        human chromosome 22° Dunham, et al. (1999) Nature 402:489-495
                Strand: Indicates DNA strand from which exons were predicted
                Nt_position: Indicates nucleotide positions of predicted exons
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<b>5</b> ·	406255	7417729	Ptus	2959-3200
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	406481	9864741	Minus	91439-91579
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10	406605	8272666	Minus	23275-23493,23723-23903

TABLE 6A lists about 68 genes highly down-regulated in ovarian cancer compared to normal ovaries. These were selected as for Table 5A, except the "average" ovarian cancer level was set to the maximum value amongst various ovarian cancers and the "average" normal ovary level was set to the minimum value from various non-malignant ovary specimens, and the ratio was greater than or equal to 2.5 (i.e. 2.5-fold down-regulated in the highest tumor vs. the lowest normal ovary). This has the overall effect of increasing stringency, and reducing the number of false-positives.

TABLE 6A: ABOUT 68 HIGHLY DOWN-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY

Pkey: Primekey
Ex. Accn: Exemplar Accession
UG ID: UniGene ID
Title: UniGene Title
ratio: ration of normal ovary vs. tumor

05					
25	Pkey	Ex. Acon	UG ID	Tille	ratio 7.9
	424851 437690	AA676441 AA804362	Hs.119059 Hs.180544	ESTs ESTs	4.7
	437630	AA642418	Hs.17381	ESTs	4.1
	407437	AF220264	15.17501	gb:Homo sapiens MOST-1 mRNA, complete cds.	4.1
30	437787	Al908263	Hs.291625	ESTs	4.0
	453282	AK000043	Hs.32922	hypothetical protein FLJ20036	4.0
	440987	AA911705	Hs.130229	ESTs	3.8
	443131	AI033833	Hs.132689	ESTs	3.8
25	431075	BE267477		gb:601189542F2 NIH_MGC_7 Homo sapiens cDNA do	3.6
35	412637	AA115097	Hs.261313	ESTs .	3.6
	408141	U69205	Hs.45152	ESTs, Moderately similar to neurogenic basic-helix-loop	3.5 3.5
	420122	AA255714	Hs.284153	Fanconi anemia, complementation group A ESTs	3.4
	430653 401308	AW902062	Hs.30280	blagicted exou	3.4
40	41075B	BE535988		gb:601062418F1 NIH_MGC_10 Homo sapiens cDNA c	3.4
40	421418	AA806639		gb:ob88g05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA	3.4
	450061	Al797034	Hs.201115	ESTs	3.3
	409725	T40760	Hs.90459	EST	3.3
4.0	434738	AA836265		gb:od17e02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA	3.3
45	431644	AW972822	Hs.169248	cytochrome c .	3.3
	450938	AW753734	Hs.277215	ESTs	3.2
	420497	AW206285	Hs.253548	ESTs	3.2
	439426	Al131502	Hs.143135	ESTS, Weakly similar to FAFY_HUMAN PROBABLE C	3.2 3.2
50	407596 448683	R86913 AA167642	Hs.14632	gb:yq30f05.r1 Soares fetal liver spleen 1NFLS Homo sap ESTs	3.2
50	431982	AW419296	Hs.105754	ESTs	3.1
	452320	AA042873	Hs.160412	ESTs	3.1
	419401	AW804663	110.100112	gb:QV4-UM0094-160300-135-d06 UM0094 Homo sapim	3.1
	402105			predicted exan	3.1
55	444997	A1204451	Hs.146196	ESTs	3.1
	403283		•	predicted exon	3.0
	455388	AW936234		gb:QV0-DT0020-090200-106-g05 DT0020 Homo sapie	3.0
	428559	H24338	Hs.27041	ESTs	29
60	419002	T78625	Hs.268594	ESTs	29
60	404868		11- 403405	predicted exon	2.9 2.9
	409090	W56067	Hs.103105	ESTs and interest and	29
	406605 441202	AI632143	Hs.135853	predicted exon ESTs	28
	422046	Al638562	113,100000	gb:ts50a10.x1 NCI_CGAP_Ut1 Homo sapiens cDNA d	2.8
65	442865	N57659	Hs.114541	ESTs. Weakly similar to neuronal thread protein AD7c-N	2.8
••	444431	AW513324	Hs.42280	ESTs	2.8
	426294	AA374185		gb:EST86289.HSC172 cells I Homo sapiens cDNA 5' en	2.8
	412480	BE142364		gb:CM0-HT0143-270999-062-d12 HT0143 Homo sapie	2.8
-	449858	AW205979	Hs.196065	ESTs	2.8
70	401464	AF039241	Hs.9028	histone deacetylase 5	2.7
	439126	AF085984		gb:Homo sapiens full length insert cDNA clone YT99F0	27
	403277	11004740		predicted exon	2.7 2.7
	450078	Al681743	Hs.56213	gb:tx38g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA ESTs, Highly similar to FXD3_HUMAN FORKHEAD D	27
75	458090 420620	AL282149 AA278807	Hs.173343	ESTs	27
, 5	459054	AW798466	Hs.82396	2,5-oligoadenylate synthetase 1	2.6
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cys-X-Cys), mem	2.6
	454338	AW381251	Hs.1050	pleckstrin homology, Sec7 and coiled/coil domains 1(cyt	2.6
	454529	Z45439	Hs.270425	ESTs	2.6
80	446877	A1559472	Hs.270720	ESTs	2.6
	412588	AW993055	Hs.44024	ESTs	2.6
	449862	A1672277	Hs.199475	ESTs	26
	446694	AV659942	Hs.258132	ESTs	2.6 2.6
	424029	AB014594	Hs.137579 .	KIAA0694 gene product	20
				1 4 7	

```
454102
                                                         gb:RC0-CT0201-270999-011-f03 CT0201 Homo sanien
                         AW752363
           430922
                         AW373747
                                        Hs.183337
                                                                                                                                      2.6
2.5
2.5
2.5
2.5
           420289
                         N55394
                                        Hs.96398
                                                        8-oxoguanine DNA glycosylase
           410495
                         N95428
                                                        gb:zb80d09.s1 Soares_senescent_fibroblasts_NbHSF Ho
gb:RC1-DT0029-030200-012-d02 DT0029 Homo sapien
  5
           412319
                         AWGREGUR
                                                         gb:PM3-HT0344-071299-003-c08 HT0344 Homo sapien
           409699
                         BE154650
           445832
                         A1261545
                                                         gb:qz30a07.x1 NCI_CGAP_Kid11 Homo saplens cDNA
           429755
                         NM_001364
                                        Hs.215839
                                                         discs, large (Drosophila) homolog 2 (chapsyn-110)
                                                                                                                                      25
           445755
                         AW294870
                                        Hs.223672
                                                        ESTs
10
           TABLE 68:
           Pkey: Unique Eos probeset identifier number
           CAT number: Gene cluster number
           Accession: Genbank accession numbers
15
           Pkev
                         CAT Number
           407596
                         1003489_1
                                            R86913 R86901 H25352 R01370 H43764 AW044451 W21298
           409699
                         1149033_1
                                            BE154650 BE154785 AW468343 BE154816 BE154667
           410495
                         1205826_1
                                            N95428 W24040 AW751366 H81987
20
                                            BE535988 AW801777
AW936903 AW936907 AW936908 AW936914
BE142364 BE142341 AA112025
           410758
                         1219899_1
                         1288602_1
           412319
                         129929_1
184454_1
           412480
           419401
                                            AW804663 AW805017 AA236969
           421418
                         202288_1
                                            AA806639 AA291008 AA836274 AW978806
25
                                            Al638562 T16929 H13401 F07773 R55836
AA374185 AW956180 H38344
BE267477 AA491488 AW836723
                         210744_1
           422046
           426294
                         263994_1
           431075
                         327638 1
                         392562_1
                                            AA836265 AA648266 AW974440
           434738
                         46887_1
           439126
                                            AF085984 H95905 H95906
30
           445832
                         651925_1
                                            AI261545 N59134 AW875371 AW875247
                                            AJ681743 AW897287 AW897205 AW897284
AW752363 BE147120 N22640
                         823882_1
1011603_1
           450078
           454102
                         1287904_1
                                            AW936234 AW936074 AW936181 AW936179 AW936217 AW936077 AW936227 AW936191
           455388
35
           TABLE 6C: ·
           Pkey: Unique number corresponding to an Eos probeset
           Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled 'The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495

Strand: Indicates DNA strand from which exons were predicted
40
           Nt_position: Indicates nucleotide positions of predicted exons
           401308
                         9212516
                                                     169019-169649
                                       Phis
           402105
                         8131588
                                                     22856-24055
                                       Minus
                                                     27494-27642
           403277
                         8072597
                                       Minus
45
           403283
                         8076905
                                                    71124-71996
                                       Minus
           404868
                         9454593
                                       Plus
                                                     39954-40430
           406605
                         8272656
                                       Minus
                                                     23275-23493,23723-23903
50
           Table 7A lists about 770 genes up-regulated in ovarian cancer compared to normal adult tissues. These were selected from 35403 probesets on the Affymetrix/Eos-Hu01
           GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult lissues was greater than or equal to 2.5. The "average" ovarian cancer level was set to
           the 2nd highest amongst various ovarian cancers. The "average" normal adult tissue level was set to the 7th highest amongst various non-malignant tissues. In order to remove
           gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.
55
           TABLE 7A: ABOUT 770 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES
           Pkey: Primekey
           Ex. Accn: Exemplar Accession
           UG ID: UniGene ID
60
           Title: UniGene Title
           ratio: ration tumor vs. normal tissues
           Pkey
109680
                       Fx. Accn.
                                       UGID
                                                        Title
                                                                                                                      ratio
                       F09255
                                       Hs.4993
                                                        ESTs
                                                                                                                      23.2
65
                                                                                                                       22.0
           119743
                       W70242
                                       Hs.58086
                                                        ESTs
                       AA283006
                                       Hs.50758
            132528
                                                        chromosome-associated polypeptide C
           129571
                       X51630
                                       Hs.1145
                                                         Wilms tumor 1
                                                                                                                       20.0
           102151
130941
                       U17280
D49394
                                       Hs.3132
                                                         steroidogenic acute regulatory protein
                                                                                                                       19.6
                                       Hs.2142
                                                         5-hydroxytryptamine (serotonin) receptor 3A
                                                                                                                       17.5
70
            132624
                        AA164819
                                       Hs.53631
                                                        ESTs
                                                                                                                       15.9
            102610
                        U65011
                                       Hs.30743
                                                        preferentially expressed antigen in melanoma
                                                                                                                       15.4
                                                         protein kinase C; iota
           101249
                       1.33881
                                       Hs.1904
                                                                                                                       14.5
                        AA460530
                                       Hs 256579
            122802
                                                         ESTs
                                                                                                                       14.5
                        M74093
            135242
                                       Hs.9700
                                                        cyclin E1
                                                                                                                       13.8
75
            101804
                        M86699
                                       Hs.169840
                                                        TTK protein kinase
                                                                                                                       12.2
```

12.0 11.5

11.4

10.9

10.9

10.8

10.5

10.3

10.1

123005

114965

115536

132191

121853

115881

119780

104301

132632

80

AA479726

AA250737

AA347193

AA449431

AA425887

AA435577

W72967

D45332

N59764

Hs.105577

Hs.72472

Hs.62180

Hs.158688

Hs.98502

Hs.184942

Hs.191381

Hs.6783

Hs.5398

**ESTs** 

**ESTs** 

**ESTs** 

**ESTs** 

KIAA0741 gene product

G nontein-counted receptor 64

guanine-monophosphate synthetase

ESTs; Weakly similar to hypothetical protein

	105298	A 4 222 4 ED	11- 00200	ESTs .	0.7
	103233	AA233459 AA133250	Hs.26369 Hs.62180	ESTS	9.7 9.1
	113168	T53592	Hs.161586	EST	9.0
_	115892	AA435946	Hs.50831	ESTs	8.9
5	125666	AA199856	Hs.118811	ESTs	8.9
	102200	U21551	Hs.157205	branched chain aminotransferase 1; cytosolic	8.8
	108055 132572	AA043562 AA448297	Hs.62637	ESTs signal recognition particle 72kD	8.6 8.6
	115909	AA436666	Hs.237825 Hs.59761	ESTs	8.5
10	109166	AA179845	Hs.73625	RAB6 interacting; kinesin-like (rabkinesin6)	8.3
	121779	AA422036	Hs.98367	ESTs	8.3
	102915	X07820	Hs.2258	matrix metalloproteinase 10 (strometysin 2)	8.0
	105317	AA233926	Hs.23635	ESTs	7.8
15	125250	W87465	Hs.222926	ESTs; Weakly similar to D2092.2 [C.elegans]	7.8
13	126960 122969	AA317900 AA478539	Hs.161756 Hs.104336	ESTs ESTs	7.8 7.7
	130376	R40873	Hs.155174	KIAA0432 gene product	7.7
	123339	AA504253	Hs.101515	ESTs	7.7
	134972	M19720	Hs.169252	Human L-myc protein gene; complete cds	7.6
20	111234	N69287	Hs.21943	ESTs; Weakly similar to ORF YGL221c [S.cerevi	7.5
	123689	AA609556	Hs.256562	ESTs	7.5
	123494	AA599786	Hs.112110	ESTs	7.4
	131985	AA434329	Hs.36563	ESTs	7.4 7.4
25	106738 108768	AA470145 AA127741	Hs.25130 Hs.61345	ESTs ESTs	7.3
25	106474	AA450212	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (from ci	7.2
	123308	AA496211	Hs.103538	ESTs	7.2
	106124	AA423987	Hs.7567	ESTs	7.2
20	111345	N89820	Hs.14559	ESTs	7.1
30	105200	AA195399	Hs.24641	ESTs	7.1
	116416 118846	AA609219 N80567	Hs.39982 Hs.50895	ESTs ESTs	7.1 7.1
	133434	AA278852	Hs.250786	ESTs	7.1
	120472	AA251875	Hs.104472	ESTs; Wealdy similar to Gag-Pol polyprotein [	6.9
35	115291	AA279943	Hs.122579	ESTs	6.9
	111185	N67551	Hs.12844	EGF-like-domain; multiple 6	6.9
	108778	AA128548	Hs.90847	general transcription factor IIIC; polypeptid	6.9
	132939	U76189	Hs.61152	exostoses (multiple)-like 2	6.9 6.9
40	134520 114724	N21407 AA131701	Hs.257325 Hs.256287	ESTs ESTs; Highly similar to SPERM SURFACE PROTEIN	6.8
70	116296	AA489033	Hs.62601	Homo sapiens mRNA; cDNA DKFZp586K1318 (from c	6.8
	102136	U15552	Hs.85769	acidic 82 kDa protein mRNA	6.7
	132725	L41887	Hs.184167	splicing factor; arginine/serine-rich 7 (35kD)	6.5
15	109648	F04600	Hs.7154	ESTs	6.4
45	116401	AA599963	Hs.59698	ESTs	6.4
	127563 104252	Al367707 AF002246	Hs.150587 Hs.210863	ESTs cell adhesion molecule with homology to L1CAM	6.4 6.4
	120438	AA243441	Hs.99488	ESTs; Wealdy similar to ORF YKR074w [S.cerevi	6.2
	131978	D80008	Hs.36232	KIAA0186 gene product	6.2
50	134621	L02547	Hs.172865	cleavage stimulation factor; 3' pre-RNA; subu	6.2
	120571	AA280738	Hs.128679	ESTs	6.2
	102627	U66561	Hs.158174	zinc finger protein 184 (Kruppel-like)	6.1
	100661 118204	HG2874-HT3 N59859	Hs.48443	Ribosomal Protein L39 Homolog ESTs	6.1 6.0
55	131386	AA096412	Hs.173135	dual-specificity tyrosine-(Y)-phosphorylation	6.0
-	129097	S50223	110.110.00	HKR-T1=Kruppel-like zinc finger protein [huma	5.9
	131228	AA279157	Hs.24485	chondroifin sulfate proteoglycan 6 (barnacan)	5.9
	106369	AA443828	Hs.25324	ESTs .	5.9
60	108255	AA063157	Hs.172608	ESTs	5.8
60	125370	AA256743 N52966	Hs.151791 Hs.142838	KIAA0092 gene product	5.8 5.8
	130010 131945	M87339	Hs.35120	ESTs replication factor C (activator 1) 4 (37kD)	5.7
	116238	AA479362	Hs.47144	DKFZP586N0819 protein	5.7
	102221	U24576		LIM domain only 4	5.6
65	130757	R00641	Hs.18925	ESTs; Wealdy similar to cDNA EST yk339a7.5 co	5.6
	131278	U81523	Hs.25195	endometrial bleeding associated factor (left-	5.6
	101383 131836	M14113 AA610086	Hs.79345 Hs.32990	coagulation factor VIIIc; procoagulant compon DKFZP566F084 protein	5.5 5.5
	129628	U26727	Hs.1174	cyclin-dependent kinase inhibitor 2A (melanom	5.5
70	106523	AA453441	Hs.31511	ESTs	5.5
-	111772	R28287	Hs.237146	ESTs	5.5
	101255	L34600	Hs.149894	mitochondrial translational initiation factor	5.5
	106895	AA489665	Hs.25245	ESTs	5.5 5.5
75	104943 129229	AA065217 AA211941	Hs.169674 Hs.109643	ESTs polyadenylate binding protein-interacting pro	5.5 5.4
, ,	102305	U33286	Hs.90073	chromosome segregation 1 (yeast homolog)-like	5.4 5.4
	106553	AA454967	Hs.5887	ESTs; Highly similar to RNA binding motif pro	5.4
	112305	R54822	Hs.26244	ESTs	5.3
00	123972	C14782	Hs.70337	immunoglobulin superfamily; member 4	5.3
80	102676	U72514	Hs.12045	pulative protein	5.3 5.3
	106459 107865	AA449741 AA025104	Hs.4029 Hs.61252	glioma-amplified sequence-41 ESTs	5.2 5.2
	121121	AA399371	Hs.189095	ESTs; Wealthy similar to zinc finger protein S	5.2
	127162	N76398	Hs.21187	ESTs	5.2

	131646	AA171895	Hs.30057	Homo sapiens clone 24749 and 24750 mRNA seque	5.2
	121770	AA421714	Hs.11469	KIAA0896 protein	5.2
	122512				5.1
		AA449311	Hs.98658	budding uninhibited by benzimidazoles 1 (yeas	
_	105870	AA399623	Hs.23505	ESTs	5.1
5	100341	D63506	Hs.8813	syntaxin binding protein 3	5.1
-	116848	H65187	Hs.39001	ESTs	5.1
	120821	AA347419	Hs.96870	Homo saplens mRNA full length insert cDNA cto	5.1
	130690	AA084286	Hs.139033	paternally expressed gene 3	5.1
	122661	AA454936	Hs.245541	ESTs	5.1
10					
TO	123169	AA488892	Hs.104472	ESTs; Weakly similar to Gag-Pol polyprotein [	5.1
	108810	AA130596	Hs.71331	ESTs; Weakly similar to POTENT HEAT-STABLE PR	5.0
	110799	N26101	Hs.7838	Human ring zinc-finger protein (ZNF127-Xp) ge	5.0
	120619			ESTs	5.0
		AA284372	Hs.111471		
	122792	AA460225	Hs.99519	ESTs	5.0
15	129912	AA047344	Hs.107213	ESTs; Highly similar to NY-REN-6 antigen [H.s	5.0
	102823	U90914	Hs.5057	carboxypeptidase D	4.9
	129890	M13699	Hs.111461	ceruloplasmin (ferroxidase)	4.9
	101084	L054 <b>25</b>		Homo sapiens autoantigen mRNA; complete cds	4.9
	134859	D87716	Hs.90315	KIAA0007 protein	4.9
20					4.9
20	115955	AA446121	Hs.44198	Homo sapiens BAC clone RG054D04 from 7q31	
	105516	AA257971	Hs.21214	ESTs	4.9
	114932	AA242751	Hs.16218	KIAA0903 protein	4.9
	106672	AA461300	Hs.30643	ESTs	4.8
	106126	AA424006	Hs.22972	ESTs; Moderately similar to H5AR (M.musculus)	4.8
25	110695	H93463	Hs.124777	ESTs	4.B
	102025	U03911	Hs.78934	mutS (E. coli) homolog 2 (colon cancer; nonpo	4.8
	133282	U52960	Hs.250855	SRB7 (suppressor of RNA polymerase B; yeast)	4.8
	119708	W67810	Hs.57904	mago-nashi (Drosophila) homolog; proliferatio	4.7
	120695	AA291468		ESTs	4.7
30			11- 400405		
οu	128651	AA446990	Hs.103135	ESTs	4.7
	103152	X66533	Hs.77890	guanylate cyclase 1; soluble; beta 3	4.7
	108699	AA121514	Hs.70832	ESTs	4.7
	115094	AA255921	Hs.88095	ESTs	4.7
	121429	AA406293	Hs.193498	ESTs	4.7
35	123203	AA489671	Hs.89709	glutamate-cysteine ligase (gamma-glutamylcyst	4.7
55					
	126802	AA947601	Hs.97056	ESTs	4.7
	130527	C17384	Hs.184227	F-box protein 21	4.7
	134470	X54942	Hs.83758	CDC28 protein kinase 2	4.7
					4.7
40	100449	D87470	Hs.75400	KIAA0280 protein	
40	110970	N51374	Hs.96870	Homo sapiens mRNA full length insert cDNA do	4.7
	115901	AA436403	Hs.86909	ESTs; Moderately similar to Frizzled-6 [H.sap	4.7
	109799	F10770	Hs.180378	Homo sapiens clone 669 unknown mRNA; complete	4.6
	116195	AA465148	Hs.72402	ESTs	4.6
	132122	U65092	Hs.40403	Cbp/p300-interacting transactivator; with Glu	4.6
45	108990	AA152296	Hs.72045	ESTs	4.6
43					
	109055	AA160529	Hs.48524	ESTs	4.6
	115937	AA443269	Hs.30991	KIAA0957 protein	4.6
	133520	X74331	Hs.74519	primase; polypeptide 2A (58kD)	4.6
					4.6
<b>50</b>	131200	AA609427	Hs.210706	ESTs; Moderately similar to !!!! ALU SUBFAMIL	
50	121369	AA405657	Hs.128791	Human DNA sequence from clone 967N21 on chrom	4.5
	132880	AA444369	Hs.177537	ESTs	4.5
					4.5
	127386	Al457411	Hs.106728	ESTs	
	120067	W93592	Hs.47343	ESTs	4.5
	122986	AA479063	Hs.102947	ESTs	4.5
55					4.5
55	135286	AA401269	Hs.97849	ESTs	
	130155	L33404	Hs.151254	kallikrein 7 (chymotryptic; stratum comeum)	4.5
	106103	AA421104	Hs.12094	ESTs	4.5
	102654	U68494	Hs.24385	Human hbc647 mRNA sequence	4.4
<b>C</b> C	107876	AA025315	Hs.61184	Novel human gene mapping to chomosome X	4.4
60	109454	AA232255	Hs.46912	ESTs	4.4
	125960	D63307	Hs.145968	ESTs .	4.4
				hect (homologous to the E6-AP (UBE3A) carboxy	4.4
	126892	Al160190	Hs.76127		
	100269	D38550	Hs.1189	E2F transcription factor 3	4.4
	134161	U97188	Hs.79440	IGF-II mRNA-binding protein 3	4.3
65					4.3
UJ	100502	HG1496-HT1		Adrenal-Specific Protein Pg2	
	105542	AA261858	Hs.8241	ESTs; Weakly similar to heat shock protein hs	4.3
	109787	F10610	Hs.34853	inhibitor of DNA binding 4; domlnant negative	4.3
	110759	N21671	Hs.19025	ESTs	4.3
70	129970	AA478975	Hs.200434	ESTs	4.3
70	134666	AA482319	Hs.8752	putative type II membrane protein	4.3
	117693	N40939	Hs.44162	ESTs; Weakly similar to cDNA EST yk342h12.5 c	4.3
	111008	N53388	Hs.7222	ESTs	4.3
	120977	AA398155	Hs.97600	ESTs	4.2
	105808	AA393808	Hs.21490	KIAA0438 gene product	4.2
75					
75	121381	AA405747	Hs.97865	ESTs; Weakly similar to WASP-family protein [	4.2
	100893	HG4557-HT	4962	Small Nuclear Ribonucleoprotein U1, 1snrp	4.2
	107176	AA621762	Hs.7576	ESTs	4.2
	118976	N93629	Hs.93391	ESTs	4.2
	130703	N63295	Hs.18103	ESTs	4.2
80	106540	AA454607	Hs.38114	ESTs; Weakly similar to coded for by C. elega	4.2
-					4.2
	119367	T78324	Hs.90905	ESTs -422	
	133633	D21262	Hs.75337	nucleolar phosphoprotein p130	4.2
	105520	AA258068	Hs.33085	WD repeat dornain 3	4.2
					4.1
	114264	Z40074	Hs.27595	, ESTs	7.1

	131046	X02530	Hs.2248	IP10; 'small inducible cytokine subfamily 8 (	4.1
	105220	AA210695	Hs.17212	ESTs	4.1
	103111	X63187	Hs.2719	epididymis-specific; whey-acidic protein type	4.1
5	125640 110561	R37700 H59617	Hs.208261 Hs.5199	ESTs ESTs; Wealty similar to UBIQUITIN-CONJUGATING	4,1 4,1
•	118092	N54915	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (from c	4.1
	134891	F03517	Hs.90787	ESTs	4.1
	112364 120699	R59312 AA291716	Hs.197642	ESTs; Weakly similar to DNA-DIRECTED RNA POLY ESTs	4.1 4.1
10	106272	AA432074	"Hs.97258 Hs.32538	ESTs	4.1
- •	112041	R43300	Hs.22929	ESTs	4.1
	131689	AA599653	Hs.30696	transcription factor-like 5 (basic helix-loop	4.1 4.1
	116134 107638	AA460246 AA009528	Hs.50441 Hs.42743	ESTs; Hightly stmilar to CGI-04 protein [H.sap ESTs; Weakly similar to predicted using Genef	4.1
15	131941	D62657	Hs.35086	ubiquifin-specific protease 1	4.0
	106154	AA425304	Hs.6994	ESTs	4.0
	105546 106319	AA262032 AA436606	Hs.26089 Hs.7392	ESTs; Weakly similar to 62D9.a [D.melanogaste ESTs; Weakly similar to Gu protein (H.sapiens	4.0 4.0
	121816	AA424814	Hs.187509	ESTs	4.0
20	122851	AA463627	Hs.99598	ESTs	4.0
	123337	AA504153	Hs.132797	ESTs; Weakly similar to ORF YGL050w [S.cerevi	4.0
	128643 129011	N40212 S72869	Hs.102958 Hs.107932	ESTs DNA segment; single copy; probe pH4 (transfor	4.0 4.0
	130895	AA609828	Hs.21015	ESTs; Highly similar to tetracycline transpor	4.0
25	132323	AA436102	Hs.256559	ESTs	4.0
	134255 102827	J05032 U91327	Hs.80758 Hs.6456	aspartyl-tRNA synthetase chaperonin containing TCP1; subunit 2 (beta)	4.0 4.0
	102123	U14518	Hs.1594	centromere protein A (17kD)	4.0
20	102813	U90651	Hs.151461	embryonic ectoderm development protein	3.9
30	113970	W86748	Hs.8109	ESTs	3.9 3.9
	107145 114212	AA621108 Z39338	Hs.173001 Hs.21201	ESTs DKFZP56680846 protein	3.9
	106614	AA458934	Hs.179912	ESTs	3.9
2.5	132742	AA490862	Hs.55901	ESTs; Weakly similar to C43H8.1 [C.elegans]	3.9
35	120948 129337	AA397822 R63542	Hs.104650 Hs.110488	ESTs; Highty similar to similar to mago nashi KIAA0990 protein	3.9 3.9
	103835	AA172215	Hs.93748	ESTs; Moderately similar to TRANSCRIPTION FAC	3.9
	133330	U42360	Hs.71119	Putative prostate cancer tumor suppressor	3.9
40	133928	N34096	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homologou	3.9 3.9
40	133640 133350	D83004 AA135468	Hs.75355 Hs.71573	ubiquitin-conjugating enzyme E2N (homologous ESTs	3.9
	115623	AA401475	Hs.39733	postsynaptic protein CRIPT	3.9
	101973	SB2597	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polypeptid	3.9
45	102669 134248	U71207 AA292677	Hs.29279 Hs.80624	eyes absent (Drosophila) homolog 2 ESTs	3.9 3.9
7.7	102380	U40434	Hs.155981	mesothelin	3.9
	116157	AA461063	Hs.44298	ESTs; Highly similar to HSPC011 [H.sapiens]	3.8
	106691	AA463453	Hs.23259	ESTs; Weakly similar to ACTIN; CYTOPLASMIC 2	3.8 3.8
50	115844 107159	AA430124 AA621340	Hs.234607 Hs.10600	ESTs ESTs; Weakly similar to ORF YKR081c [S.cerevi	3.8
-	106498	AA452141	Hs.7171	ESTs	3.8
	134405	J04177	Hs.82772	collagen; type XI; alpha 1	3.8
	106260 109864	AA431448 H02554	Hs.5250 Hs.30323	ESTs; Weakly similar to BACR37P7.g [D.melanog ESTs	3.8 3.8
55	124648	N91948	Hs.125034	ESTS	3.8
	134719	L07515	Hs.89232	chromobox homolog 5 (Drosophila HP1 alpha)	3.8
	113702	T97307	Hs.161720	ESTs; Moderately similar to !!!! ALU SUBFAMIL	3.8 3.8
	128639 111299	N91246 N73808	Hs.102897 Hs.24936	ESTs ESTs	3.6
60	129351	AA167268	Hs.62349	Human ras inhibitor mRNA; 3' end	3.7
	119741	W70205	Hs.43670	kinesin family member 3A	3.7
	105012 128734	AA116036 AA343629	Hs.9329 Hs.104570	chromosome 20 open reading frame 1 kallikrein 8 (neuropsin/ovasin)	3.7 3.7
	130567	L07493	Hs.1608	replication protein A3 (14kD)	3.7
65	114253	Z39909	Hs.14831	ESTs	3.7
	103169 111269	X68560 N70711	Hs.44450 Hs.18885	Sp3 transcription factor ESTs; Highly similar to CGI-116 protein (H.sa	3.7 3.7
	112876	T03488	Hs.4842	ESTs	3.7
~~	118261	N62780	Hs.94122	ESTs	3.7
70	130385	AA126474	Hs.155223	stanniocalcin 2	3.7 3.7
	129300 134388	C20976 M15841	Hs.110165 Hs.82575	ESTs; Highly similar to ribosomal protein L26 small nuclear ribonucleoprotein polypeptide B	3.7
	106968	AA504631	Hs.26813	ESTs; Weakly similar to hypothetical 43.2 kDa	3.7
75	100906	HG4716-HT		Guanosine 5-Monophosphale Synthase	3.7
75	100418 101484	D86978 M24594	Hs.84790 Hs.20315	KIAA0225 protein interferon-induced protein 56	3.7 3.7
	102547	U57911	Hs.46638	chromosome 11 open reading frame 8	3.7
	103587	Z29083	Hs.82128	5T4 oncofetal trophobiast glycoprotein	3.7
80	130600	AA478601	Hs.258737 Hs.104558	ESTs ESTs	3.7 3.7
JU	128733 134375	AA328993 AA412720	Hs.104556 Hs.82389	ESTs; Highly similar to CGI-118 protein (H.sa	3.7
	134098	X06323	Hs.79086	ribosomal protein; mitochondrial; L3	3.6
	101188	120320	Hs.184298	cyclin-dependent kinase 7 (homolog of Xenopus	3.6
	132149	T10822	Hs.4095	ESTs	3.6

	116200	AA465358	Hs.118793	ESTs; Highly similar to p621 [H.sapiens]	3.6
	121920	AA428300	Hs.161841	ESTs	3.6
	128609	AA234365	Hs.102456	survival of motor neuron protein interacting	3.6
_	101078	L04510	Hs.792	ADP-ribosylation factor domain protein 1; 64k	3.6
5	108693	AA121289	Hs.49597	ESTs; Highly similar to retinoic acid-induced	3.6
	109139	AA176121	Hs.59757	zinc finger protein 281	3.6
	111870	R37778	Hs.18685	ESTs; Weakly similar to hypothetical protein	3.6
	113848	W60080	Hs.27099	DKFZP564J0863 protein	3.6
10	127947	AI432475	Hs.146327	ESTs	3.6
10	128056	A1379480	Hs.125449	ESTs; Weakly similar to MaxiK channel beta 2	3.6
	129914	U22377	Hs.13321	rearranged L-myc fusion sequence	3.6
	13214B	AA283988	Hs.4094	ESTs	3.6
	134644	S83308	Hs.87224	SRY (sex-determining region Y)-box 5	3.6
1.5	115047	AA252627	Hs.22554	homeo box 85	3.6
15	102398	U42359		Human N33 protein form 1 (N33) gene, exon 1 a	3.6
	127479	AA513722	Hs.179729	collagen; type X; alpha 1 (Schmid metaphyseal	3.6
	105545	AA262030	Hs.5152	ESTs; Weakly similar to katanin p80 subunit [	3.6
	101483	M24486	Hs.76768	procollagen-proline; 2-oxoglutarate 4-dioxyge	3.6
20	105709	AA291268	Hs.26761	DKFZP586L0724 protein	3.6
20	122636	AA454103	Hs.110031	ESTs	3.6
	124792	R44357	Hs.132784	ESTs; Weakly similar to cDNA EST EMBL:T01421	3.6
	103621	Z47727	Hs.150675	polymerase (RNA) II (DNA directed) polypeptid	3.5
	105427	AA251330	Hs.28248	ESTs	3.5
0.5	121553	AA412488	Hs.48820	ESTs . *	3.5
25	115167	AA258421	Hs.43728	hypothetical protein	3.5
	134570	U66615	Hs.172280	SWI/SNF related; matrix associated; actin dep	3.5
	110787	N24716 ·	Hs.12244	ESTs; Weakly similar to C44B9.1 [C.elegans]	3.5
	131621	U77665	Hs.139120	ribonuclease P (30kD)	3.5
20	132813	N72116	Hs.57435	solute carrier family 11 (proton-coupled diva	3.5
30	116370	AA521256	Hs.236204	ESTs; Moderately similar to NUCLEAR PORE COMP	3.5
	131965	W90146	Hs.35962	ESTs	3.5
	115221	AA262942	Hs.79741	ESTs	3.5
	116093	AA456020	Hs.50848	ESTs; Weakly similar to KIAA0862 protein (H.s	3.5
~ =	123507	AA600176	Hs.112345	ESTs	3.5
35	129801	F11087	Hs.239666	ESTs	3.5
	115084	AA255566	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (from cl	3.5
	123442	AA598803	Hs.111496	ESTs .	3.5
	115061	AA253217	Hs.41271	ESTs	3.5
40	100146	D13645	Hs.2471	KIAA0020 gene product	3.5
40	115140	AA258030	Hs.55356	ESTs; Weakly similar to supported by GENSCAN	3.5
	115360	AA281950 °	Hs.5057	carboxypeptidase D	3.5
	130261	D83767	Hs.153678	reproduction 8	3.4
	100824	HG4058-HT4		Oncogene Aml1-Evi-1, Fusion Activated	3.4
4.5	102287	U31814	Hs.3352	histone deacetylase 2	3.4
45	102788	U86602	Hs.74407	nucleolar prolein p40	3.4
	118836	N79820	Hs.50854	ESTs	3.4
	102423	U44754	Hs.179312	small nuclear RNA activating complex; polypep	3.4
	106300	AA435840	Hs.19114	high-mobility group (nonhistone chromosomal)	3.4
	106156	AA425354	Hs.4210	ESTs	3.4
50	106483	AA451676	Hs.30299	IGF-II mRNA-binding protein 2	3.4
	107868	AA025234	Hs.61260	ESTs	3.4
	108187	AA056538	Hs.27842	ESTs; Weakly similar to similar to 1-acyl-gly	3.4
	116123	AA459282	Hs.43756	ESTs	3.4
	119501	W37721	Hs.151363	ESTs	3.4
55	129121	AA127459	Hs.108788	ESTs; Weakly similar to zeste [D.melanogaster	3.4
	131638	D87120	Hs.29882	predicted osteoblast protein	3.4
	132962	N34893	Hs.6153	ESTs; Highly similar to CGI-48 protein (H.sap	3.4
	133767	D63875	Hs.173288	KIAA0155 gene product	3.4
<b>C</b> 0	111823	R35253	Hs.24944	ESTs	3.4
60	134372	D63877	Hs.82324	KIAA0157 protein	3.4
	130938		Hs.21398	ESTs; Moderately similar to PUTATIVE GLUCOSAM	3.4
	120220	AA013250			
	115169	AA258427	Hs.58427	ESTs	3.4
				ESTs ESTs	3.4 3.4
	115169	AA258427	Hs.58427	ESTs ESTs; Weakly similar to PROTEIN PHOSPHATASE P	
65	115169 123978	AA258427 C20653	Hs.58427 Hs.170278	ESTs	3.4
65	115169 123978 108807	AA258427 C20653 AA129968	Hs.58427 Hs.170278 Hs.49376	ESTs ESTs; Weakly similar to PROTEIN PHOSPHATASE P ESTs; Weakly similar to beta-TrCP protein E3R ESTs; Weakly similar to ORF YGR200c (S.cerevi	3.4 3.4 3.4 3.4
65	115169 123978 108807 132581	AA258427 C20653 AA129968 R42266	Hs.58427 Hs.170278 Hs.49376 Hs.52256	ESTs ESTs; Weakly similar to PROTEIN PHOSPHATASE P ESTs; Weakly similar to beta-TrCP protein E3R	3.4 3.4 3.4 3.4 3.4
65	115169 123978 108807 132581 134654	AA258427 C20653 AA129968 R42266 W23625	Hs.58427 Hs.170278 Hs.49376 Hs.52256 Hs.8739	ESTs ESTs; Weakly similar to PROTEIN PHOSPHATASE P ESTs; Weakly similar to beta-TrCP protein E3R ESTs; Weakly similar to ORF YGR200c (S.cerevi	3.4 3.4 3.4 3.4 3.4 3.3
	115169 123978 108807 132581 134654 105730 111295 102009	AA258427 C20653 AA129968 R42266 W23625 AA292701 N73275 U02680	Hs.58427 Hs.170278 Hs.49376 Hs.52256 Hs.8739 Hs.5364 Hs.21275 Hs.82643	ESTs ESTs; Weakly similar to PROTEIN PHOSPHATASE P ESTs; Weakly similar to beta-TrCP protein E3R ESTs; Weakly similar to ORF YGR200c [S.cerevi DKFZP564I052 protein ESTs; Weakly similar to ubiquitin-conjugating protein tyrosine kinase 9	3.4 3.4 3.4 3.4 3.3 3.3
65 70	115169 123978 108807 132581 134654 105730 111295	AA258427 C20653 AA129968 R42266 W23625 AA292701 N73275	Hs.58427 Hs.170278 Hs.49376 Hs.52256 Hs.8739 Hs.5364 Hs.21275	ESTs ESTs; Weakly similar to PROTEIN PHOSPHATASE P ESTs; Weakly similar to beta-TrCP protein E3R ESTs; Weakly similar to ORF YGR200c (S.cerevi OKFZP564(052 protein ESTs; Weakly similar to ubiquitin-conjugating	3.4 3.4 3.4 3.4 3.3 3.3 3.3
	115169 123978 108807 132581 134654 105730 111295 102009 114161 130604	AA258427 C20653 AA129968 R42266 W23625 AA292701 N73275 U02580 Z38904 X03635	Hs.58427 Hs.170278 Hs.49376 Hs.52256 Hs.8739 Hs.5364 Hs.21275 Hs.82643 Hs.22385 Hs.1657	ESTs ESTs; Weakly similar to PROTEIN PHOSPHATASE P ESTs; Weakly similar to beta-TrCP protein E3R ESTs; Weakly similar to ORF YGR200c (S.cerevi DKFZP5641052 protein ESTs; Weakly similar to ubiquitin-conjugating protein tyrosine kinase 9 ESTs; Weakly similar to KIAA0970 protein [H.s estrogen receptor 1	3.4 3.4 3.4 3.4 3.3 3.3 3.3
	115169 123978 108807 132581 134654 105730 111295 102009 114161 130604 100103	AA258427 C20653 AA129968 R42266 W23625 AA292701 N73275 U02680 Z38904 X03635 AF007875	Hs.58427 Hs.170278 Hs.49376 Hs.52256 Hs.8739 Hs.5364 Hs.21275 Hs.82643 Hs.22385 Hs.1657 Hs.5085	ESTs ESTs; Weakly similar to PROTEIN PHOSPHATASE P ESTs; Weakly similar to beta-TrCP protein E3R ESTs; Weakly similar to ORF YGR200c [S.cerevi DKFZP564l052 protein ESTs; Weakly similar to ubiquitin-conjugating protein tyrosime kinase 9 ESTs; Weakly similar to KIAA0970 protein [H.s estrogen receptor 1 dolichyl-phosphate mannosyltransferase polype	3.4 3.4 3.4 3.3 3.3 3.3 3.3 3.3
	115169 123978 108807 132581 134654 105730 111295 102009 114161 130604 100103	AA258427 C20653 AA12968 R42266 W23625 AA292701 N73275 U02680 Z38904 X03635 AF007875 AA421171	Hs.58427 Hs.170278 Hs.49376 Hs.52256 Hs.8739 Hs.5364 Hs.21275 Hs.82643 Hs.22385 Hs.1657 Hs.5085 Hs.234545	ESTs ESTs; Weakly similar to PROTEIN PHOSPHATASE P ESTs; Weakly similar to beta-TrCP protein E3R ESTs; Weakly similar to ORF YGR200c [S.cerevI OKFZP5641052 protein ESTs; Weakly similar to ubiquitin-conjugating protein tyrosine kinase 9 ESTs; Weakly similar to KIAA0970 protein [H.s estrogen receptor 1 dofichyl-phosphate mannosyltransferase polype ESTs	3.4 3.4 3.4 3.3 3.3 3.3 3.3 3.3 3.3
70	115169 123978 108807 132581 134654 105730 111295 102009 114161 130604 100103	AA258427 C20653 AA129968 R42266 W23625 AA292701 N73275 U02580 Z38904 X03635 AF007875 AA421171 AA463745	Hs.58427 Hs.170278 Hs.49376 Hs.52256 Hs.8739 Hs.5364 Hs.21275 Hs.82643 Hs.22385 Hs.1657 Hs.5085	ESTs ESTs; Weakly similar to PROTEIN PHOSPHATASE P ESTs; Weakly similar to beta-TrCP protein E3R ESTs; Weakly similar to ORF YGR200c (S.cerevi DKFZP564I052 protein ESTs; Weakly similar to ubiquitin-conjugating protein tyrosine kinase 9 ESTs; Weakly similar to KIAA0970 protein [H.s estrogen receptor 1 dotichyl-phosphate mannosyltransferase polype ESTs ESTs; Weakly similar to PROBABLE ATP-DEPENDEN	3,4 3,4 3,4 3,3 3,3 3,3 3,3 3,3 3,3 3,3
	115169 123978 108807 132581 134654 105730 111295 102009 114161 130604 100103	AA258427 C20653 AA12968 R42266 W23625 AA292701 N73275 U02580 Z38904 X03635 AF007875 AA421171 AA463745 S77154	Hs.58427 Hs.170278 Hs.49376 Hs.52256 Hs.8739 Hs.5364 Hs.21275 Hs.82643 Hs.22385 Hs.1657 Hs.5085 Hs.234545 Hs.2345445 Hs.234545	ESTs ESTs; Weakly similar to PROTEIN PHOSPHATASE P ESTs; Weakly similar to beta-TrCP protein E3R ESTs; Weakly similar to ORF YGR200c (S.cerevi DKFZP5641052 protein ESTs; Weakly similar to ubiquitin-conjugating protein tyrosine kinase 9 ESTs; Weakly similar to KIAA0970 protein [H.s estrogen receptor 1 dofichyi-phosphate mannosyltransferase polype ESTs ESTs; Weakly similar to PROBABLE ATP-DEPENDEN nuclear receptor subfamily 4; group A; member	3.4 3.4 3.4 3.3 3.3 3.3 3.3 3.3 3.3 3.3
70	115169 123978 108807 132581 134654 105730 111295 102009 114161 130504 100103 121748 106698	AA258427 C20653 AA129968 R42266 W23625 AA292701 N73275 U02580 Z38904 X03635 AF007875 AA421171 AA463745	Hs. 58427 Hs. 170278 Hs. 49376 Hs. 52256 Hs. 8739 Hs. 25364 Hs. 21275 Hs. 82643 Hs. 22385 Hs. 1657 Hs. 5085 Hs. 234545 Hs. 234545 Hs. 234545 Hs. 28403 Hs. 82120 Hs. 79404	ESTs ESTs; Weakly similar to PROTEIN PHOSPHATASE P ESTs; Weakly similar to beta-TrCP protein E3R ESTs; Weakly similar to ORF YGR200c [S.cerevi OKFZP5641052 protein ESTs; Weakly similar to ubiquitin-conjugating protein tyrosine kinase 9 ESTs; Weakly similar to KIAA0970 protein [H.s estrogen receptor 1 dofichyl-phosphate mannosyltransferase polype ESTs ESTs; Weakly similar to PROBABLE ATP-DEPENDEN nuclear receptor subfamily 4; group A; member neuron-specific protein	3,4 3,4 3,4 3,3 3,3 3,3 3,3 3,3 3,3 3,3
70	115169 123978 108807 132581 134654 105730 111295 102009 114161 130604 100103 121748 106698 134353	AA258427 C20653 AA12968 R42266 W23625 AA292701 N73275 U02580 Z38904 X03635 AF007875 AA421171 AA463745 S77154	Hs.58427 Hs.170278 Hs.49376 Hs.52256 Hs.8739 Hs.5364 Hs.21275 Hs.82643 Hs.22385 Hs.1657 Hs.5085 Hs.234545 Hs.2345445 Hs.234545	ESTs ESTs; Weakly similar to PROTEIN PHOSPHATASE P ESTs; Weakly similar to beta-TrCP protein E3R ESTs; Weakly similar to ORF YGR200c [S.cerevi DKFZP564I052 protein ESTs; Weakly similar to ubiquitin-conjugating protein tyrosins kinase 9 ESTs; Weakly similar to KIAA0970 protein [H.s estrogen receptor 1 dotichyl-phosphate mannosyltransferase polype ESTs ESTs; Weakly similar to PROBABLE ATP-DEPENDEN nuclear receptor subfamily 4; group A; member neuron-specific protein ESTs	3.4 3.4 3.4 3.3 3.3 3.3 3.3 3.3 3.3 3.3
70	115169 123978 108807 132581 134654 105730 111295 102009 114161 130604 100103 121748 106698 134353 134154	AA258427 C20653 AA129968 R42266 W23625 AA292701 N73275 U02580 Z38904 X03635 AF007875 AA421171 AA463745 S77154 AA211320 F03321 N50641	Hs. 58427 Hs. 170278 Hs. 49376 Hs. 52256 Hs. 8739 Hs. 25364 Hs. 21275 Hs. 82643 Hs. 22385 Hs. 1657 Hs. 5085 Hs. 234545 Hs. 234545 Hs. 234545 Hs. 28403 Hs. 82120 Hs. 79404	ESTs ESTs; Weakly similar to PROTEIN PHOSPHATASE P ESTs; Weakly similar to beta-TrCP protein E3R ESTs; Weakly similar to ORF YGR200c [S.cerevi DKFZP564I052 protein ESTs; Weakly similar to ubiquitin-conjugating protein lyrosine kinase 9 ESTs; Weakly similar to KIAA0970 protein [H.s estrogen receptor 1 dotichyl-phosphate mannosyltransferase polype ESTs ESTs; Weakly similar to PROBABLE ATP-DEPENDEN nuclear receptor subfamity 4; group A; member neuron-specific protein ESTs Homo sapiens mRNA; cDNA DKFZp588C1723 (from c	3.4 3.4 3.4 3.4 3.3 3.3 3.3 3.3 3.3 3.3
70 75	115169 123978 108807 132581 134654 105730 111295 102009 114161 130604 100103 121748 106698 134353 134154	AA258427 C20653 AA129968 R42266 W23625 AA292701 N73275 U02680 Z38904 X03635 AF007875 AA421171 AA463745 S77154 AA211320 F03321	Hs.58427 Hs.170278 Hs.49376 Hs.52256 Hs.8739 Hs.5364 Hs.21275 Hs.82643 Hs.22385 Hs.1657 Hs.5685 Hs.234545 Hs.29403 Hs.292120 Hs.879404 Hs.65874	ESTs ESTs; Weakly similar to PROTEIN PHOSPHATASE P ESTs; Weakly similar to beta-TrCP protein E3R ESTs; Weakly similar to ORF YGR200c (S.cerevi DKFZP564l052 protein ESTs; Weakly similar to ubiquitin-conjugating protein tyrosine kinase 9 ESTs; Weakly similar to KIAA0970 protein [H.s estrogen receptor 1 dofichyl-phosphate mannosyltransferase polype ESTs ESTs; Weakly similar to PROBABLE ATP-DEPENDEN nuclear receptor subfamily 4; group A; member neuron-specific protein ESTs Homo sapiens mRNA; cDNA DKFZp586C1723 (from c ESTs	3.4 3.4 3.4 3.3 3.3 3.3 3.3 3.3 3.3 3.3
70	115169 123978 10887 132581 134654 105730 111295 102009 114161 130604 100103 121748 106698 134353 134154 133142 124461	AA258427 C20653 AA129968 R42266 W23625 AA292701 N73275 U02580 Z38904 X03635 AF007875 AA421171 AA463745 S77154 AA211320 F03321 N50641	Hs.58427 Hs.170278 Hs.49376 Hs.52256 Hs.8739 Hs.5364 Hs.21275 Hs.82643 Hs.22385 Hs.1657 Hs.5085 Hs.234545 Hs.234545 Hs.29403 Hs.82120 Hs.79404 Hs.558874 Hs.80285	ESTs ESTs; Weakly similar to PROTEIN PHOSPHATASE P ESTs; Weakly similar to beta-TrCP protein E3R ESTs; Weakly similar to ORF YGR200c [S.cerevi DKFZP564I052 protein ESTs; Weakly similar to ubiquitin-conjugating protein tyrosine kinase 9 ESTs; Weakly similar to KIAA0970 protein [H.s estrogen receptor 1 dotichyl-phosphate mannosyltransferase polype ESTs ESTs; Weakly similar to PROBABLE ATP-DEPENDEN nuclear receptor subfamity 4; group A; member neuron-specific protein ESTs Homo sapiens mRNA; cDNA DKFZp588C1723 (from c	3.4 3.4 3.4 3.3 3.3 3.3 3.3 3.3 3.3 3.3
70 75	115169 123978 108807 132581 134654 105733 111295 102009 114161 130604 100103 121748 106698 134353 134154 133142 124461 104903	AA258427 C20653 AA129968 R42266 W23625 AA292701 N73275 U02580 Z38904 X03635 AF007875 AA421171 AA463745 S77154 AA211320 F03321 N50641 AA055534	Hs. 58427 Hs. 170278 Hs. 49376 Hs. 52256 Hs. 8739 Hs. 5364 Hs. 22365 Hs. 22365 Hs. 1657 Hs. 5085 Hs. 234545 Hs. 29403 Hs. 82120 Hs. 79404 Hs. 65874 Hs. 80205 Hs. 124134	ESTs ESTs; Weakly similar to PROTEIN PHOSPHATASE P ESTs; Weakly similar to beta-TrCP protein E3R ESTs; Weakly similar to ORF YGR200c (S.cerevi DKFZP564l052 protein ESTs; Weakly similar to ubiquitin-conjugating protein tyrosine kinase 9 ESTs; Weakly similar to KIAA0970 protein [H.s estrogen receptor 1 dofichyl-phosphate mannosyltransferase polype ESTs ESTs; Weakly similar to PROBABLE ATP-DEPENDEN nuclear receptor subfamily 4; group A; member neuron-specific protein ESTs Homo sapiens mRNA; cDNA DKFZp586C1723 (from c ESTs	3.4 3.4 3.4 3.3 3.3 3.3 3.3 3.3 3.3 3.3
70 75	115169 123978 108807 132581 134654 105730 111295 102009 114161 1305043 100103 121748 100609 134353 134154 133142 124461 104903 106772	AA258427 C20653 AA129968 R42266 W23625 AA292701 N73275 U02580 Z38904 X03635 AF007875 AA421171 AA463745 S77154 AA211320 F03321 N50641 AA055534 AA478106	Hs. 58427 Hs. 170278 Hs. 49376 Hs. 52256 Hs. 8739 Hs. 2364 Hs. 22365 Hs. 1657 Hs. 5085 Hs. 234545 Hs. 22403 Hs. 82120 Hs. 65874 Hs. 65874 Hs. 65874 Hs. 60265 Hs. 124134 Hs. 12692	ESTs ESTs; Weakly similar to PROTEIN PHOSPHATASE P ESTs; Weakly similar to beta-TrCP protein E3R ESTs; Weakly similar to ORF YGR200c [S.cerev! OKFZP5641052 protein ESTs; Weakly similar to ubiquitin-conjugating protein tyrosine kinase 9 ESTs; Weakly similar to KIAA0970 protein [H.s estrogen receptor 1 dofichyl-phosphate mannosyltransferase polype ESTs ESTs; Weakly similar to PROBABLE ATP-DEPENDEN nuclear receptor subfamily 4; group A; member neuron-specific protein ESTs Homo sapiens mRNA; cDNA DKFZp586C1723 (from c ESTs ESTs; Weakly similar to protein phosphatase-1	3.4 3.4 3.4 3.3 3.3 3.3 3.3 3.3 3.3 3.3
70 75	115169 123978 108807 132581 134654 105730 111295 102009 114161 130604 100103 121748 106698 13435 134154 124461 104903 106772 109704	AA258427 C20653 AA129968 R42266 W23625 AA292701 N73275 U02680 Z38904 X03635 AF007875 AA421171 AA463745 S77154 AA21 1320 F03321 N50641 AA078106 F09687	Hs.58427 Hs.170278 Hs.49376 Hs.52256 Hs.8739 Hs.5364 Hs.21275 Hs.22385 Hs.1657 Hs.5085 Hs.234545 Hs.234545 Hs.234545 Hs.29403 Hs.82120 Hs.879404 Hs.65874 Hs.80285 Hs.124134 Hs.12692 Hs.12876	ESTs ESTs; Weakly similar to PROTEIN PHOSPHATASE P ESTs; Weakly similar to beta-TrCP protein E3R ESTs; Weakly similar to ORF YGR200c [S.cerevi DKFZP564I052 protein ESTs; Weakly similar to ubiquitin-conjugating protein tyrosins kinase 9 ESTs; Weakly similar to KIAA0970 protein [H.s estrogen receptor 1 dolichyl-phosphate mannosyltransferase polype ESTs ESTs; Weakly similar to PROBABLE ATP-DEPENDEN nuclear receptor subfamily 4; group A; member neuron-specific protein ESTs Homo sapiens mRNA; cDNA DKFZp586C1723 (from c ESTs ESTs; Weakly similar to protein phosphatase-1 ESTs	3.4 3.4 3.4 3.3 3.3 3.3 3.3 3.3 3.3 3.3

	118528	N67889	Hs.49397	ESTs	3.3
	124027	F03625	Hs.107537	ESTs	3.3
	131699	R68657	Hs.90421	ESTs; Moderately similar to IIII ALU SUBFAMIL	3.3
_	111044	N55443	Hs.23625	ESTs	3.3
5	103768	AA089997	Hs.180320	ESTs; Weakly similar to GOLGI 4-TRANSMEMBRANE	3.3
	131882	N49091	Hs.3385	ESTs; Highly similar to CGI-134 protein (H.sa	3.3
	123673	AA609471	Hs.112712	ESTs	3.3
	132936	AB002305	Hs.6111	KIAA0307 gene product	3.3
10	103023	X53793	Hs.117950	multifunctional polypeptide similar to SAICAR	3.3
10	120572	AA280794	Hs.258787	ESTs	3.3
	132384	AA479933	Hs.46967	Human DNA sequence from clone 167A19 on chrom	3.3
	105658	AA282914	Hs.10176	ESTs	3.2
	105086	AA147719	Hs.159441	ESTs	3.2
15	118695	N71781	Hs.50081	Homo sapiens mRNA full length insert cDNA do	3.2
13	112092	R44538	Hs.140889	ESTs	3.2
	125154	W38419	Hs.24936	ESTs	3.2
	108040	AA041551	Hs.48644	ESTs	3.2 3.2
	133453	M68941	Hs.73826	protein tyrosine phosphatase; non-receptor ty	3.2
20	124006	D60302	Hs.108977	ESTS ESTS: Woodshi similar to UEAT SUCCY 70 KD BBOT	3.2
20	116083 106753	AA455653 AA476944	Hs.44581 Hs.7331	ESTs; Weakly similar to HEAT SHOCK 70 KD PROT ESTs	3.2
	102621	U66075	Hs.50924	GATA-binding protein 6	3.2
	103330	X85373	Hs.77496	small nuclear ribonucleoprotein polypeptide G	3.2
•	128926	AA481403	Hs.107213	ESTs; Highly similar to NY-REN-6 antigen [H.s.	3,2
25	101167	L15309	Hs.193677	zinc finger-protein 141 (clone pHZ-44)	3.2
	104055	AA393755	Hs.117211	ESTs; Highly similar to CGI-62 protein [H.sap	3.2
	112917	T10196	Hs.4263	ESTs; Wealdy similar to /prediction	3.2
	120358	AA213459	Hs.100932	transcription factor 17	3.2
	121857	AA426017	Hs.62694	ESTs; Highly similar to DNA-REPAIR PROTEIN CO	3.2
30	122124	AA434257	Hs.186679	ESTs; Moderately similar to !!!! ALU SUBFAMIL	3.2
	132231	H99131	Hs.42635	ESTs	3.2
	134272	X76040	Hs.223014	protease; serine; 15	3.2
	115860	AA431719	Hs.61809	ESTs	3.2
	115278	AA279757	Hs.67466	ESTs; Wealdy similar to BACN32G11.d [D.melano	3.2
35	134125	R38102	Hs.50421	KIAA0203 gene product	3.2
	129160	AA131252	Hs.109007	ESTs	3.2
	121710	AA419011	Hs.96744	DKFZP586D0823 protein	3.2
	102242	U27185	Hs.32943	retinoic acid receptor responder (tazarotene	3.2
	104956	AA074880	Hs.120975	ESTs; Weakly similar to hypothetical protein	3.2
40	113047	T25867	Hs.7549	ESTs	3.2
	115017	AA251880	Hs.179982	turnor protein p53-binding protein	3.2
	133780	M14219	Hs.76152	decorin	3.1
	129453	AA421213	Hs.111632	Lsm3 protein	3.1
16	130353	X86018	Hs.172210	MUF1 protein	3.1
45	106036	AA412505	Hs.10653	ESTs	3.1
	102234	U26312	Hs.8123	chromobox homolog 3 (Drosophila HP1 gamma)	3.1
	106133	AA424346	Hs.107573	sialyltransferase	3.1 3.1
	116803	H47357 AA465194	Hs.6670	ESTs; Moderately similar to weak similarity t ESTs	3.1
50	106721 107115	AA610108	Hs.27693		3.1
50	133228	N90029	Hs.6831	ESTs; Highly similar to CGI-124 protein [H.sa Homo sapiens clone 1400 unknown protein mRNA;	3.1
	104733	AA019498	Hs.23071	ESTs	3.1
	103879	AA228148	Hs.50252	ESTs; Weakly similar to putative [C.elegans]	3.1
	103038	X54941	Hs.77550	CDC28 protein kinase 1	3.1
55	135154	AA126433	Hs.173242	sorting nexin 4	3.1
	114860	AA235112	Hs.106227	ESTs; Moderately similar to similar to murine	3.1
	102437	U46569	Hs.221986	aquaporin 5	3.1
	100352	D64159		Homo sapiens mRNA for 3-7 gene product, parti	3.1
	103631	Z48570		H.sapiens Sp17 gene	3.1
60	104238	AB002364	Hs.27916	a disintegrin-like and metalloprotease (repro	3.1
	108613	AA100967	Hs.69165	EST <sub>\$</sub>	3.1
	115915	AA436884	Hs.48926	ESTs	3.1
	120640	AA286945	Hs.163933	ESTs	3.1
	124068	H03099	Hs.101619	EST <sub>8</sub>	3.1
65	130375	U91931	Hs.155172	adaptor-related protein complex 3; beta 1 sub	3.1
	131632	AA443671	Hs.29826	ESTs .	3.1
	131523	H88801	Hs.201676	M phase phosphoprotein 10 (U3 small nucleolar	3.1
	115827	AA427890	Hs.44426	ESTs; Weakly similar to PHOSPHOLIPID HYDROPER	3.1
70	108828	AA131584	Hs.71435	DKFZP564O0463 protein	3.1
70	112198	R49483	Hs.22159	ESTs; Weakly similar to ZINC FINGER PROTEIN H	3.1
	123960	AA621785	Hs.170008	methylmalonate-semialdehyde dehydrogenase	3.1
	131538	Z29331	Hs.28505	ubiquitin-conjugating enzyme E2H (homologous	3.1
	105616	AA280670	Hs.24968	ESTs	3.1
75	101228	1.27706	Hs.82916	chaperonin containing TCP1; subunit 6A (zeta	3.1
75	100280	D42085	Hs.155314	KIAA0095 gene product	3.1
	132744	X54326	Hs.55921	glutamyl-prolyl-IRNA synthetase	3.1
	103105	X61970	Hs.76913	proteasome (prosome; macropain) subunit; alph	3.1
	106984	AA521201	Hs.7129	ESTs ESTs; Wealdy similar to contains similarity t	3.1 3.1
80	105127	AA158132 U33052	Hs.11817 Hs.69171	protein kinase C-like 2	3.1
30	102302 117708	N45114	Hs.46476	ESTs	3.1
	111314	N74574	Hs.33922	H.sapiens novel gene from PAC 117P20; chromos	3.0
	132902	AA490969	Hs.168147	ESTs	3.0
	130356	X84373	Hs.155017	nuclear receptor interacting protein 1	3.0
	.50000				

	128420	AI088155	Hs.14146	ESTs; Weakly similar to unknown [H.sapiens]	3.0
	108746	AA126974	Hs.43388	ESTs	3.0
	127236	Al341818	Hs.98658	budding uninhibited by benzimidazoles 1 (yeas ESTs	3.0 3.0
5	114208 107071	Z39301 AA609053	Hs.7859 Hs.35198	ESTs	3.0
-	104957	AA074919	Hs.10026	ESTs; Wealdy similar to ORF YJL063c [S.cerevi	3.0
	124073	H05394	Hs.127376	KIAA0266 gene product	3.0
	130869 101232	AA128100 L28997	Hs.2057 Hs.242894	uridine monophosphate synthetase (orotate pho ADP-ribosylation factor-like 1	3.0 3.0
10	104276	C02193	Hs.85222	ESTs; Weakly similar to R27090_2 [H.sapiens]	3.0
	126160	N90960	Hs.247277	ESTs; Weakly similar to transformation-relate	3.0
	128584	M11433	Hs.101850	retinol-binding protein 1; cellular	3.0
	100405 101335	D86425 L49054	Hs.82733	nidogen 2 Homo sapiens t(3;5)(q25.1;p34) fusion gene NP	3.0 3.0
15	108761	AA127514	Hs.61603	ESTs	3.0
	111346	N89829	Hs.13259	ESTs	3.0
	114988	-AA251089	Hs.94576	ESTs; Wealdy similar to phosducin; retinal [H	3.0 3.0
	116008 116545	AA449338 D20313	Hs.48589 Hs.74899	ESTs; Weakly similar to finger protein HZF6; ESTs	3.0
20	117873	N49967	Hs.46624	ESTs	3.0
	121463	AA411745	Hs.239681	ESTs; Weakly similar to KIAA0554 protein [H.s	3.0
	128625	AA242816 M25753	Hs.102652 Hs.23960	ESTs; Weakly similar to KIAA0437 [H.sapiens] cyclin B1	3.0 3.0
	131185 134380	D38073	Hs.179565	minichromosome maintenance deficient (S. cere	3.0
25	105740	AA293206	Hs.10852	ESTs -,	3.0
	130919	AA291710	Hs.21276	collagen; type IV; alpha 3 (Goodpasture antig	3.0 3.0
	134423 104896	W96151 AA054228	Hs.83006 Hs.23165	ESTs; Highly similar to CGI-139 protein [H.sa ESTs	3.0
	134407	X72964	Hs.82794	caltractin (20kD calcium-binding protein)	3.0
30	106378	AA445994	Hs.21331	ESTs	3.0
	112283	R53545	Hs.20952	Homo sapiens clone 24411 mRNA sequence	3.0 3.0
	109018 114239	AA156960 Z39742	Hs.114992 Hs.222478	ESTs ESTs	3.0
	114959	AA250775	Hs.87747	ESTs	3.0
35	116408	AA608752	Hs.71969	Homo sapiens mRNA; cDNA DKFZp564P0823 (from c	3.0
	115286 105809	AA279803 AA393827	Hs.82204 Hs.20104	ESTs ESTs	2.9 2.9
	113811	W44928	Hs.4878	ESTs ·	2.9
40	107248	D59894	Hs.34782	ESTs	2.9
40	134489	U09284	Hs.112378	LIM and senescent cell antigen-like domains 1 KIAA0244 protein	2.9 2.9
	134064 127370	D87685 AI024352	Hs.78893 Hs.70337	immunoglobulin superfamily; member 4	29
	113277	T65797	Hs.11774	protein (peptidyl-protyl cis/trans isomerase)	2.9
15	132783	N74897	Hs.5683	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide	2.9
45	109010 130095	AA156460 F01831	Hs.44229 Hs.14838	dual specificity phosphatase 12 ESTs	2.9 2.9
	106618	AA459249	Hs.8715	ESTs; Weakly similar to Similarity with snail	29
	103427	X97303	•	H.sapiens mRNA for Ptg-12 protein	2.9
50	133980	D00760	Hs.181309	proteasome (prosome; macropain) subunit; alph ESTs	29 29
50	111353 105344	N90430 AA235303	Hs.6616 Hs.8645	ESTs	2.9
	134498	M63180	Hs.84131	threonyl-IRNA synthetase	2.9
	117910	N50828	Hs.12940	zinc-fingers and homeoboxes 1	2.9
55	118903 121713	N90774 AA419198	Hs.132207 Hs.105577	ESTs; Moderately similar to !!!! ALU SUBFAMIL ESTs	2.9 2.9
55	129080	H19307	Hs.108507	ESTs	2.9
	129404	AA172056	Hs.111128	ESTs	2.9
	129457 130352	X55330 D87450	Hs.207776 Hs.154978	aspartylglucosaminidase KIAA0261 protein	2.9 2.9
60	133415	X69699	Hs.73149	paired box gene 8	2.9
	120649	AA287115	Hs.99697	ESTs	2.9
	131257	AA256042	Hs.24908	ESTS	2.9 2.9
	134480 116734	AA024664 F13789	Hs.83916 Hs.93796	NADH dehydrogenase (ubłquinone) 1 alpha subco DKFZP586D2223 protein	2.9
65	105028	AA126719	Hs.25282	ESTs	2.9
	114986	AA251010	Hs.87807	ESTs	2.9
	105651 1017:14	AA282481 M68874	Hs.18439	ESTs Hurnan phosphatidylcholine 2-acythydrolase (cP	2.9 2.9
	123398	AA521265	Hs.105514	ESTs	2.9
70	106007	AA411462	Hs.11042	ESTs; Weakly similar to veli 1 [H.sapiens]	2.9
	109450	AA232183	Hs.173042	ESTs; Weakly similar to !!!! ALU SUBFAMILY J Human BAC clone GS025M02 from 7q21-q22	2.9 2.9
	104685 108677	AA010530 AA115629	Hs.9599 Hs.118531	ESTs	2.9
	116028	AA452112	Hs.42644	thioredoxin-like	2.9
75	105404	AA243303	Hs.21187	ESTs	29
	132365 119638	AA598694 W52480	Hs.46541 Hs.56148	Homo sapiens PAC clone DJ0894A10 from 7q32-q3 ESTs; Moderately similar to NY-REN-58 antigen	29 29
	124637	N80716	Hs.75798	Human DNA sequence from clone 1183121 on chro	29
00	130588	AA287735	Hs.16411	Human DNA sequence from clone 1189824 on chro	2.9
80	105640	AA281623	Hs.7525	ESTs; Weakly similar to KIAA0742 protein [H.s	2.9 2.9
	131818 119298	Z39297 T23820	Hs.3281 Hs.155478	neuronal pentraxin II cyclin T2	2.9
	128742	D00763	Hs.251531	proteasome (prosome; macropain) subunit; alph	2.9
	115089	AA255876	Hs.86919	. ESTs; Weakly similar to !!!! ALU SUBFAMILY J	2.9

	100468	D89289	Hs.118722	fucosyltransferase 8 (alpha (1:6) fucosyltran	2.8
	132920	L06133	Hs.606	ATPase; Cu++ transporting; alpha polypeptide	2.8 2.8
	113490 133451	T88700 Y00764	Hs.173374	ESTs ubiquinol-cytochrome c reductase hinge protei	2.8
5	128770	H98645	Hs.73818 Hs.143460	protein kinase C; nu	2.8
_	129122	N62515	Hs.108790	ESTs	2.8
	104827	AA035630	Hs.8551	PRP4/STKWD splicing factor	2.8
	111348	N90041	Hs.9585	ESTs	2.8 2.8
10	130987 102139	R45698 U15932	Hs.21893 Hs.2128	ESTs; Weakly similar to cAMP inducible 2 prot dual specificity phosphatase 5	2.8
10	114902	AA236359	Hs.39504	ESTs	2.8
	106094	AA419461	Hs.18127	ESTs	2.8
	126438	N93125	Hs.137300	ESTs	2.8
15	107129	AA620553	Hs.4756	flap structure-specific endonuclease 1	2.8
15	104491	N71513	Hs.39328	ESTs ESTs; Wealdy similar to CD4.2 (C.elegans)	2.8 2.8
	105043 106855	AA132239 AA486182	Hs.11810 Hs.17975	ESTs, Wearly stituted to OD4.2 (Gelegials)	28.
	109695	F09530	Hs.180591	ESTs; Weakly similar to R06F6.5b [C.elegans]	2.8
	120455	AA251083	Hs.104347	ESTs	2.8
20	130861	N23393	Hs.20509	ESTs	2.8
	131649	AA481254	Hs.30120	ESTs	2.8 2.8
	128517	AA280617 HG1112-HT11	Hs.100861	ESTs; Weakly similar to p60 katanin [H.sapien Ras-Like Protein Tc4	2.8
	100486 116729	F13700	Hs.115823	ribonuctease P; 40kD subunit	2.8
25	101851	M94250	Hs.82045	midkine (neurite growth-promoting factor 2)	2.8
	115465	AA286941	Hs.43691	ESTs	2.8
	100137	D13627	Hs.15071	chaperonin containing TCP1; subunit 8 (theta)	2.8
	125837	H05323	Hs.146401	endothelial monocyte-activating polypeptide	2.8 2.8
30	131562 129445	U90551 AA306121	Hs.28777 Hs.111515	H2A histone family; member L ESTs; Weakly similar to predicted using Genef	2.8
50	129239	D31544	Hs.109701	ESTs; Moderately similar to weak similarity t	2.8
	106507	AA452584	Hs.91585	protein phosphatase 1; regulatory (inhibitor)	2.8
	101664	M60752	Hs.121017	H2A histone family; member A	2.8
25	129426	AA412087	Hs.168272	EST; Highly similar to protein inhibitor of a	2.8
35	103437 129821	X98260	Hs.82254 Hs.12696	M-phase phosphoprotein 11 cortactin SH3 domain-binding protein	2.8 2.8
	130160	F11019 Z39228	Hs.151344	UDP-Gat:betaGicNAc beta 1;3-galactosyltransfe	2.8
	104257	AF006265	Hs.9222	estrogen receptor-binding fragment-associated	2.8
	116204	AA465701	Hs.108646	ESTs	2.8
40	125914	AA262925	Hs.180034	cleavage stimulation factor; 3' pre-RNA; subu	2.8
	131510	AA207114	Hs.27842	ESTs; Weakly similar to similar to 1-acyl-gly ESTs	2.8 2.8
	106291 122761	AA435551 AA459296	Hs.30824 Hs.105039	ESTs; Weakly similar to !!!! ALU SUBFAMILY J	2.8
	107056	AA600310	Hs.18720	programmed cell death 8 (apoptosis-inducing f	2.8
45	108535	AA084505	Hs.226440	Homo sapiens clone 24881 mRNA sequence	2.8
	116226	AA478729	Hs.76450	ESTs	2.8
	120266	AA173939	Hs.193902	ESTs; Wealdy similar to inner centromere prot	2.8 2.8
	128654 116726	H20689 F13681	Hs.103180 Hs.42309	actin-like 6 ESTs	2.7
50	132640	U33821	153.72505	Tax1 (human T-cell teukemia virus type I) bin	2.7
	133273	AA147725	Hs.69469	dendritic cell protein	2.7
	108846	AA132983	Hs.44155	DKFZP586G1517 protein	2.7
	105621	AA280865	Hs.6375	Homo sapiens mRNA; cDNA DKFZp564K0222 (from c	2.7 2.7
55	129164 133618	AA282183 U78524	Hs.109045 Hs.75251	ESTs DEAD/H (Asp-Glu-Ala-Asp/His) box binding prot	2.7
55	120521	AA258785	Hs.107476	ATP synthase; H+ transporting; mitochondrial	2.7
	116429	AA609710	Hs.82837	Human chromosome 3p21.1 gene sequence	2.7
	110984	N52006	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polypeptid	2.7
60	100372	D79997	Hs.184339	KIAA0175 gene product	27
OU	125134 129254	W19228	Hs.100748 Hs.1098	ESTs deoxynucleotidyltransferase; terminal	2.7 2.7
	102339	AA453624 U37022	Hs.95577	cyclin-dependent kinase 4	2.7
	106589	AA456646	Hs.28661	ESTs	2.7
	119118	R44122	Hs.42743	ESTs; Wealdy similar to predicted using Genef	2.7
65	105973	AA406320	Hs.21201	DKFZP566B0846 protein	2.7
	106317	AA436568	Hs.172140	ESTs	2.7 2.7
	115551 103789	AA365527 AA096178	Hs.177861 Hs.70337	ESTs; Highly similar to CGI-110 protein [H.sa immunoglobulin superfamily; member 4	2.7
	105079	AA143190	Hs.12677	ESTs; Highly similar to CGI-147 protein (H.sa	27
70	109299	AA205649	Hs.86371	zinc finger protein 254	2.7
	122089	AA432136	Hs.98682	ESTs	2.7
	129108	L20321	Hs.1087	serine/threonine kinase 2	2.7
	129385	D82675	Hs.110950	Homo sapiens clone 25007 mRNA sequence SELENOPHOSPHATE SYNTHETASE; Human selenium d	27 27
75	131412 104052	U34044 AA393164	Hs.124027 Hs.97644	mammaglobin 2	2.7
	116254	AA481146	Hs.41086	ESTs; Wealty similar to OXYSTEROL-BINDING PRO	2.7
	106878	AA488872	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (from c	2.7
	114652	AA101416	Hs.107149	ESTs; Weakly similar to PTB-ASSOCIATED SPLICI	2.7
80	106831	AA482014	Hs.29463	centrin; EF-hand protein; 3 (CDC31 yeast homo	2.7 2.7
30	101445 124428	M21259 N36881	Hs.1066 Hs.82202	small nuclear ribonucleoprotein polypeptide E ribosomal protein L17	27
	114471	AA028074	Hs.103387	ESTs	2.7
	102051	U07550	Hs.1197	heat shock 10kD protein 1 (chaperonin 10)	2.7
	106916	AA490814	Hs.24170	. ESTs; Weakly similar to ribosomal S1 protein	2.7

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	116142	AA460649	Hs.39457	ESTs	2.7
	109912	H05509	Hs.24639	ESTs	2.7
	103193 102046	X70476	Hs.75724 Hs.182215	coatomer protein complex; subunit beta 2 (bet ADP-ribosytation factor-like 3	2.7 2.7
5	104567	U07151 R64534	Hs.101469	ESTs	27
•	112996	T23539	Hs.7165	zinc finger protein 259	2.7
	118138	N57773	Hs.93560	ESTs; Weakly similar to trg [R.norvegicus]	2.7
	123095 124315	AA485724 H94892	Hs.192119	ESTs v-rat simian leukemia virat oncogene homolog	2.7 2.7
10	124447	N48000	Hs.6906 Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (from cl	27
	132834	H77546	Hs.57898	ESTs; Highly similar to NY-REN-49 antigen [H.	27
	107529	Y12065	Hs.5092	nucleolar protein (KKE/D repeat)	2.7
	130648	AA075427	Hs.17296	ESTs; Weakly similar to /prediction	2.7 2.6
15	106685 133848	AA461551 AA093287	Hs.16251 Hs.76728	ESTs; Highly similar to 73 kDA subunit of de ESTs ·	26
15	134880	AA092376	Hs.90606	15 kDa selenoprotein	2.6
	128871	AA400271	Hs.106778	Homo sapiens mRNA for putative Ca2+-transport	2.6
	106846	AA485223	Hs.34892	ESTs	2.6 2.6
20	119892 132309	W84548 AA460917	Hs.94896 Hs.2780	ESTs jun D proto-oncogene	26
20	132923	U21858	Hs.60679	TATA box binding protein (TBP)-associated fac	2.6
	114365	Z41688	Hs.18653	ESTs	2.6
	114162	Z38909	Hs.22265	ESTs	2.6 2.6
25	133370 106818	AA156897 AA480890	Hs.72157 Hs.3542	OKFZP56411922 protein ESTs	2.6
23	133501	W16684	Hs.74284	ESTs; Moderately similar to Similar to S.cere	2.6
	100530	HG1869-HT1		Male Enhanced Antigen	2.6
	130553	AA430032	Hs.252587	pituitary tumor-transforming 1	2.6 2.6
30	108917 122249	AA137078 AA436679	Hs.173648 Hs.258543	ESTs ESTs; Highly similar to CGI-07 protein [H.sap	26
50	119598	W45531	Hs.94642	ESTs	2.6
	119902	W84865	Hs.40094	Human DNA sequence from clone 167A19 on chrom	2.6
	133272	AA465016	Hs.69423	kallikrein 10	26
35	132575	AA045365	Hs.5188	ESTs; Weakly similar to 60S RIBOSOMAL PROTEIN	2.6 2.6
33	130459 133083	AA460264 N70633	Hs.155983 Hs.6456	KIAA0577 gene product chaperonin containing TCP1; subunit 2 (beta)	2.6
	131130	T19399	Hs.23255	nucleoporin 155kD	2.6
	112043	R43317	Hs.26312	glioma amplified on chromosome 1 protein (leu	2.6
40	116146	AA460701	Hs.193200	ESTs	2.6 2.6
40	122378 103134	AA446100 X65724	Hs.103617 Hs.2839	ESTs Norrie disease (pseudoglioma)	2.6
	133395	AA491296	Hs.72805	ESTs	2.6
	115652	AA405098	Hs.38178	ESTs	2.6
15	104975	AA086071	Hs.50758	chromosome-associated polypeptide C	26
45	134691 112869	M59979 T03313	Hs.88474 Hs.4747	prostaglandin-endoperoxide synthase 1 (prosta dyskeratosis congenita 1; dyskerin	2.6 2.6
	100092	AF000231	Hs.75618	RAB11A; member RAS oncogene family	2.6
	102635	U66838	Hs.79378	cyclin A1	2.6
50	104490	N71503	Hs.43087	ESTs; Weakly similar to dysferlin [H.sapiens]	2.6
50	106813 106872	AA479922 AA487907	Hs.181022 Hs.18282	ESTs ESTs; Highly similar to unknown [H.sapiens]	2.6 2.6
	107022	AA599041	Hs.28866	programmed cell death 10	2.6
	107113	AA610073	Hs.23900	ESTs; Weakly similar to digophrenin-1 like p	2.6
55	113281	T66300	Hs.112356	Homo sapiens mRNA for lipoyltransferase; comp	2.6 2.6
55	115586 115779	AA399218 AA424183	Hs.92423 Hs.70945	ESTs ESTs	2.6
	122895	AA469946	Hs.105325	ESTs	2.6
	124726	R15740	Hs.104576	carbohydrate (keratan sulfate Gal-6) sulfotra	2.6
<i>(</i> 0	129775	R94659	Hs.12420	ESTs	2.6
60	131991	AA251909	Hs.36708	budding uninhibited by benzimidazoles 1 (yeas	2.6 2.6
	132518 134612	D57975 AA451712	Hs,5064 Hs.171581	ESTs ESTs; Highly similar to ubiquitin C-terminal	2.6
	130313	AA620323	Hs.154320	ubiquitin-activating enzyme E1C (homologous t	26
	131971	R70167	Hs.3611	ESTs	26
65	133175	AA134767	Hs.66666	ESTs	2.6 2.6
	102083 125670	U10323 AI432621	Hs.75117 Hs.82685	interteukin enhancer binding factor 2; 45kD CD47 entigen (Rh-related antigen; integrin-as	26
	121822	AA425107	Hs.97016	ESTs; Moderately similar to SH3 domain-bindin	2.6
<b>~</b> ^	106719	AA465171	Hs.236844	ESTs	2.6
70	130029	AA236412	Hs.236510	ESTs; Moderately similar to PFT27 [M.musculus	2.6
	124328	H97781 AA236951	Hs.14415 Hs.108636	ESTs; Highly similar to CGI-108 protein (H.sa chromosome 1 open reading frame 9	2.6 2.6
	105387 103073	X59417	Hs.74077	proteasome (prosome; macropain) subunit; alph	2.6
	116294	AA489000	Hs.93748	ESTs: Moderately similar to TRANSCRIPTION FAC	2.6
75	135339	D59269	Hs.127842	Homo sapiens mRNA full length insert cDNA clo	2.6
	125390	H95094	Hs.75187	translocase of outer mitochondrial membrane 2 Human mariner1 transposase gene; complete con	2.6 2.6
	102504 131076	U52077 H44386	Hs.247948 Hs.22666	ESTs	2.6
	114096	Z38342	Hs.27007	chromosome condensation 1-like	2.6
80	120402	AA234339	Hs.50282	GTP-binding protein ragB	2.6
	102125	U14550	Hs.107573	sialyltransferase	2.6 2.6
	134653 101959	AA452818 S80343	Hs.87385 Hs.180832	ESTs arginyl-IRNA synthetase	2.6
	116766	H13260	Hs.95097	. ESTs	2.6

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	104954	AA074514	Hs.26213	ESTs; Weakly similar to protein [H.sapiens]	2.5
	108771	AA127924	Hs.71034	ESTs	2.5
	116439	AA610068	Hs.43913	PIBF1 gene product	2.5 2.5
5	133859	U85782	Hs.178761	26S proteasome-associated pad1 homolog	2.5
,	132792 129620	AA401903 AA010686	Hs.242985 Hs.239720	hemoglobin; gamma G ESTs; Weakly similar to KIAA0691 protein [H.s	2.5
	120296	AA191353	Hs.22385	ESTs; Weakly similar to KIAA0970 protein (H.s	2.5
	115615	AA401186	Hs.48617	ESTs	2.5
	102983	X17620	Hs.118638	non-metastafic cells 1; protein (NM23A) expre	2.5
10	106288	AA435536	Hs.24336	ESTs	2.5
	107444	W28391	Hs.5181	proliferation-associated 2G4; 38kD	2.5
	104525	R16007	Hs.75355	ubiquitin-conjugating enzyme E2N (homologous	2.5
	128917	AA204876	Hs.206097	oncogene TC21	2.5 2.5
15	102299	U32907 AA282071	Hs.155545 Hs.152759	37 kDa laucine-rich repeat (LRR) protein activator of S phase kinase	25
13	115363 130399	AA449417	Hs.155356	Homo sapiens mRNA for putative glucosyltransf	25
	130752	D50927 ·	Hs.18895	tousled-like kinase 1	25
	132724	AA417962	Hs.55498	geranylgeranyl diphosphate synthase 1	2.5
	106743	AA476352	Hs.21938	ESTs; Weakly similar to KIAA0704 protein [H.s	2.5
20	128949	AA190993	Hs.8850	a disintegrin and metalloproteinase domain 12	2.5
	125685	AI040346	Hs.4943	hepatocellular carcinoma associated protein;	2.5
	105826	AA398243	Hs.21806	ESTs; Moderately similar to similar to NEDD-4	2.5
	110841	N31610	Hs.18645	ESTs; Weakly similar to partial CDS [C.elegan	2.5 2.5
25	111987 132669	R42036 AA188378	Hs.6763 Hs.54602	KIAA0942 protein ESTs; Weakly similar to 60S RIBOSOMAL PROTEIN	2.5
23	100398	D84557	Hs.155462	minichromosome maintenance deficient (mis5; S	2.5
	130800	AA223386	Hs.19574	ESTs; Weakly similar to kalanin p80 subunit [	2.5
	114481	AA033562	Hs.151572	ESTs	2.5
20	113404	T82323	Hs.70337	immunoglobulin superfamily; member 4	2.5
30	100260	D38491	Hs.174135	KIAA0117 protein	2.5
	103563	Z22534	Hs.150402	activin A receptor; type I	2.5
	104573 105025	R68952 AA126336	Hs.29780	ESTs ESTs; Weakly similar to ZINC FINGER PROTEIN 1	2.5 2.5
	105524	AA258158	Hs.22744 Hs.22153	ESTs; Weakly similar to KIAA0352 [H.saplens]	2.5
35	106157	AA425367	Hs.32094	ESTs	2.5
-	107243	D59489	Hs.34727	ESTs	2.5
	109920	H05733	Hs.30558	ESTs ·	2.5
	109981	H09552	Hs.26090	ESTs; Weakly similar to T20B12.1 [C.elegans]	. 2.5
40	114518	AA046407	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like 1	2.5
40	114768	AA149007	Hs.182339	Ets homologous factor	2.5 2.5
	118906 119025	N91000 N98926	Hs.94433 Hs.55209	ESTs ESTs; Weakly similar to DMR-N9 PROTEIN (H.sap	2.5
	131712	N29502	Hs.30991	KIAA0957 protein	2.5
	132233	X04706	Hs.93574	homeo box D3	2.5
45	132740	AA227751	Hs.55896	ESTs	2.5
	115239 .	AA278550	Hs.73291	ESTs; Wealdy similar to similar to the beta t	2.5
	128820	F10338	Hs.106309	Friend of GATA2	2.5
	124049	F10523	Hs.74519	primase; polypeptide 2A (58kD)	2.5 2.5
50	128781 121361	X85372 AA405494	Hs.105465 Hs.183052	small nuclear ribonucleoprotein polypeptide F ESTs	2.5
50	134133	X93920	Hs.180383	dual specificity phosphatase 6	2.5
	102502	U51678	Hs.78050	small acidic protein	2.5
	115875	AA433943	Hs.43946	ESTs; Weakly similar to Weak similarity to Ye	2.5
	132874	AA425776	Hs.58609	ESTs	2.5
55	109646	F04543	Hs.5028	DKFZP56400423 protein	2.5
	111197	N68093	Hs.22909	ESTs	2.5
	102968	X16396	Hs.154672 Hs.123645	methylene tetrahydrofolate dehydrogenase (NAD ESTs	2.5 2.5
	124911 106628	R88992 AA459657	Hs.123045	Homo sapiens clone 23570 mRNA sequence	2.5
60 -	116988 -		113.12311	ys69e12.s1 Soares relina N2b4HR Homo sapiens	2.5
-	131075	Y00757	Hs.2265	secretory granule; neuroendocrine protein 1 (	2.5
	133578	X78627	Hs.75066	translin	2.5
	100420	D86983	Hs.118893	p53-responsive gene 2	2.5
<b>C E</b>	130743	W87710	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (from d	2.5
65	122465	AA448164	Hs.99153	ESTs; Highly similar to CGI-73 protein [H.sap	25 25
	115117 124582	AA256492 N68477	Hs.49007 Hs.108408	poly(A) polymerase ESTs; Highly similar to CGI-78 protein [H.sap	2.5
	104771	AA025911	Hs.24994	ESTs; Highly similar to CGI-53 protein [H.sap	2.5
	108059	AA043944	Hs.62663	ESTs	2.5
70	105628	AA281251	Hs.35696	ESTs; Wealty similar to putative zinc finger	25
	109261	AA195255	Hs.61779	ESTS	2.5
	119789	W73140	Hs.50915	kalikrein 5	2.5
	130512	AA045304	Hs.181271	ESTs; Highly similar to CGI-120 protein [H.sa	2.5 2.5
75	134402 104769	U25165 AA025887	Hs.82712 Hs.114774	fragile X mental retardation; autosomal homol ESTs; Weakly similar to !!!! ALU SUBFAMILY J	2.5
, 5	125787	AA744748	Hs.29403	ESTS; Weakly similar to PROBABLE ATP-DEPENDEN	2.5
	131775	AA459555	Hs.31921	KIAA0648 protein	2.5
	•				

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TABLE 7B:
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

	Pkey	CAT Number	Accession
5	101335	46413_1	L49054 N87447 AA248791 AA452193 AI015525 AI762070 AA781526 AW183498 AA625682 AI268713 AA400391 AI193725 AW590304 W56360 AA936067 AI99398 AA466183 AA628688 AA844206 AA621117 AI141092 AI808150 BE379750 AI351482 AA693527 AA405119 AA400562 AW368723 AA463811 AW242927 R50034 W56334 F21257 AA164314 BE074125 AA470924 AI307439 W16738 AA026647 T33599 T19178 AA164313 AI744010 AI015466 AI014921
	100906	4312_1	AU076916 BE298110 AW239395 AW672700 NM_003875 U10860 AW651755 BE297958 C03806 Al795876 AA644165 T36030 AW392852 AA446421 AW881856 Al469428 BE548103 T96204 R94457 N78225 AI564549 AW004984 AW780423 AW675488 AW087890 AA971454 AA305698 AA879433 AA535069 AI394371 AA928053 AI378367 N59764 AI364000 AI431285 T81090 AW674657 AW674987 AA897396 AW673412 BE063175 AW674408 AI202011 R00723 AI753769 AI460161 AW079585 AW275744 AI873729 D25791 BE537646 T81139
10	102221	3861_1	R00722 NM_006769 U24576 AW161961 AW160473 AW160465 AW160472 AW161069 AI824831 AW162635 AI990356 AW162477 AW162571 AI520836 AW162352 AW162351 AW162752 AI962216 AI537346 AA853902 H17667 BE045346 BE559802 BE255391 AA985217 AA235051
15			A1129757 AW366451 T34489 D56106 D56351 AI936579 AW023219 AW889335 AW889120 AW889232 AW889175 BE093702 AW889349 AA147546 AI952998 AA912579 A1143356 AW902211 R64717 AW157236 AI815242 D45274 AW263991 AA442920 AA129965 AL035713 AI923255 AI949082 AI142826 AI684160 AI701987 AI678954 AI887349 BE4636353 AW628092 AW302281 AA493203 BE348856 BE536419 AW193969 AW673561 AW592609 AI224044 H43943 AA091912 R49632 R48353 AI568409 R48256 AI198046 H27986 H43899 AI678759 AI680310 AI624220 H17052 AA156410 N56062 AI699430 AA664529 T09406 T10459 AA627505 AI379584 N83831 N88633 AW022651
			AA971281 AA248036 Al039197 Al914689 AA973825 AL047305 AA129966 Al798369 AW264348 Al445879 Al658759 N67924 Al933507 Al216121 Al333174 T10972 Al375028 Al186756 Al273778 AA610487 Al797946 AA853903 AA903939 Al338587 Al278494 AW627595
20	101714	30725_1	AA904019 M68874 AL022147 M72393 AL049797 BE439441 T27650 AI766240 AW150345 AW778943 AI627464 BE439479 AA587049 AI277900
	116803	55078_4	A1984983 A1630935 H47357 W33034 H55976 H55975 R67830 AA527091 F24482 AW841585 R66514
25	116988 132640	185904_1 179_1	AW953679 AW953680 AA244436 H82527 AA361046 AA244483 H82526 AW162087 AA224538 AA471218 AA088655 AA375275 BE440052 AF090891 AA324435 AF063549 Al110675 AA322223 AW953306 AA233590 AW949864 AW949859 AA383721 AA081878 U33821 NM_006024 AA350900 AA081588 Al148087 AF268075 AA088185 Al142478 AA081824 Al887930 AA070570 BE185248 A459825 BE257794 AA420459 AA420859 AA777997 AA081219 AW815721 AW854758 AA157932 BE018208 AW378974 AL041212 Al247564 AW581897 Al002897 BE543242 Al811690 AW852076 AW852270 AA360869 AA094943 AA090680 AW601554 AA099673 AA662226 AA356814 AA330174 AA187544 C02751 AA315460 BE168358
30			AA300399 AA403945 AA632422 AW156901 AW95973 AA604222 AA359614 AA359174 AA167944 C02731 AA5154600 ET IBD538 AW080447 AI813764 AI624222 AW156901 AI956923 AW473780 AI861975 AA173643 AW511541 AI951492 BE301686 AA669760 BE182212 AA081009 T69431 AI186207 AA604124 AA707346 AA173953 AI016700 AI125916 AA358962 AI673719 T90593 T90497 T10776 AW513002 AW304292 AA724885 AW474759 AI811621 AW068925 AA666305 AI580161 AI128023 AW471151 AA534849 AA666358 AI078833 AI139223 AI244874 AI381658 AW263441 AI432440 AW602882 N66401 AA224251 AI167469 AI141060 AA099214 AI537130 AL 120426 AA948655 D53110 AA076099 AA938617 AA826543 AI357914 AA556098 AA807694 AI288812 AA632832 AA157933 AA639802
35			AA634268 AA282337 AA551431 AA557374 AA256923 AA872943 AA003665 H83626 AA810385 T92925 T36145 AA632190 AA130438 AI686635 AA130437 AW392904 AW392839 AW392848 AW392836 AA729737 AA070450 AW392890 W04825 AA771848 AA084634 AA481985 A1263840 AI801006 AA235380 AI954229 A1559330 A1208724 AA887638 T25894 AA041269 W44443 AI581770 W46171 AA878485 W46535 AA197336 AA894945 AA394224 A1766834 A1582590 A1033007 AA481889 AW190598 AW392855 R27279 AA398137 A1248407 A1241386 A1991753 A1825585 AA865699 A1096806 A1833030 AA041279 AW888745 A1703279 N70572 A1912553 BE549931
40			A1240422 AW376187 AW591692 AA975905 AW614967 AA009666 W44332 AA664659 T06561 BE468150 Al650695 AA587920 Al473310 A1032991 AA256499 AW104241 BE163782 AI984973 BE163613 Al263906 AA628191 AA282072 BE163769 BE163775 Al492939 Al473315 D56907 AA587930 H69480 Al362373 AA598483 D56595 A167590 C16223 Al935415 D62565 D62884 D63130 Al760286 Al650286 AW173598 Al499145 Al122566 AW903408 AI810569 AA854936 BE049510 D62065 D61900 D62101 R27475 Al469835 Al669086 N80399 N49922 N48746 AA481381 R222588 H13912 AC004549 AW602500 AW768788
45	103427	43892_1	N40522 N4074 9 0-0451361 N22536 R15312 AC004245 AVX105705 BE514383 AA071273 AW247987 AW673286 BE312102 AW749824 BE071985 AW577383 BE071945 BE072005 AW577355 BE071965 AW239231 BE072000 BE071960 AW577360 AW749830 AW373020 X97303 AW999522 BE000192 BE562219 BE266655 BE264970
	103631	152_34	R64730 AF214731 T19173 BE258318 AF161446 BE542228 BE383856 BE266748 BE543260 AA640735 AA788907 BE251313 BE221852 AW855357 AA224407 AW855346 BE150454 AW070651 BE326867 AW051698 A1829278 A1470927 AW855345 A1804942 A1971004
50			BEC46620 A1863664 AA808492 A1915971 BE046949 AW590711 A1468066 BE409685 AA332653 BE385394 AA852623 BE255591 BE254968 AA211871 BE255493 BE257727 BE255389 BE257491 BE262528 BE261296 BE313277 BE261714 BE314316 Z28434 AA315545
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60	•		AA872914 W31065 N54216 AJ568741 H56262 NM_017425 Z48570 AJ831777 T75007 AA354867 AA427988 AJ922844 AA733170 AW821145 BE081547 AW881571 AW881573 AW055249 AA204724 AJ417415 A1127303 AJ355013 AJ039527 AW593259 AA576745 AJ457317 AW593236 H93126 BE396072 AL134941 AW629175 AJ424011 AA115732 AA179986 AJ334944 AW367922 AW152304 AA806752 AJ312418 AW935023 BE301136 AA032258 AJ829922 AJ372405 BE177074 AW513734 AJ151526 AA975643 AA478034 AJ814200 AW080063 AJ032624 BE177107 AA319768 AW935098 AJ017620 AA974477 D51441 C14225 AL043583 D80145 AJ690771 AW09711 AW881570
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	120695	9683_3	AA976503 AI917802 AA953664 AA404613 AA428771 BE280542 AW194691 AI927301 AI740458 AI796100 AI935603 AW052210 AA970201 AI633384 AA425910 AI017004 AI241295 AA402816 AA291468

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	100352	37786_1		887 D64159 AF112218 AI766633 AL039303 AL133888 E 141 BE620065	BE620604 AW976259 AW262792 AW591383 AI365413 N36652 AA807027	
	101084	13883_1	AW409	9934 AW245855 AU077157 AW163245 AW161434 AW2	50083 AA316055 BE621134 AA171883 BE272494 L05425 BE250310	
5			AL 135 BE250 AW15 AA483	350 AW996947 AA403201 AA446682 W79685 AW24624 413 AW250833 BE076336 A!925558 A!907634 AW8041 7242 AA934590 Al628921 Al470650 AW409935 AW1727 514 AA125418 AA722289 AA780182 AW768894 AW183	3518 BE394454 AA126101 AA581348 AA303227 AA058438 AA126544 19 AW577783 AW002316 AA320025 AW753913 A7798554 AW070650 93 AW804270 AA902387 AW804232 AW804255 AW607751 A1909114 193 AA401208 AW162279 AA888018 BE206452 AI826742 AA857353 1014 AW156969 AI244063 AA863491 AI376281 AA582490 AA846248	
10	100502	26409_1	AA493 U1597 BE259 AA701	881 W81287 AA515590 AA659297 AA635139 AA65929: 9 X17544 W52755 NM_003836 Z12172 AW370136 BE2 1532 D16897 AA885610 AA911283 AA319627 R94472 R 996 AW418723 N53220 AA602813 AA576128 AA59378	62564 T49116 AA333753 BE262238 BE313737 H39153 AW583056 R28890 29022 AA443405 R96397 W04904 W01746 W01204 N74203 N58621 6 AA911577 AA575957 A1149135 AW57305B AA772985 A1188918 A1372065	
15			BE467 AW93	454 T49117 Al268620 AA928248 AA449494 ÁA318817 `	135742 AA235245 W32706 AA447372 R96355 N59573 AA904616 A1291224 T49929 R94473 H38154 A1076649 AW935307 AW605112 AW935433 15384 A184857 AA319871 T29465 C21134 Z19785 AA329107 T52079 1346673 R82547 T50006	
	102398	entrez_U4	2359 U4235	9		
<ul><li>20</li><li>25</li></ul>	GeneChip the 3rd hig gene-spec	array such that hest amongst v ific background	the ratio of "ave arious ovarian c	rage" ovarian cancer to "average" normal adult tissues w ancers. The "average" normal adult tissue level was set i ecific hybridization, the 15th percentile value amongst the	nese were selected from 35403 probesets on the Affymetrix/Eos-Hu01 as greater than or equal to 4.0. The "average" overlan cancer tevel was set to the 4th highest amongst various non-malignant tissues. In order to remove a non-malignant tissues was subtracted from both the numerator and the	)
30	Pkey: Prin Ex. Acon: UG ID: Ur Title: Unio	nekey Exemplar Acce niGene ID	ssion	GENES, OVARIAN CANCER VERSUS NORMAL ADULT	TISSUES	
35	Pkey 130941 101249 132528	Ex. Accn D49394 L33881 AA283006	UG ID Hs.2142 Hs.1904 Hs.50758	Title 5-hydroxytryptamine (serotonin) receptor 3A protein kinase C; tota chromosome-associated polypeptide C	ratio 12.1 11.8 11.5	
40	102610 115536 129571 105298 121779	U65011 AA347193 X51630 AA233459 AA422036	Hs.30743 Hs.62180 Hs.1145 Hs.26369 Hs.98367	preferentially expressed antigen in melanoma ESTs Wilms tumor 1 ESTs ESTs	11.0 10.0 9.3 7.8 7.3	
45	104301 132191 102136 101804 132572	D45332 AA449431 U15552 M86699 AA448297	Hs.6783 Hs.158688 Hs.85769 Hs.169840 Hs.237825	ESTs KIAA0741 gene product ecidic 82 kDa protein mRNA TTK protein kinase signal recognition particle 72kD	6.9 6.7 6.6 6.5 5.9	

132572 AA448297 AA470145 Hs.237825 Hs.25130 signal recognition particle 72kD ESTs 106738 108857 AA133250 Hs.62180 ESTs 50 115291 AA279943 Hs.122579 **ESTs** 5.8 5.8 5.7 5.7 guanine-monophosphale synthetase ESTs 132632 N59764 Hs.5398 Hs.59698 Hs.184167 116401 AA599963 splicing factor, arginine/serine-rich 7 (35kD HKR-T1=Kruppel-like zinc finger protein (huma 132725 129097 L41887 S50223 55 134520 N21407 Hs.257325 **ESTs** Hs.90847 Hs.24485 108778 AA128548 general transcription factor IIIC; polypeptid 5.4 chondrollin sulfate proteoglycan 6 (bamacan) DKFZP586N0819 protein 5.2 5.2 131228 AA279157 AA479362 AA043562 Hs.47144 Hs.62637 116238 5.1 5.1 108055 **ESTs** 60 U76189 Hs.61152 exostoses (multiple)-like 2 132939 5.0 115909 AA436666 Hs.59761 ESTs; Weakly similar to ORF YKR074w [S.cerevi 120438 123494 109648 Hs.99488 Hs.112110 Hs.7154 5.0 AA243441 5.0 AA599786 **ESTs** F04600 ESTs 4.9 65 132624 AA164819 Hs.53631 **ESTs** 4.9 4.9 4.9 4.8 4.7 111234 N69287 Hs.21943 ESTs; Wealty similar to ORF YGL221c [S.cerevi 135242 M74093 Hs.9700 cyclin E1 AA479726 Hs AA489033 Hs HG2874-HT3018 **ESTs** 123005 Hs.105577 Homo sapiens mRNA; cDNA DKFZp586K1318 (from c Ribosomal Protein L39 Homolog 116296 100661 Hs.62601 70 4.6 4.5 4.5 4.5 4.4 4.4 4.4 4.2 4.2 4.2 4.1 111345 N89820 Hs.14559 ESTs 102627 U66561 Hs.158174 zinc finger protein 184 (Kruppel-like) AA449741 U33286 AA211941 R40873 glioma-amplified sequence-41 chromosome segregation 1 (yeast homolog)-like polyadenylate binding protein-interacting pro KIAA0432 gene product 106459 Hs.4029 102305 129229 Hs.90073 Hs.109643 75 130376 Hs.155174 120619 AA284372 Hs.111471 **ESTs** Hs.256579 Hs.39982 Hs.88095 ESTs ESTs 122802 AA460530 AA509219 AA255921 116416 115094 126802 80 ESTs AA947601 Hs.97056 **ESTs** hect (homologous to the E6-AP (UBE3A) carboxy 126892 AI160190 Hs.76127 105516 AA257971 Hs.21214 **ESTs** 131985 AA434329 Hs.36563 . ESTs

				507		4.0	
	114965 120821 134621	AA347419 H L02547 H	ts.72472 ts.96870 ts.172865	ESTs Homo sapiens mRNA full length insert cleavage stimulation factor; 3' pre-RNA	cDNA clo t; subu	4.0 4.0 4.0	z.
5	134161	U97188 H	ts.79440	IGF-II mRNA-binding protein 3		4.0	
	CAT numb	: que Eos probeset i er: Gene cluster n : Genbank accessi	umber	ber			
10	Accession	Genuani accessi	ion numbers				
	Pkey 101249	CAT Number 2520_1	L18964 NI AW08751	4_002740 l33881 AA095249 BE080871 1 A1480090 A1873147 T57875 A1217404 1 A1032193 A1953696 A1630583 AA0626	AA827196 Al279471 AA969	093 AA815168 AA988896 AI7	467131 AW088338 AW937631 54623 T28044 AW950302
15	100661 116401	23182_1 95855_1	BE623001 AW89394	L05096 AA383604 AW966416 N53295 D AW978851 AA034240 Al686323 Al767 A835700 AA599963 T20152 AA533167	AA460213 AW571519 AA60	3655	AA835698 AA447216 Al623248
	116416	373989_1	AW75367	6 R11789 AW001886 AA609219 AW780 42970 R63752	420 A1860557 A1280331 A13	34300 Al288870 AA669343 N	29918 BE537790 AA934687
20	132191	54683_4	AA507576 Al189144 Al743979 Al380330	Al610269 Al380079 R40309 Al203932 Al016691 W45515 AA551452 AA44943 Al283341 AW340338 AA774643 AW104 Al247787 AA770467 Al200154 Al08965 AA907692 N21250 AW904736 Al90932	. T10046 AA424059 N62822 778 A1078020 N21487 H975 3 A1089890 A1695738 W885	AW197701 AA465242 AI4189 62 AA970063 BE327945 F038 24 AI471010 AA700191 AA778	989 A1942433 A1891115 BE302316 880 F03885 AA970699 A1298468 8937 BE440182 R79225 AA338236
25			AA465598	AA321185 AW130492 AI824479 AI682	992		
	130941 115909	2774_1 47548_1	AW24890 AW87252	59 D49394 BEŹ52349 AW249320 AW24 3 AA731733 AA804189 AA703169 A1435 7 AA453863 AA442475 AF086541 AA36	6492 A1076288 AA912176 A\ 5801 A1692575 AW131631 A	N248713 AA743457 R08170 C	C06167 R02351
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33			Al206773	AI879827 R64193			
40	102136	17647_1	BE169677 AW00226	i U15552 NM_014597 AA223318 AA171 I AW117711 AW366303 AW366302 AW 6 BE064947 BE064722 T10372 AW8386	366308 AW366304 AW3663 381 Al811119 AW262098 AA	00 A1908432 AW591937 A1358 588547 A1916666 A1440083 A	B420 AW272622 C75067 A1926471 N078150 F24260 AA512919
40			AI953413 AW74793	A1064798 A1420425 AA191324 BE5032 6 A1589491 AA559096 A1090265 AA548	22 A1632721 AA180035 AA5 959 AA223220 AW515936 A	58329 W44843 T10610 W384 W368395 AW368407 BE5407	42 BE542869 AI125024 BE279566 76 AI039762 AI584020 AA171691
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55			AI868711 AI278406 BE39797 AA45950	IE094097 AI826398 H58956 T17222 AW AA582354 AA524392 R01549 R01641 I AW609291 AA137249 AA142866 AA63 I AW609285 T65602 T99684 T97378 AV 3 N95643 AW821210 AW813461 AW588 I6 AW582079 AW609276 AW609280 AV	Z21083 AA528463 T39127 A 9198 AW609271 AW149760 N609366 T85647 AI572235 2064 AW609293 AW609320	A989472 F09450 AA084485 E A1025112 AA236620 AA9372 F99083 AA199583 AW303874 AW609270 AW582085 AW58	BE004378 AW974353 AA137250 48 U90736 AW005487 AW674427 I T35523 AA586445 Z39669 2071 AW609318 AW813451
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	109548 132528	708849_1 11027_8		N362549 A1671064 T23526 F03426 F04 A284422 AA283006	694 F04600 Al635856 Z387	5 F02039 AW022635	
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70			AW0818 Al921404 N74716 / T90801 /	10 W93905 W96519 A1863832 AA44317 19 AA714970 A1122630 W04887 AW662 1 AA143770 AA587675 BE302192 AA81: 10W969249 AA468581 AA516399 A12747 1383246 A1740957 T86758 A1471248 A1 1 T99348 A1924643 AW103910 A180290	427 AA602680 W93645 AA5 3080 A1493386 AW327435 A 26 A1131244 A1572604 A192 864233 AA910590 A1079094	82946 AW008812 AA311187 .W340871 Al143616 AA68723 9236 AW327971 R65637 N90 ! AW805781 AA709025 AW19	AA463631 Al421918 Al400518 I1 AA218961 Al362249 Al378345 I309 H07877 W96486 Al358806 I6707 AW327436 Al903790
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	132624	42095_1	AA32610	8 W74020 AW612698 A1750909 AA487 AA525338 AA526640 HB4308 AA27894:	800 AJ270695 AA044941 H2 2 AA164818 AA847110 T823		
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			AA961206 N41430 N41439 AW630477 W37595 BE394538 AA365256 N47771 N34873 AA988105 AI242138 AW146523 AI978761 N50882 AA527448 AW086200 AI750910 N50868 AA709437 N51946 AI222179 AA732883 H96742 AW0815360 N53720 W37490 R87362 AA613273 H98999 AI465022 AI368442 AI460122 N20486 N24087 AA164819 N24878 AW471270 AW790458 R68240 AA594434 N20460 AI419626 AW500664 AI033658 AA593215 AA907408 AA713508 AI42267 H85551 AA923571 D62680 AW627456 H96206 AA016289 AA485896 N25691
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25	•		AA662222 AA664912 AA244152 AW611553 BE503285 AA211023 AA383016 AI698174 AW195381 AA948229 AI768495 AI690437 N30025 AI718952 AI953572 BE464509 AA777315 AI337221 AW070910 AI953848 AW674561 H54177 AW510890 AW078699 AI436178 AA630759 BE502074 AA278769 AI499038 AW465072 AA778071 AW236753 AI933033 AI690458 AIZ76691 AW768235 AI952118 AA425156 AA610579
23			W73953 AA244153 W86Q34 A194872 A1952678 AW087811 A1333591 A1659883 A1926911 W48865 AL048024 AA214485 A1972522 A1151368 W48738 AA214467 AA334640 A1678170 AA927525 AA581588 W96283 AA365470 A1471919 AW611488 AA211834 A1365198 A1698365 AW002238 AA507624 W98150 AA446490 ALD48025 AA852400 AA362221 A1338376 R35083 AA299812 R10397 A4975988 AW736462 Z43032 H16969 F13487 D19858 AA452207 BE085942 AA344396 AW949533 AA279472 AW902405 AW070440 BE395195 H00835 AA300750
30			AA729303 AA420591 AA385025 AA420542 R69155 AA420592 AA281747 N88502 Al458206 AJ700996 AW418607 AW341202 Al825692 W00640 AA214405 AA044744 Al950617 BE467493 AW474113 AA446310 BE326705 Al911573 AW243968 Al628622 AW173020 AW079958 Al140387 AW051969 AW299438 Al127170 AW769164 Al422435 Al307116 BE549519 Al371116 AV243968 AA701073 AA679948 BE551197 N50345 AW338776 BE326601 Al142892 AW470687 Al989568 AA911241 AW294822 Al174414 AA804366 Al004725 AW271994 Al559313 Al270102 Al351542 AW768904 AA765964 Al961708 Al149231 AA995907 Al094280 Al185753 H01219 AW768846 AA747500 AA970106 Al601238 AA513452 AW612802 BE075163 R39171 Al565328 Al375559 F10356 AA284625 BE241509 Al702889 AW193010 AA649847
35	111234	83711_2	AW439150 AA721407 AA810333 AA706384 Al049887 BE569015 BE622280 BE566618 AW967342 R69269 AA902656 Al185915 R43705 H15150 H09794 AA832464 Al697438 Al3454538 Al436354 AA946272 AA928143 Al091263 R41658 Al352580 A1122948 AA946670 Al340088 Al275007 N70255 AA721176 Al934162 AA827098 AA935934 AA827088 Al081207 AA992399 AW130757 Al805667 AA035556 Al379266 Al093901 Al095234 AA909079 AA516079 Al572357 AA205969 Al432383 AA905290 AW628920 AW182996
40			A1266084 N49879 AW024457 A1246246 A1934031 A1369270 A1003836 AA010063 AA494361 A1284151 A1919536 N34884 N69287 AW510465 A1388609 AW081421 AA706205 A1086317 A1140633 A1347104 AA602547 A1686707 AA872686 AA694028 A1094546 Z40832 A1382838 AA610132 AA501433 H84120 A1140722 AW674839 BE503822 AW663895 BE327472 AW393494 A1340087 W04189 AW393499 H56506 BE089878 BE301950 A1025475 AA724446 BE275324 H15210 AW957667
45	134161	16074_1	AAB34543 AI682259 AF117108 BE395917 NM_006547 U97188 U76705 BE560799 BE396918 BE269531 BE560268 BE560346 AA836048 AL023775 BE545535 AA427803 C18804 D58801 AA303353 U46218 BE539704 AA187956 AA252545 AA261821 D63197 AI824109 A1088047 AI424833 AI807368 AI250857 AA741476 AI146832 AA169615 AI809821 AI274288 AW136704 AI206172 AA917039 AA243584 AI808611 AW674709 AA935733 AW450092 AA905172 AA471196 AA302256 AW673348 AI352044 AW511295 AA247134 W81035 AA722962 AW662471 R64432 AW044616 A1086619 AW628546 AW043682 AA425750 AI743038 AI368723 AA187143 AI376987 AI803976 AI275537 AW471358 AW104877 AA195464 W81072 AW197351 AA932674 AI393420 AI434998 R63822 AW085083 AI240272 W87006 AA011347 H58428 AI497895 R23223
50	132939	11857_1	AB009284 AF000416 AA022636 BE082610 AW367997 AA491410 AA337477 AA336421 W38526 AA625283 AA773685 AA490078 T66134 AA847838 AA022647 AW054726 AI918001 AA431966 AI263596 AI804298 AW469314 U76189 AA779001 AA625945 AL042357 AI674730 AA410350 AK001450 AV654353 AA058443 D81618 AA853665 W31930 AA334445 AW955767 N47777 AA883784 AA428916 AI652062 AA3470350 AI417923 AI435031 AA708791 AI989636 AI220345 AI239913 AI220102 AI3575 AI076731 AI377049 AI039173 AW972638 N90076 AW263652 BE440048 BE440013 AA577463 AI038774 AW204992 AA846580 AA501952 AA342058 AA508525 D61670 W31725 AI689499
55	111345	6692_1	AI955969 AA526628 AI282717 T66198 AW263155 AA314512 AW408152 AA360413 BE206274 AK001402 AA307665 AW954678 W39078 AW369236 AW369115 AW369096 AW753235 AW369072 AW361194 AW369125 AW364187 H94225 T79502 AA131908 BE071359 AW368503 AW801517 AW801322 AI674163 AA861077 AJ738568 AI830199 AW118577 AI478895 AI688497 H92996 AW083479 AW970625 AW613124 AI632234 AI654210 AI696847
60	104301	145380_1	A1923423 AA131909 AA806530 AA806158 AW592520 R96509 AA813923 AA502823 AW467889 AA960972 AA994566 A1280346 AA884588 AA633653 A1200023 N89820 AW768792 C00145 R96554 T79416 AA768491 AA476251 AA809748 A1186268 AA621244 A1379029 BE550341 AA651915 A1216376 A1215585 A1471780 AA772159 AW181980 A1511189 AA759270 A1675769 A1018776 AA757335 AA148511 A138378 AA504167 A1420617 AW261930 AW872797 N51769 AW614403 A1860533 AW573108 N64830 A1693732 A1436159 BE501089 A1436163 AA971485 A1269364 A1935358 A1222050 AW303978 AW573247
65	134520	13358_3	AIB71154 T16758 AI765893 AW969018 AA744720 BE094085 AA743769 AI476407 AA156619 AI768535 R81435 D45332 N75682 N51177 AW207406 AA425184 R20997 AA504168 Z43298 BE091005 BE541579 AW387738 AW386083 H13769 AW377820 AW369180 AW753239 AW672695 BE379572 AW021732 AW891450 AW891416 BE091338 N50375 BE091354 BE091355 BE091361 BE091363 BE091360 AA353863 AA845510 N21407 AW770981 AI361577
70	135242	5782_1	AA526557 AA525443 AW893622 AA630898 Al418983 BE172016 AA550754 AA664574 C16147 AA355902 AW958586 N51590 C20995 BE544186 A337578 AA090549 Al807374 AW450654 BE067578 AA446781 AA44708 T10807 AA457082 Al267703 Al880220 BE568979 AW380506 BE150744 AW380468 AW380546 BE150713 D60029 H88099 BE546301 BE150731 AW368467 BE091348 AI583187 M73812 AW339829 M74093 BE252510 BE252518 BE536901 U40788 W95578 BE018493 BE544205 N83837 Al671049 AW439693 AW330786 AW374970 AA592950 Al215885 AL215884 BE302101 A186210 AW771831 T54213 AW452924 AA834019 W95471 AA628312
75	134621	27351_1	AW304866 AA570076 Al559873 T54121 AA037145 L02547 NM_001324 AW411516 AA314711 AA143605 BE394455 AA325731 AA093227 AA083307 BE299438 BE295669 AA370886 AA38272 AA166862 BE304837 BE298306 R60507 AW238966 N72750 AW505406 AW994153 AA309742 AA309929 BE090721 AW904189 AW904214 AA363564 R94127 AA352101 R28249 AA206337 AW577208 AA385473 AA355463 AA400696 AA075587 W72815 AA554033 AA075530 AA620555 AA554034 T27804 AW950014 AI570740 AI266538 AA704423 AW411517 AI278646 AW339924 AI668917 AI796034
80	126802	116467_4	AA994601 R94082 AW027137 AA400552 AW299746 W72816 AA988494 AA146582 AW087489 AA992763 AW516454 AA992759 AW270444 AA227188 Al208929 AA167720 Al052527 AA865660 AA569368 Al888464 Al570003 AA827620 AA507543 Al888385 R88418 AW959083 AI341077 Al825719 BES52285 AA738076 AW085903 R28242 AW805510 AW805503 AW805500 AW805819 AW517040 AW473670 AW516701 T30141 AA894497 BE349504 Al272007 Al985274 BE501962
	126892	38252_1	AW102975 AI801727 AW197918 T24046 AA947601 AW900958 AF121856 BE242657 U83194 AA226732 AI160190 AA948725 AI079958 AW513369 W39443 AW408479 W06854 AA094683 AI985095
	120032	سسد	AA316647 H96313 N78438 R81582 H95034 R79674 AA488552 W25292 W31697 W19918 T30640 R08686 H78637 AA165100 Z41909

5			AA165080 R34212 AA150886 T82168 N77082 W56864 R19848 AA888217 AA314539 AW750293 N62714 R58039 AA845453 N63268 W03474 N41923 AI264123 AI808533 AA824288 AW198143 N99916 AA902465 AA775397 AA772387 AI567675 AA227473 AI082614 R58034 N78878 R34329 AW438902 AA164685 AA558790 AI590102 AA863422 BE002625 AA934039 AI298102 W15351 H93997 AA725326-BE180993 W05350 AI510771 W06941 AA488414 R79863 N91264 R76884 AA312948 T71267 AW959659 AI086695 N90421 AI278098 AA164538 AI300271 AA854381 R81331 AA700449 H06174 AW518427 AA876634 AA150778 N32393 H78585 T85364 BE002808 AW663196 N90337 BE252097 T71401 H06438 N40268 N31015 R77046 T99588 T85462 W25298 T59815 H09416 T85403 W32150 N79109 R78812
10	105298	8689_1	BE387790 BE276849 BE246825 BE246900 AA380487 AA332996 AW408727 AK000294 AI636887 AW197272 AW590657 AW594006 AI768979 AI751632 AA580098 AA313261 AA300475 AA133237 AA233499 BE242126 BE242597 BE242254 AA314374 AW961210 AW999345 AA173535 AA305779 R99373 AA128304 AA447246 AA476365 T34973 BE254878 N25149 224939 BE263038 AA128317 AK06082 H23504 AW378551 AA088533 AA442625 H15235 H79172 AA344697 AA344742 AL040280 BE173256 BE173129 T59749 AA088410 BE242311 AA173576 AA455337 AA129715 AA582953 AW612637 AA917038 AW340019 AW006315 AW593024 H05915 AW294592 Al146814 AW1955659 AW440271 AI209090 AI286689 H98630 H15174 AI214454 AI569471 AA085808 AW188361 AI751631 AW440477 AW300860 AA516088 AI365108 AI305805 AI264064 AI246276 AA442611 AA807059 AA233459 AA875987 AI374653 AA9172665 AA947515 AA436867 AI216423 AI657181
15	120438	166102_1	ALG80306 AA436854 AL537153 AA883723 Z28659 AA705973 Z40741 AA463884 AL216025 AL564986 AA476316 AL432566 AL571662 AA447126 AW293675 AL675617 AW009004 H23498 AW015242 AA831493 AL292346 AL076966 AL191561 AA243441 AL183309 AA252613 AL038422 AL306531 AW051480 AL348605 AA195119 AL817119 AL091896 AA738440 AA195013 AA976687 AA459659 AL246250 BE219252 AL703457 AA243291 AA243401 AA989100 AA931640 AA459782
20	105516	9334_1	AK001269 AL354613 AA147472 AA490803 BE207628 AW816113 AA085574 AW503392 AA299910 AW750305 BE079539 BE079484 BE512838 AK001593 AW968772 AW967440 AW206280 AA251270 Al627886 AA303599 AA147473 BE206616 AA490611 AA715039 AW590866 AW590447 Al8644512 AA204731 AA894490 BE001136 AA612785 AA237035 AA149960 Z44257 R12986 AA448446 AI734041 AA422167 BE220551 R66041 R32927 R32942 AA258773 AW386142 R63730 N54624 AW880296 AA253485 AW954441 H98989 AW614348 AI654838 AA779783 AW237213 N66635 A186812 AA497479 BE158011 Al859480 AW805579 N52010 AA806305 AI628445 AW270990
25		•	AA778165 AA149949 AI650728 AA749108 AA687257 AI261661 AA747442 AA481351 AA206339 AA903407 AW473306 AI688930 AA262281 AA48310 AA748820 AI347430 BE465692 R32839 AW510564 AA436408 AA257971 AA253362 AA938330 AA513150 AA976840 AA687117 AI281547 AAQ46243 R32825 AI631554 AW139818 AI244536 R52946 AW235443 R40183 AA299909 AA811958 AI302918 Z40213 BE158047 BE158060 AA767245 AW748159 AW500735 AA094074
	129097	25953_1	BE243933 AA355449 T29766 F08396 N83324 NM_006963 S50223 AI207648 AA258092 AA113952 AI311718 AI128612 AW607449 M77172
30	·		A1951311 X52346 AA903307 A1569810 N55421 W77876 R37223 R83788 AA031666 H47092 AA133451 AA311095 AA906963 H87667 N56058 AA933593 W24864 H10710 F06925 F07239 AW386140 AA325018 AA235950 AW373176 N57158 AA258093 N39467 R21609 BE089979 R34173 AW889005 AA745644 A1693852 AA424914 AA744771 W72632 A1291213 AA524318 A1472134 A1911230 AA528418 AA115745 AA775720 A1671134 AA975044 AW298117 AA321015 N26288 AW952194 A1743379 A1204233 A1801026 AA830890 A146990 AW104611 A1338576 R21507 A1667623 BE244484 A1263308 AA031667 A1684346 AA731989 AA988943 AA235951 AA807887 AA642645 A1246489 N29739 A1216718 A1383349 A1038618 A1351476 AA806031 A1914178 H10711 A1095573 H89220 AW470854 AA729015 R83353 AA782239
35			R34295 H87165 AW419059 Al653689 Z40349 H89114 AW074506 AA397785 AA888377 Al911228 F03193 Al468783 AA702615 Al830829
	120619 129229	169895_1 20927_1	AA748323 R37224 AA424915 AA731647 H47183 AW955339 AL045632 AA333229 Al806195 AA284372 AA206108 AA682533 AW449514 AA804785 Al215473 Al357263 Al651208 Al651753 AF013758 NM_006451 Al538709 AA209236 AA300293 AA367274 AA126598 AA324825 AW955225 F11436 AW374740 AW374714 AW374774 AW751514 W74780 Al909015 AW997079 AW997087 AW379344 AW363397 W38589 AA043823 BE169280 Al909016 AW994851 Al740638
40			AW148560 AW368339 AI858333 AA314718 AW954872 AW468734 AI681980 AW519045 AW055171 AA579286 AW069164 AW615004 AA345052 A446735 AI142106 AA662683 AW002813 AI418280 AW613203 AI613333 AJ354480 AI929755 AI146977 W74674 AW799610 AI798529 AI589422 AA043957 AI223043 AA157016 AI446759 D56729 AI587471 F30716 AA6121125 AI537301 AA663347 D11966 AI434383 AA598533 AI287254 AW139140 AW051033 AA601911 AI702506 AA737460 T30221 AI12981 N90213 AA605225 AI798518 BE001071 T10841 W20199 AW664594 AW195667 D60123 D61496 AW468018 AI720097 N90553 AA829375 AW513266 H92758 AA585324 C14767 AI922391
45	120821	19274_2	D60124 D60666 AW071558 BE044120 AA728821 AA211941 Y19062 NM_014393 AW28601 AK001576 AL079288 W16667 Z45664 A1768561 AL079286 R12736 AW080147 AW136530 A1202958 AW241579 R21013 AA347419 A1929333 AW196689 A1040867 F13437 AA918240 A1869798 A1365176 AW440030 AW440072 N80992 AW242030 Z44807 R12417 AA436784 AA442041 AA046503 AL157526 A1929265 AA055542 AA045462 AA683542 N51374 AW193508
50	106459	3897_1	AI873524 AW473151 AW004719 AI810504 AI581093 AA493977 Z40600 F04553 R46130 F09321 AA789081 AW408328 NM_006530 U61384 AA449841 AW138216 AA448598 AJ245746 AI365301 N44728 AA255743 AA360783 BE550380 AW593925 AI962209 AA322097 AW964625 AI695988 AW672827 BE543256 AK001413 AW603395 AA651700 AA449053 AA465540 AW083185 T62128 Z78373 AW673713 AW468061 BE350755 AW673958 AW675504 AA995709 AW574841 AA835883 AI248439 AA54884 T62072 N33193 AA814046 AI376210 AI340020 AA449766 AA703407 AA427613 AI470108 AI298757 AA507602 AI658941 AA449478 AA67346F AA440741 A A934914 AA934917 AA927698 AW672015
55	115094	190995_1	AA633165 AA449741 AA831821 AA903673 AA682588 AW673075 AA255920 AI817197 AA255921 AI612925 AW874669 AA493440
	129571	1726_1 287665_1	X51630 M80232 X61631 S75264 AA172249 AA134066 AA130278 AA130187 AA130291 AA031554 A1246677 Z21455 AI745434 AW273544 AW088613 AW471307 AI745483 AI399854 AI683952 AA031555 AA298075 AI935945 T29809 AA172099 AA356120 AW513143 AA422036 AI821669 AW514232 AA477828 AW772009 AW439799 AW089884
60	106738	174703_1	AW149266 R49246 AW237401 AA938113 AW665871 AI969698 AI950812 AW874276 AI571939 AA741222 AI869822 AW104061 AI569994 AW972559 AA506012 AI553704 AA470145 AI332421 AA218990 AW131361 AI709076 AW392488 AW392477 AI970981 AW392476 D61949 H44981 BE172698
	123005	75629_1	AW369771 AW748174 AA290801 AA419198 AA044331 AA127909 AW995442 AI480343 AA044582 AW956159 AA373451 AA127965 AL134913 AW994956 BE622314 BE006298 BE006312 BE006305 BE006317 BE006303 AA043906 AA234175 AA479726
<i></i>	108055	100690_1	AJ404672 AJ289819 AW976000 AA043561 AW450885 AW452879 AA043562 AA788832 AJ564338 AJ564330 AJ368875 AA643607 AA994375
65	115291	22325_1	AA810342 Al367704 BE545072 Al540751 AA301103 Al916675 N85422 BE563965 AA327978 Al816094 AK001515 BE501319 AA279943 BE138895 AA343765
	110231	22020_1	AW963051 AW082308 Al823992 Al653752 Al589007 Al816135 Al565535 BE501307 AW272765 AW242239 AA766315 Al014927 AA578848 Al354483 Al476548 Al038579 AA973322 AA992180 AW472921 BE504789 Al392988 AA506076 AA769228 Al370562 AL137710 BE005656 AW965920
70	130376 115536	248274 61_1	R40873 AK001468 AA190315 AA374980 AW961179 AA307782 AA315295 AA347194 AW953073 AW368190 AW368192 AA280772 AA251247 N85676 AI215522 AI216389 N87835 R12261 R57094 AI660045 AA347193 R16712 AW119006 N55905 N87768 AW900167 AI341261 AI818674 D20285 AI475165 AA300756 R40626 A1122827 AA133250 AI952488 AA970372 AA889845 AW069517 AI524385 AA190314 AI673359 AA971105 AI351088 AI872789 AI919056 AI611216 AK001472 BE568761 AA581004
75	114965 131228	153955_1 8262_1	AI733881 AA165164 AI826437 AI972791 AA165165 BE219575 AI732586 AI821571 AA250737 AW136875 AIS84273 AI249271 AW207469 AL079814 AA354351 AF020043 AW291398 BE550484 NM_005445 BE046917 AW994249 AI651554 AI631515 AW771344 AI969758 AI699982 AA247175 AI244676 D44780 AW593978 AI638479 AI373676 AW089547 AL121432 AA554698 AI016991 AI087260 AW49939 AF067163 W40482 AW316558 AI537184 AW381979 W40150 AI810562 AA573151 AI630288 AI675561 AI674420 AW840733
80			AWD22653 AA114219 AJ005015 AL046587 AA878141 AW271896 AW085287 AA150465 BE536295 AA463412 BE093222 AA213739 AA485586 AI825913 AA706307 AI337348 R31995 AI819641 R32095 AW976653 AA742375 AA142957 AI808214 AW468303 AI205987 AI206347 AI769095 BE501640 AA113866 AI093931 AI752855 AA612743 AA463411 AA279157 AI123791 AA213570 AI207305 AW627814 R31945 R32040
	116238	10772_1	AV660717 NM_015437 AL050285 R95774 Al857094 AA443833 Al367670 AA609046 Al440298 Al613139 Al291826 AW028954 Al123242 Al824715 AW079750 AA479362 AW150151 Al952267 AA814094 Al168431 Al566595 Al521422 Al920793 AW051241 N70051 Al689429

			AI783813 AI769315 AI743691 AI915645 AA479473 C21435 N50944 N50902 AW978102 H23837 BE087538 AA316516
	122802	287993_1	AI687303 AW571681 AI554465 AI684252 AI581056 AA604098 AI628160 AI859843 AA424021 AA460530 BE042778 AW273200 AW273223
			AW167288 AW083347 AI654306 AW517496 AW104706 AW273214 BE139512 AW189487 AW130822 AW167419 AI289485 AW150010
-			H88004 AI743745 AW088710
)	123494	21202_1	AW179019 AW179011 AF135160 NM_014050 AF078860 BE018005 AK000285 AF151038 BE245156 AW179007 AA345114 BE619758
			BE619209 W25509 AA314339 AA336674 AA337956 AW954843 AW390412 N46796 AA316235 AA314286 R15686 BE535633 N57134 N46483
			AW368462 AA923517 AA665223 Al418513 AA837523 Al359320 Al309273 Al522278 N40939 AA904977 AA938272 N30240 AA887965
			AI671972 AI028109 AA094652 AA883262 AA887781 AI744447 AW592944 AI077790 AW860883 AW148667 N89861 AA557195 AI191824
			AI433166 AI719760 AA453089 AA630656 AA300976 AA639620 AW675033 AA284393 AW886987 AI476335 AI332939 BE301513 AA452920
10			AW674302 Al925483 AW170412 Al698717 Al375985 BE220535 Al688151 AW514809 AW062346 AA599786 BE350848 Al560848 Al023075
			AA864875 AA166871 Al807947 AW514579 Al978602 Al860340 AA830886 Al374788 Al283592 AA683152 AA743159 Al379932 Al432056
			AI128904 AW150433 N38909
	116296	11967_2	AW149502 Z43342 AW002826 AL049382 AA442545 AW971471 BE220243 AW968952 AA043607 AW299245 AA659892 Al038768 H26330
			BE463534 AI628252 AA836139 AI277291 AA489033 AA741239 AI209064 AI300253 AI275761 Z39417 C01835
15			

Table 9A lists about 382 genes up-regulated in ovarian cancer compared to normal ovaries. These were selected from 35403 probesets on the Affymetrix/Eos-Hu01 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult ovaries was greater than or equal to 10. The "average" ovarian cancer level was set to the 2nd highest amongst various ovarian cancers. The "average" normal adult ovaries level was set to the arithmetic mean amongst various non-malignant ovaries. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues (see Table 7A) was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 9A: 382 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY Primekey

Pkey: Primekey
Ex. Acon: Exemplar Accession
UG ID: UniGene ID
Title: UniGene title

ratio: ratio tumor vs. normal tissues

30	Pkey	Ex. Acon	UGID	Title	ratio
	134454	L33930	Hs.173996	CD24 antigen (small cell lung carcinoma clust	86.2
	102927	X12876	Hs.65114	keratin 18	84.7
	115909	AA436666	Hs.59761	ESTs	72.3
	123169	AA488892	Hs.104472	ESTs; Weakly similar to Gag-Pol polyprotein [	66.8
35	115674	AA406542	Hs.71520	ESTs	65.4
JJ	102193	U20758	Hs.313		63.1
		M93036		secreted phosphoprotein 1 (osteopontin; bone	56.8
	101839		Hs.692	membrane component; chromosomal 4; surface ma	56.1
	115221	AA262942	Hs.79741	ESTs	
40	108059	AA043944	Hs.62663	ESTs	52.3
40	121853	AA425887	Hs.98502	ESTs	47.8
	133504	W95070	Hs.74316	desmoplakin (DPI; DPII)	47.0
	103546	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	46.5
	100147	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin I-lik	45.5
45	102979	X17042	Hs.1908	proteoglycan 1; secretory granule	44.6
43	130967	AA134138	Hs.182579	Homo sapiens leucine aminopeptidase mRNA; com	44.5
	102009	U02680	Hs.82643	protein tyrosine kinase 9	40.4
	126960	AA317900	Hs.161756	ESTs	39.6
	103111	X63187	Hs.2719	epididymis-specific; whey-acidic protein type	39.1
50	133829	AA453783	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (from c	39.0
50	111223	N68921	Hs.34806	ESTs; Weakly similar to neogenin [H.sapiens]	38.9
	102803	U89916	Hs.26126	claudin 10	38.8
	104943	AA065217	Hs.169674	ESTs	38.7
	106605	AA457718	Hs.21103	Homo saplens mRNA; cDNA DKFZp564B076 (from cl	38.4
	120655	AA287347	Hs.238205	ESTs .	38.1
55	102968	X16396	Hs.154672	methylene tetrahydrofolate dehydrogenase (NAD	36.3
	104052	AA393164	Hs.97644	mammaglobin 2	36.0
	109166	AA179845	Hs.73625	RAB6 interacting; kinesin-like (rabkinesin6)	35.9
	101332	L47276		Homo sapiens (cell line HL-6) alpha topolsome	35.0
	106167	AA425906	Hs.7956	ESTs	34.5
60	101042	J05428	Hs.10319	UDP glycosyltransferase 2 family; polypeptide	34.3
	125852	H09290	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (from c	33.7
	101201	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin; uteri	32.3
•	126410	R51912	Hs.12409	somatostatin	32,1
	134326	U16306	Hs.81800	chondroitin sulfate proteoglycan 2 (versican)	32.0
65	125739	AA428557	Hs.92137	v-myc avian myelocytomatosis viral oncogene h	31.6
	132254	L20826	Hs.430	plastin 1 (1 isoform)	31.4
	112610	R79392	Hs.23643	ESTs	30.9
	101441	M21005	Hs.100000	S100 calcium-binding protein A8 (calgranulin	30.6
	116345	AA496981	Hs.199067	HER3 receptor tyrosine kinase (c-erbB3; ERBB3	30.1
70	108860	AA133334	Hs.129911	ESTs	29.8
	133859	U86782	Hs.178761	26S proteasome-associated pad1 homolog	29.2
	107295	T34527	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polypeptid	28.9
	106210	AA428239	Hs.10338	ESTs	28.9
	134711	XD4011	Hs.88974	cytochrome b-245; beta polypeptide (chronic g	28.0
75	125769	Al382972	Hs.82128	5T4 oncofetal trophoblast glycoprotein	27.5
	107222	D51235	Hs.82689	tumor rejection antigen (gp96) 1	27.4
	102260	U28386	Hs.159557	karyopherin alpha 2 (RAG cohort 1; importin a	26.9
	134691	M59979	Hs.88474	prostaglandin-endoperoxide synthase 1 (prosta	26.8
	105588	AA279215	Hs.10867	ESTs	26.3
80	130718	N70196	Hs.18376	ESTs	26.3
	111185	N67551	Hs.12844	EGF-like-domain; multiple 6	25.6
	131965	W90146	Hs.35962	ESTs	25.6
	132903	AA235404	Hs.5985	Homo sapiens done 25186 mRNA sequence	25.6
	114359	Z41589	Hs.153483	ESTs: Moderately similar to H1 chloride chann	25.5
	114359	241309	ns. 153463	CO12! windstates) arriver on the emotion engine	ພພ

	404405	Ltoome	Hs.170087	aryl hydrocarbon receptor	25.2
	101185 128742	L19872 D00763	Hs.251531	proteasome (prosome; macropain) subunit; alph	25.1
	116724	F13665	Hs.65641	ESTs	24.9
	111929	R40057	Hs.112360	prominin (mouse)-like 1	24.9
5	102915	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin 2)	24.8
	131210	AA430047	Hs.24248	ESTs	24.7
	101714	M68874		Human phosphatidylcholine 2-acylhydrolase (cP	24.6
	100154	D14657	Hs.81892	KIAA0101 gene product	24.6 24.3
10	134656	X14787	Hs.87409 Hs.75454	thrombospondin 1 antioxidant protein 1	23.9
10	100294 104080	D49396 AA402971	Hs.57771	kallikrein 11	23.7
	107056	AA600310	Hs.18720	programmed cell death 8 (apoptosis-inducing f	23.7
	115697	AA411502	Hs.63325	ESTs; Weakly similar to airway trypsin-like p	23.7
	130350	U02020	Hs.239138	pre-B-cell colony-enhancing factor	23.7
15	105870	AA399623	Hs.23505	ESTs	23.6
	118528	N67889	Hs.49397	ESTs	23.4
-	105309	AA233790	Hs.4104	ESTs; Weakly similar to cDNA EST yk386g7.5 co	23.2 23.2
	109680	F09255	Hs.4993 Hs.181307	ESTs H3 histone; family 3A	23.2
20	131501 100824	'AA121127 HG4058-HT4:		Oncogene Amil-Evi-1, Fusion Activated	23.1
20	111890	R38678	Hs.12365	ESTs	23.0
	101543	M31166	Hs.2050	pentaxin-related gene; rapidly induced by IL-	22.8
	102095	U11313	Hs.75760	sterol carrier protein 2	22.8
	114988	AA251089	Hs.94576	ESTs; Weakly similar to phosducin; retinal [H	22.8
25	120695	AA291468		ESTs	22.8
	130941	D49394	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3A	22.8 22.7
	106654	AA460449 AA176428	Hs.3784	ESTs; Highly similar to phosphoserine aminotr ESTs	22.6
	109141 102345	U37283	Hs.193380 Hs.58882	Microfibril-associated glycoprotein-2	22.6
30	115652	AA405098	Hs.38178	ESTs	22.4
50	100103	AF007875	Hs.5085	dolichyl-phosphate mannosyltransferase polype	22.3
	105463	AA253370	Hs.32646	ESTs	22.2
	132624	AA164819	Hs.53631	ESTs	22.2
25	119743	W70242	Hs.58086	ESTs	22.0
35	132528	AA283006	Hs.50758	chromosome-associated polypeptide C	22.0 · 21.8
	107174 134495	AA621714 D63477	Hs.25338 Hs.84087	ESTs KIAA0143 protein	21.8
	131985	AA434329	Hs.36563	ESTs	21.5
	105832	AA398346	Hs.21898	ESTs	21.2
40	126160	N90960	Hs.247277	ESTs; Weakly similar to transformation-relate	21.2
	114846	AA234929	Hs.44343	ESTs	20.9
	109703	F09684	Hs.24792	ESTs; Weakly similar to ORF YOR283w (S.cerevi	20.9
	135154	AA126433	Hs.173242	sorting nextn 4	20.8 20.7
45	131185	M25753	Hs.23960	cyclin 81 ESTs	20.7
45	105616 131148	AA280670 C00038	Hs.24968 Hs.23579	ESTs	20.2
	129337	R63542	Hs.110488	KIAA0990 protein	20.2
	133640	D83004	Hs.75355	ubiquitin-conjugating enzyme E2N (homologous	20.1
	127479	AA513722	Hs.179729	collagen; type X; alpha 1 (Schmid metaphyseal	19.9
50	133711	J04130	Hs.75703	small inducible cytokine A4 (homologous to mo	19.8
	131818	Z39297	Hs.3281	neuronal pentraxin II	19.7
	125303	Z39821	Hs.107295	ESTs	19.6 19.5
	109112 105376	AA169379 AA236559	Hs.72865 Hs.8768	ESTs ESTs; Wealty similar to IIII ALU SUBFAMILY SQ	19.2
55 °	103605	Z35402	Hs.194657	cadherin 1; E-cadherin (epithelial)	19.1
-	100661	HG2874-HT3		Ribosomal Protein L39 Homolog	19.1
	129571	X51630	Hs.1145	Wilms tumor 1	19.0
	115239	AA278650	Hs.73291	ESTs; Weakly similar to similar to the beta t	18.9
<b>60</b>	131562	U90551	Hs.28777	H2A histone family; member L	18.9
60	131272	AA423884	Hs.139033	paternatly expressed gene 3 ESTs; Weakly similar to APICAL-LIKE PROTEIN [	18.9 18.8
	130343 103245	AA490262 X76648	Hs.15485 Hs.28988	glutaredoxin (thioltransferase)	18.7
	101809	M86849	F15.20500	Homo sapiens connexin 26 (GJB2) mRNA, complet	18.6
	105344	AA235303	Hs.8645	ESTs	18.4
65	135225	AA455988	Hs.9667	butyrobetaine (gamma); 2-oxoglutarate dioxyge	18.4
	116786	H25836	Hs.83429	tumor necrosis factor (ligand) superfamily; m	18.3
	131510	AA207114	Hs.27842	ESTs; Weakly similar to similar to 1-acyl-gly	18.2
	124059	F13673	Hs.99769	ESTs	18.0 17.9
70	103352 132742	X89398 AA490862	Hs.78853 Hs.55901	uracil-DNA glycosylase ESTs; Weakly similar to C43H8.1 [C.elegans]	17.9
, 0	135242	M74093	Hs.9700	cyclin E1	17.9
	123494	AA599786	Hs.112110	ESTs	17.8
	129168	T90621	Hs.109052	chromosome 14 open reading frame 2	17.7
75	128517	AA280617	Hs.100861	ESTs; Weakly similar to p60 katanin [H.sapien	17.6
75	130160	Z39228	Hs.151344	UDP-Gal:betaGlcNAc beta 1;3-galactosyltransfe	17.6
	103448	X99133	Hs.204238	tipocalin 2 (oncogene 24p3)	17.5
	119708	W67810	Hs.57904	mago-nashi (Drosophila) homolog; proliferatio ESTs	17.5 17.5
	122946 125819	AA477445 AA044840	Hs.105341 Hs.251871	CTP synthase	17.5
80	131689		Hs.30696	transcription factor-like 5 (basic helix-loop	17.5
	115061	AA253217	Hs.41271	ESTs	17.3
	113702	T97307	Hs.161720	ESTs; Moderately similar to IIII ALU SUBFAMIL	17.3
	115291		Hs.122579	ESTs	17.3
	102567	U59863	Hs.146847	TRAF family member-associated NFKB activator	17.2
				4 74	

	400000	11044044	11 400040	and and ampleto hinding analytic internation and	47.0
	129229	AA211941	Hs.109643	polyadenylate binding protein-interacting pro	17.2
	129351	AA167268	Hs.62349	Human ras inhibitor mRNA; 3' end	17.2
	110769	N22222		yw34b06.s1 Morton Fetal Cochlea Homo sapiens	17.1
_	113182	T55234	Hs.9676	Human DNA sequence from clone 30M3 on chromos	17.0
5	115892	AA435946	Hs.50831	ESTs	17.0
	123114	AA486407	Hs.105235	ESTs; Moderately similar to KIAA0454 protein	17.0
	123442	AA598803	Hs.111496	ESTs	17.0
	123339	AA504253	Hs.101515	ESTs	16.9
10	123689	AA609556	Hs.256562	ESTs	16.9
10	131941	D62657	Hs.35086	ubiquitin-specific protease 1	15.8
	120649	AA287115	Hs.99697	ESTs	16.8
	102139	U15932	Hs.2128	dual specificity phosphatase 5	16.8
	115522	AA331393	Hs.47378	ESTs	16.7
1.5	135243	AA215333	Hs.97101	putative G protein-coupled receptor	16.6
15	131257	AA256042	Hs.24908	ESTs	16.5
	109508	AA233892	Hs.55902	ESTs; Weakly similar to IIII ALU SUBFAMILY SX	16.3
	132701	AA279359	Hs.55220	BCL2-associated athanogene 2	16.3
	134449	L34155	Hs.83450	laminin; alpha 3 (nicein (150kD); kalinin (16	16.3
20	126180	R18070	Hs.3712	ubiquinol-cytochroma c reductase; Rieske iron	16.3
20	106124	AA423987	Hs.7567	ESTs	16.2
	115363	AA282071	Hs.152759	activator of S phase kinase	16.2
	117588	N34895	Hs.44648	ESTs	16.1
	131245	AA620599	Hs.24766	DKFZP564E1962 protein	16.1 16.0
25	101674	M61916	Hs.82124	laminin; beta 1	16.0
23	126819	AA305536	Hs.161489	ESTs	16.0
	134039 130648	S78569	Hs.78672	laminin; alpha 4 ESTs; Weakly similar to Iprediction	15.9
	102823	AA075427 U90914	Hs.17296 Hs.5057	carboxypeptidase D	15.8
	128470	AA447504	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (from cl	15.8
30	115844	AA430124	Hs.234607	ESTs	15.7
20	132543	AA417152	Hs.5101	protein regulator of cytokinesis 1	15.7
	130155	L33404	Hs.151254	kallikrein 7 (chymotryptic; stratum comeum)	15.7
	101008	J04162	Hs.763	Fc fragment of IgG; low affinity Illa; recept	15.7
	120472	AA251875	Hs.104472	ESTs; Weakly similar to Gag-Pol polyprotein [	15.6
35	116844	H64938	Hs.38331	ESTs	15.6
55	106753	AA476944	Hs.7331	ESTs	15.6
	114767	AA148885	Hs.154443	minichromosome maintenance deficient (S. cere	15.5
	114768	AA149007	Hs.182339	Ets homologous factor	15.5
	127370	AI024352	Hs.70337	immunoglobulin superfamily; member 4	15.5
40	101507	M27492	Hs.82112	interleukin 1 receptor; type (	15.4
. •	102519	U52969	Hs.80296	Purkinje cell protein 4	15.4
	102610	U65011	Hs.30743	preferentially expressed antigen in melanoma	15.4
	111244	N69556	Hs.24724	MFH-amplified sequences with leucine-rich tan	15.4
	120404	AA234921	Hs.96427	KIAA1013 protein	15.3
45	130455	X17059	Hs.155956	N-acetyltransferase 1 (arylamine N-acetyltran	15.2
	129519	AA298786	Hs.112242	ESTs	15.1
	106553	AA454967	Hs.5887	ESTs; Highly similar to RNA binding motif pro	15.0
	109502	AA233837	Hs.44755	ESTs; Weakly similar to membrane glycoprotein	14.9
<b>~</b> ^	115967	AA446887	Hs.42911	ESTs	14.9
50	104636	AA004415	Hs.106106	ESTs	14.9
	134133	X93920	Hs.180383	dual specificity phosphatase 6	14.9
	134444	X04470	Hs.251754	secretory leukocyte protease inhibitor (antil	14.8
	132998	Y00062	Hs.170121	protein tyrosine phosphalase; receptor type;	14.8
	131997	D82399	Hs.136644	Homo sapiens clone 23714 mRNA sequence	14.6
55	134056	R27358	Hs.7886	ESTs; Weakly similar to Pelle associated prot	14.6
	101249	L33881	Hs.1904	protein kinase C; iota	14.5
	105298	AA233459	Hs.26369	ESTs	14.5
	107119	AA620307	Hs.27379	ESTs	14.5
60	115839	AA429038	Hs.40541	ESTs	14.5
60	122802	AA460530	Hs.256579	ESTS	14.5
	129896	AA043021	Hs.13225 Hs.168352	UDP-Gal:betaGlcNAc beta 1;4- galactosyltransf	14.3 14.3
	130269	AA284694		nucleoporin-like protein 1	
	134374	D62633	Hs.8236	ESTs	14.3
65	106370	AA443841	Hs.18676	sprouty (Drosophila) homolog 2	14.2 14.1
UJ	130919	AA291710	Hs.21276	collagen; type IV; alpha 3 (Goodpasture antig	14.1
	132923	U21858	Hs.60679	TATA box binding protein (TBP)-associated fac	14.1
	107968 125390	AA034020 H95094	Hs.61539 Hs.75187	ESTs translocase of outer mitochondrial membrane 2	14.1
		AA621131		ESTs: Weakly similar to W01A11.2 gene product	14.1
70	107148 110788	N24730	Hs.5889 Hs.1 <b>5420</b>	ESTs: Weakly similar to WOTATT.2 gene product	14.1
70	109481	AA233342	Hs.90680	ESTs; Weakly similar to WD40 protein Ciao 1 (	13.9
	105646	AA282147	Hs.5888	ESTs	13.9
	106030	AA412251	Hs.12802	development and differentiation enhancing fac	13.8
	132618	AA253330	Hs.5344	adaptor-related protein complex 1; gamma 1 su	13.7
75	133230	S82240	Hs.6838	ras homolog gene family; member E	13.7
	124803	R45480	Hs.164866	cyclin K	13.6
	121381	AA405747	Hs.97865	ESTs; Weakly similar to WASP-family protein [	13.6
	105200		Hs.24641	ESTs	13.5
	105627	AA281245	Hs.23317	ESTs	13.5
80	114986		Hs.87807	ESTs	13.5
- •	118036	N52844	Hs.196008	ESTs	13.5
	134672	N79749	Hs.87627	ESTs; Weakly similar to cDNA EST EMBL:T00542	13.5
	110915		Hs.29724	ESTs	13.3
	· 117984		Hs.47368	ESTs	13.3

	132550	AA029597	Hs.170195	bone morphogenetic protein 7 (osteogenic prot	13.3
	124315	H94892	Hs.6906	v-ral simian leukemia viral oncogene homolog	13.2
	102547 125134	U57911 W19228	Hs.46638 Hs.100748	chromosome 11 open reading frame 8 ESTs	13.2 13.2
5	111805	R33468	Hs.24651	ESTS	13.1
_	106983	AA521195	Hs.10887	similar to hysosome-associated membrane glyco	13.0
	106498	AA452141	Hs.7171	ESTs	13.0 13.0
	110787 122860	N24716 AA464414	Hs.12244 Hs.112159	ESTs; Weakly similar to C44B9.1 [C.elegans] ESTs	13.0
10	131535	AA504642	Hs.28436	ESTs; Wealty similar to coded for by C. elega	13.0
	116188	AA464728	Hs.184598	ESTs	13.0
	107243 129300	D59489 C20976	Hs.34727 Hs.110165	ESTs ESTs; Highly similar to ribosomal protein L26	12.9 12.9
	134487	R38185	Hs.83954	Homo sapiens unknown mRNA	12.8
15	102348	U37519	Hs.87539	aldehyde dehydrogenase 8	12.8
	131839	H80622	Hs.33010	KIAA0633 protein 2-5'oligoadenylate synthetase 3	12.8 12.8
	119620 120802	W47620 AA343533	Hs.56009 Hs.128777	ESTs; Weakly similar to predicted using Genef	12.7
	102250	U28014	Hs.74122	caspase 4; apoptosis-related cysteine proteas	12.7
20	105539	AA258873	Hs.25242	ESTs	12.7
	114965 118001	AA250737 N52151	Hs.72472 Hs.47447	ESTs ESTs	12.7 12.7
	100448	D87469	Hs.57652	EGF-like-domain; multiple 2	12.6
25	130920	D50975	Hs.75525	calreticulin	12.6
25	131075 105496	Y00757 AA256323	Hs.2265 Hs.25264	secretory gracule; neuroendocrine protein 1 ( DKFZP434N126 protein	12.6 12.5
	109235	AA193592	Hs.42300	ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ	12.5
	118215	N62195	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A synthas	12.5
30	134388	M15841	Hs.82575	small nuclear ribonucleoprotein polypepiide B	12.5 12.4
30	106897 133050	AA489790 S67325	Hs.167496 Hs.63788	RAN binding protein 6 propionyl Coenzyme A carboxylase; beta polype	12.4
	109683	F09308	Hs.27607	ESTs	12.3
	121463	AA411745	Hs.239581	ESTs; Weakly similar to KIAA0554 protein [H.s	12.3
35	102876 101804	X03663 M86699	Hs.174142 Hs.169840	colony stimulating factor 1 receptor; formed TTK protein kinase	12.2 12.2
55	129017	H13108	Hs.107968	ESTs	12.1
	105812	AA394126	Hs.20814	ESTs; Highly similar to CGI-27 protein (H.sap	12.1
	106459 107059	AA449741 AA608545	Hs.4029 Hs.23044	glioma-amplified sequence-41 RAD51 (S. cerevisiae) homolog (E coli RecA ho	12.0 12.0
40	107033	AA609210	Hs.19221	ESTs	12.0
	110799	N26101	Hs.7838	Human ring zinc-finger protein (ZNF127-Xp) ge	12.0
	112253	R51818	Hs.104222	Homo sapiens mRNA; cDNA DKFZp566L034 (from cl	12.0 12.0
	116760 120314	H11054 AA194166	Hs.155342 Hs.221040	protein kinase C; delta KIAA1038 protein	12.0
45	123005	AA479726	Hs.105577	ESTs	12.0
	132572	AA448297	Hs.237825	signal recognition particle 72kD	12.0 12.0
	110561 101923	H59617 S75256	Hs.5199	ESTs; Weakly similar to UBIQUITIN-CONJUGATING HNL=neutrophil lipocalin (human, ovarian canc	11.9
	134992	H05625	Hs.92414	ESTs	11.8
50	105516	AA257971	Hs.21214	ESTs	11.8
	105248 109130	AA226968 AA172040	Hs.22826 Hs.20161	ESTs ESTs; Weakly similar to IgE receptor beta sub	11.7 11.7
	115955	AA446121	Hs.44198	Homo sapiens BAC clone RG054D04 from 7q31	11.7
<i>F F</i>	116135	AA460314	Hs.94179	ESTs	11.7
55	116284 132384	AA487252 AA479933	Hs.237809 Hs.46967	ESTs; Weakly similar to hypothetical protein  Human DNA sequence from clone 167A19 on chrom	11.7 11.7
	134753	Y09216	Hs.173135	dual-specificity tyrosine-(Y)-phosphorylation	11.7
	125136	W31479	Hs.129051	ESTs	11.7
60	133928	N34096	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homologou	11.6
JU	117395 127007	N26330 AA299360	Hs.93701	ESTs EST11857 Uterus tumor I Homo sapiens cDNA 5	11.5 11.5
	130567	L07493	Hs.1608	replication protein A3 (14kD)	11.5
	135073	AA452000	- Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (from c	11.5 11.4
65	115140 115536	AA258030 AA347193	Hs.55356 Hs.62180	ESTs; Weakly similar to supported by GENSCAN ESTs	11.4
0.0	133240	D31161	Hs.68613	ESTs	11.3
	106521	AA453431	Hs.14732	malic enzyme 1; NADP(+)-dependent; cytosolic	11.3 11.3
	107674 114149	AA011027 Z38814	Hs.41143 Hs.27196	KIAA0581 protein ESTs .	11.3
70	132478	H20906	Hs.49500	KIAA0746 protein	11.2
	104252	AF002246	Hs.210863	cell adhesion molecule with homology to L1CAM	11.2
	102436 106726	U46499 AA465339	Hs.790 Hs.7141	microsomal glutathione S-transferase 1 ESTs	11.2 11.2
	100116	D00654	Hs.77443	actin; gamma 2; smooth muscle; enteric	11.2
75	110970	N51374	Hs.96870	Homo sapiens mRNA full length insert cDNA cto	11.2
	130417 132906	U58522 AA142857	Hs.155485 Hs.234896	huntingtin-Interacting protein 2 ESTs; Highly similar to geminin (H.sapiens)	11.2 11.2
	107853	AA142657 AA024427	Hs.59461	DKFZP434C245 protein	11.2
00	103467	Y00451	Hs.78712	aminolevulinate; delta-; synthase 1	11.1
80	100438	D87448	Hs.91417	topoisomerase (DNA) II binding protein	11.1 11.1
	102654 103172	U68494 X68742	Hs.24385 Hs.116774	Human hbc647 mRNA sequence integrin; alpha 1	11.1
	106856	AA486183	Hs.15839	ESTs; Wealty similar to similar to oxysterol-	11.1
	108255	AA063157	Hs.172608	ESTs	11.1

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	124308	H93575	Hs.227146	Homo sapiens mRNA; cDNA DKFZp564J142 (from ci	11.1
	129057	X62466	Hs.214742	CDW52 antigen (CAMPATH-1 antigen)	11.1
	128845 129025	AA455658 AA420992	Hs.10649	basement membrane-induced gene ESTs; Weakly similar to testicular tektin B1-	11.1 11.0
5	107638	AA009528	Hs.103441 Hs.42743	ESTs; Weakly similar to predicted using Genef	11.0
•	134480	AA024664	Hs.83916	NADH dehydrogenase (ubiquinone) 1 alpha subco	11.0
	115262	AA279112	Hs.88594	ESTs	11.0
	102580 106614	U60808 AA458934	Hs.152981 Hs.179912	CDP-diacylglycerol synthase (phosphatidate cy ESTs	10.9 10.9
10	107115	AA610108	Hs.27693	ESTs; Highly similar to CGI-124 protein [H.sa	10.9
	115764	AA421562	Hs.91011	anterior gradient 2 (Xenepus laevis) homolog	10.9
	121770	AA421714	Hs.11469	KIAA0896 protein	10.9
	132191 133214	AA449431 Y10659	Hs.158688 Hs.250911	KIAA0741 gene product interleukin 13 receptor; alpha 1	10.9 10.9
15	133914	N32811	Hs.77542	ESTs	10.8
	101973	S82597	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polypeptid	10.8
	102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	10.8 10.8
	104147 106474	AA451992 AA450212	Hs.226799 Hs.42484	ESTs; Highly similar to HSPC039 protein (H.sa Homo sapiens mRNA; cDNA DKFZp564C053 (from cl	10.8
20	115881	AA435577	Hs.184942	G protein-coupled receptor 64	10.8
	129950	M31516	Hs.1369	decay accelerating factor for complement (CD5	10.8
	132783	N74897	Hs.5683	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide	10.8 10.8
	133784 134248	AA214305 AA292677	Hs.76173 Hs.80624	ESTs ESTs	10.8
25	105565	AA278302	Hs.18349	ESTs; Weakly, similar to partial CDS [C.elegan	10.8
	127999	AA837495	Hs.69851	ESTs; Weakly similar to Wiskott-Aldrich syndr	10.8
	108040 130367	AA041551 Z38501	Hs.48644 Hs.8768	ESTs ESTs; Weakly similar to IIII ALU SUBFAMILY SQ	10.7 10.7
	108539	AA084677	Hs.54558	ESTs; Weakly similar to protein B [H.sapiens]	10.7
30	111345	N89820	Hs.14559	ESTs	10.7
	115583	AA398913	Hs.45231	LDOC1 protein	10.7
	128965 101396	T17440 M15796	Hs.107418 Hs.78996	ESTs proliferating cell nuclear antigen	10.7 10.6
	132164	U84573	Hs.41270	procollagen-lysine; 2-oxoglutarate 5-dioxygen	10.6
35	101275	L37936	Hs.3273	Ts translation etongation factor, mitochondri	10.6
	104560	AA007160	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (from cl	10.6 10.6
	108609 112041	AA100694 R43300	Hs.69499 Hs.22929	Human DNA sequence from BAC 15E1 on chromosom ESTs	10.6
4.0	114208	Z39301	Hs.7859	ESTs	10.6
40	118537	N67974	Hs.75431	fibrinogen; gamma polypeptide	10.6
	106919 115984	AA490885 AA447687	Hs.21766 Hs.91109	ESTs ESTs	10.6 10.6
	105538	AA258860	Hs.32597	ring finger protein (C3H2C3 type) 6	10.6
45	102200	U21551	Hs.157205	branched chain aminotransferase 1; cytosolic	10.5
45	116710	F10577	Hs.70312	ESTs	10.5 10.5
	119780 112996	W72967 T23539	Hs.191381 Hs.7165	ESTs; Weakly similar to hypothetical protein zinc finger protein 259	10.5
	103029	X54489	Hs.789	GRO1 oncogene (melanoma growth stimulating ac	10.5
50	101255	L34600	Hs.149894	mitochondrial translational initiation factor	10.4
50	107032 125617	AA599472 Al287461	Hs.247309 Hs.164950	succinate-CoA ligase; GDP-forming; beta subun ESTs	10.4 10.4
	131475	Z39053	Hs.27263	ESTs	10.4
	132073	N67408	Hs.38516	ESTs	10.4
55	101469	M22877	Hs.169248	Human somatic cytochrome c (HCS) gene; comple	10.3 10.3
22	102437 104301	U46569 D45332	Hs.221986 Hs.6783	aquaporin 5 ESTs	10.3
	127236	AI341818	Hs.98658	budding uninhibited by benzimidazoles 1 (yeas	10.3
	101465	M22612	Hs.241395	protease; serine; 1 (trypsin 1)	10.3
60	113805	W42957	Hs.250617	ESTS	10.2 10.2
00	133536 109799	Y00254 F10770	Hs.177486 Hs.180378	amyloid beta (A4) precursor protein (protease  Homo sapiens clone 669 unknown mRNA; complete	10.2
	113523	T90037	Hs.16686	ESTs	10.2
	116195	AA465148	Hs.72402	ESTs	10.2
65	134542 125298	X57025 Z39255	Hs.85112 Hs.235350	insulin-like growth factor 1 (somatomedin C) YDD19 protein	10.2 10.2
03	119367	T78324	Hs.90905	ESTs .	10.2
	134470		Hs.83758	CDC28 protein kinase 2	10.2
	134288	AA430008	Hs.8117	ESTs	10.1
70	105127 110627		Hs.11817 Hs.35225	ESTs; Weakly similar to contains similarity t ESTs; Weakly similar to MBNL protein [H.sapie	10.1 10.1
, 0	115188		Hs.88367	ESTs	10.1
	132632	N59764	Hs.5398	guanine-monophosphate synthetase	10.1
	124049		Hs.74519	primase; polypeptide 2A (58kD)	10.1 10.0
75	100079 113987		Hs.23311 Hs.9641	KIAA0367 protein ESTs; Moderately similar to COMPLEMENT C10 SU	10.0
	117280		Hs.172241	ESTs	10.0
	TARLE				

TABLE 9B: Pkey: Unique Eos probeset identifier number CAT number: Gene cluster number Accession: Genbank accession numbers 80

CAT Number 23182\_1 Pkey 100661

Accession BE623001 L05096 AA383604 AW966416 N53295 AA460213 AW571519 AA603655

	101332	25130_1	J04088 NM_001067 AF071747 AJ011741 NB5424 AL042407 AA218572 BE296748 BE083981 AL040877 AW499918 AW675045 H17813 BE081283 AA670403 AW504327 BE094229 AA104024 A4471482 AJ970337 AA737616 AI827444 AW003286 AJ742333 AJ344044
			A1765634 A1948838 AW235336 AW172827 AA095289 BE046383 A1734240 W16699 A1660329 A1289433 AA933778 AW469242 AA468838 AA806983 AA625873 W76031 BE206307 AA550803 A1743147 A1990076 AA948274 AA129533 A1635399 AA605313 A1624669 AW594319
5			AI221834 AI337434 AA307706 BE550282 AI760467 AI630636 AI221521 AW674314 AW078889 AI933732 AI686969 AI186928 AW074595
_			A1127486 AL079644 A1910815 H17814 AA310903 AW137854 T19279 AA026682 AA306035 AW383390 AW383389 AW383422 AW383427
			AW383395 H09977 AA306247 AA352501 AW403639 F05421 AA224473 AA305321 H93904 AA089612 AW391543 AW402915 AW173382
			AW402701 AW403113 R94438 N73126 H93466 AA090928 AA095051 T29025 AW951071 L47277 L47276 AI375913 BE384156 W24652 AA746288 AA568223 BE090591 H93033 N57027 AA504348 AA327653 AW959913 N53767 AA843715 AI453437 AW263710 AI076594
10			AA583483 AW873194 AW575166 Al128799 Al803319 AL042776 AW074313 Al887722 Al032284 AA447521 Al123885 N29334 Al354911
			AW090687 AA236763 AA435535 AA236910 AA047124 AA236734 AW514610 H93467 AA962007 AI446783 AA127259 AI613495
			AI686720 AI587374 AA936731 AA702453 AI859757 AA216786 AI251819 AI469227 AA806022 AI092324 N71868 AA968782 AA236919
			AA809450 AA227220 AA765284 A1192007 AA768810 AA805794 AA729280 AA806238 AW768817 N71879 A1050686 AA505822
15			AA668974 Al688160 BE045915 AW466315 AA731314 AA649568 AA834316 AW591901 AW063876 AW294770 Al300266 Al336094 Al560380 AA721755 H09978 D20305 D29155 AW821790 BE150864 F01675 Al457474 AW466316 AA550969 AA630788
13	100824	5_36	AJ393237 AJ521317 AJ761348 AF025841 D43968 AW994987 L34598 AF025841 D89789 D89788 D89790 AW998932 AJ971742 AJ310238
			X90976 AW139668 AW674280 Al365552 AA877452 AV657554 C75229 AA376077 Al798056 AW609213 W25586 H30149 BE075089
			BE075190 AW580858 H99598 AA425238 AA133916 AW363478 BE158121 BE158127 AW467960 BE158135 BE158126 BE158145
20			N92860 AA847246 Al961688 Al361423 AA878154 AA043767 Al863712 Al559226 AW339007 Al371266 Al368901 AA046624 AA134739 AW449154 AA130232 Al458720 AA962511 Al700627 R70437 AW004008 AA045229 Al671572 H99599 AA043768 Al685454 Al871685
20			N2937 X90977 AA524240 A[142114 A[825750 A[557805 A[631355 A]347893 AA134740 F20669 AA046707 AW793216 AW963298
			AW959380 AA363265 A1784593 A1268201 R69451 AV657618 A1695588
	101714	30725_1	M68874 AL022147 M72393 AL049797 BE439441 T27650 AI766240 AW150345 AW778943 AI627464 BE439479 AA587049 AI277900
25	404000	32963_1	A1984983 A1630935 M86849 AA315280 NM 004004 AA315269 BE142653 AA461400 AW802042 BE152893 AW383155 AA490688 AW117930 AW384563
2.5	101809	32903_1	AW384544 AW384566 AW378307 AW378323 AW839085 AA257102 AW378317 AW276060 AW271245 AW378298 AW384497 AI598114
			AW264544 AI018136 AW021810 AA961504 AW086214 AW771489 AW192483 AI290266 AW192488 AW384490 AW007451 AW890895
			AA554460 AA613715 AW020066 AJ783695 AJ589498 AJ917637 AW264471 AW384491 AJ816732 AW368530 AW368521 AW368463
30			AA461087 AI341438 AI970613 AI040737 AI418400 AA947181 AA962716 AI280695 AW769275 AW023591 AI160977 AA055400 N71882 AA490466 AW243772 AW316636 AI076554 AW511702 N69323 H88912 AA257017 AI952506 H88913 AI912481 AA600714 BE465701
30			. AA490400 AYY243172 AYY310030 AUY0334 AYY311702 N09323 F100312 AA237017 AI932300 F100313 AI912401 AA000714 DE403701 N64149 C00523 N64240 AA677120
	101923	30543_1	X99133 X83006 W38398 AA401137 AA298242 AA366738 AA308126 AW583781 AA298668 AW845024 BE140204 AW845005 U47734
		_	AAB37575 NM_005564 AA329732 AA421943 BE171567 S75256 AI750047 AI762213 AA100735 AW612993 AI474120 AW062884
35			A1940001 AW062852 AW062899 BE182639 AW778875 AA528093 AW517424 A1939989 AA076188 BE182636 AA169569 AA167439
33			AI283967 AA167783 AA076140 AI749649 AA166792 AI708618 AA400973 AA514773 AA514789 AA164458 AA167440 AA074845 AA421944 AA514874 AA079557 AA102361 AA587027 AA642930 AA878029 AA164459 AW176400 AW475086 AA857522 AA148193
			AAB38234 AA593897 A284596 AW193324 AA148194 AW583341 Al669077 AW264913 AA074902 Al680515 AA169874 AA169614
			AA079651 AW591737 AW190644 AA076565 AA662747 AA075896 AA535642 N27757 Al306666 AA074727 N79823 AA524360 Al826800
40			AA173827 BE140374 BE004062 AW265060 BE184103 A199258 AAB57853 AA299459 AA837890 AI626104 AA503624 BE183618
40			BE183717 AA573267 AI833071 AW270590 AA506601 BE004010 AA837854 AI675895 AI810491 AI184883 AW664712 AA076046 AA515574 AW352267 AI797418 AA172395 AI749194 AI559933 AA502597 AA321220 AI866124 AI695633 AA494293 AW085635
			AA165649 AA165663
	127007	19921_1	AB037771 BE005079 AA394189 AW959650 AA299360 AA398081 W37627 AW750817 AW630138 AI522058 BE326323 AA374890
4.5		7	AW418534 AW997510 AW995214 AW959649 AA504426 D79223 D79621 AI276062 AI973155 AA653470 AA337887 AI382521 AW084427
45	440000		D57078 W37628 AIG10506 Z30230 AIG67034 AA766091 H25097 H25078 AW991507 AA319736
	110769	229824_1	BE000831 AA541787 AW173038 AA327931 AW117510 AW664665 Al066624 Al478955 Al863075 Al073744 AA490170 R46651 Al075653 F02865 N2222 AW972956
	120695	9683_3	AA976503 AI917802 AA953664 AA404613 AA428771 BE280542 AW194691 AI927301 AI740458 AI796100 AI935603 AW052210
<b>CO</b>			AA970201 AI633384 AA425910 AI017004 AI241295 AA402816 AA291468
50			

Table 10A lists about 733 genes up-regulated in ovarian cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetric/Eos-Hiu03 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" ovarian cancer level was set to the about the 80th percentile arrongst various ovarian cancers. The "average" normal adult tissue level was set to the 90th percentile value amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 10A: ABOUT 733 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES

Pkey: Primekey
Ex. Accn; Exemplar Accession
UG ID: UniGene ID
Title: UniGene title

ratio: ratio tumor vs normal tissues

65	Pkey	Ex. Acon	UGID	Title	ratio
	432938	T27013	Hs.3132	steroidogenic acute regulatory protein	56.1
•	418179	X51630	Hs.1145	Wilms tumor 1	33.5
	400292	AA250737	Hs.72472 ·	BMPR-lb; bone morphogenetic protein receptor	30.0
	452838	U65011	Hs.30743	Preferentially expressed antigen in melanoma	29.5
70	415511	AI732617	Hs.182362	ESTs	28.1
70				ESTS	28.1
	422956	BE545072	Hs.122579		
	410929	H47233	Hs.30643	ESTs	27.4
	400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin 2)	25.2
	449034	AI624049	Hs.277523	gb:ts41a09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA	23.7
75	427585	D31152	Hs.179729	collagen; type X; alpha 1 (Schmid metaphyseal	22.7
	428392	H10233	Hs.2265	secretory granule, neuroendocrine protein 1	21.9
	448243	AW369771	Hs.77496	ESTs	21.3
	430691	C14187	Hs.103538	ESTs .	21.2
	444783	AK001468	Hs.62180	ESTs	20.8
80	407638	AJ404672	Hs.288693	EST	20.1
	423739	AA398155	Hs.97600	ESTs	19.7
	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular matrix p	19.0
	451110	A1955040	Hs.301584	ESTs	18.8
	426427	M86699	Hs.169840	. TTK protein kinase	18.7

	428227	AA321649	Hs.2248	INTERFERON-GAMMA INDUCED	18.3
	419854	AW664873	Hs.87836	Homo sapiens PAC clone RP5-1087M19 from 7q11.	18.3
	439706	AW872527	Hs.59761	ESTs	18.3
					17.4
_	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	
5	410247	AF181721	Hs.61345	RU2S	17.0
	428153	AW513143	Hs.98367	hypothetical protein FLJ22252 similar to SRY-	16.9
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	16.6
	416209	AA236776	Hs.79078	MAD2 (mitolic arrest deficient, yeast, homolo	16.6
	424905	NM_002497	Hs. 153704	NIMA (never in mitosis gene a)-related kinase	16.2
10					
10	423685	BE350494	Hs.49753	Homo sapiens mRNA for KIAA1561 protein, parti	15.9
	428187	A1687303	Hs.285529	ESTs	15.9
	438817	AI023799	Hs.163242	ESTs	15.9
	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3' untr	15.9
			Hs.38018	dual-specificity tyrosine-(Y)-phosphorylation	15.7
15	407721	Y12735			
15	412723	AA648459	Hs.179912	ESTs	15.3
	424717	H03754	Hs.152213	wingless-type MMTV integration site family, m	15.2
	443646	AI085198	Hs.298699	ESTs	15.1
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT2RP20	14.8
	428976	AL037824	Hs.194695	ras homolog gene family, member I	14.6
20					
20	418738	AW388633	Hs.6682	solute carrier family 7, member 11	14.3
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to M	14.2
	436209	AW850417	Hs.254020	ESTs, Moderately similar to unnamed protein p	14.1
	427356	AW023482	Hs.97849	ESTs	.13.9
					13.8
25	418601	AA279490	Hs.86368	calmegin	
25	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	13.7
	428532	AF157326	Hs.184788	TBP-interacting protein	13.6
	402408			0	13.6
	447350	AI375572	Hs.172634	ESTs; HER4 (c-erb-84)	13.4
				DKFZP564J0863 protein	13.4
20	451807	W52854	Hs.27099		
30	423575	C18863	Hs.163443	ESTs	13.2
	443211	AI128388	Hs.143655	ESTs	13.2
	437872	AK002015	Hs.5887	RNA binding motif protein 7	13.0
	451659	BE379761	Hs.14248	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	12.7
	452904		Hs.30957	Homo sapiens mRNA; cDNA DKFZp434E0626 (from c	12.7
25		AL157581			12.5
35	442655	AW027457	Hs.30323	ESTs	
	452096	BE394901	Hs.226785	ESTs	12.4
	414972	BE263782	Hs.77695	KIAA0008 gene product	12.3
	435039	AW043921	Hs.130526	ESTs	12.3
	447033	Al357412	Hs.157601	EST - not in UniGene	12.3
40					12.2
40	433764	AW753676	Hs.39982	ESTs	
	442611	BE077155	Hs.177537	ESTs	12.0
	408562	AJ436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein, parti	11.9
	427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3A	11.8
	421478	AI683243	Hs.97258	ESTs	11.8
45				ESTs	11.8
73	426635	BE395109	Hs.129327		
	415989	A1267700	Hs.111128	ESTs	11.7
	433159	AB035898	Hs.150587	kinesin-like protein 2	11.5
	452249	BE394412	Hs.61252	ESTs	11.4
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	11.3
50					11.3
50	442353	BE379594	Hs.49136	ESTs	
	447700	Al420183	Hs.171077	ESTs, Weakly similar to similar to serine/thr	11.3
	450480	X82125	Hs.25040	zinc finger protein 239	11.3
	425176	AW015644	Hs.301430	ESTs, Moderately similar to TEF1_HUMAN TRANSC	11.2
	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-relate	11.2
55					11.1
J.J	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated protein	
	445258	AI635931	Hs.147613	ESTs	11.1
	432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polypeptid	11.0
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain-bind	10.9
	404567			0	10.8
60		AW299598	Hs.50895	homeo box C4	10.7
UU	423811				
	452891	N75582	Hs.212875	ESTs, Weakly similar to KIAA0357 [H.sapiens]	10.6
	441627	AA947552	Hs.58086	ESTs	10.3
•	443555	N71710	Hs.21398	ESTs, Moderately similar to GNPI_HUMAN GLUCOS	10.3
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkinesin6)	10.2
65				ESTs	10.1
05	427469	AA403084	Hs.269347		
	415227	AW821113	Hs.72402	ESTs	10.1
	445413	AA151342	Hs.12677	CGI-147 protein	10.0
	425734	AF056209	Hs.159396	peptidylgtycine alpha-amidating monooxygenase	10.0
	421451	AA291377	Hs.50831	ESTs	10.0
70				highly expressed in cancer, rich in leucine h	9.8
70	410044	BE566742	Hs.58169		
	427878	C05766	Hs.181022	CGI-07 protein	9.7
	408460	AA054726	Hs.285574	ESTs	9.7
	422972	N59319	Hs.145404	ESTs	9.7
	443715	AI583187	Hs.9700	cyclin E1	9.7
75		AA909358			9.6
, ,	440901		Hs.128612	ESTS	
	453160	Al263307	Hs.146228	ESTs	9.6
	415211	R64730.comp	Hs.155986	ESTs; Highly similar to SPERM SURFACE PROTEIN	9.5
	425282	AW163518	Hs.155485	huntingtin interacting protein 2	9.5
	400250			0	9.5
80		AWIESONO	Un CAEAS	nna mDNA ris avena fartor im 1695/N	9.3
00	410568	AW162948	Hs.64542	pre-mRNA cleavage factor Im (68kD)	
	442957	AI949952	Hs.49397	ESTs	9.3
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1 (yeas	9.3
	434401	AI864131	Hs.71119	Putative prostate cancer tumor suppressor	9.2
	453628	AW243307	Hs.170187	. ESTs	9.1
		10001			•••

•					
	452055	Al377431	Hs.293772	ESTs	9.1 9.1
	424086 442875	AI351010 BE623003	Hs.102267 Hs.23625	lysyl oxidase Homo sapiens clone TCCCTA00142 mRNA sequence	9.1
_	416208	AW291168	Hs.41295	ESTs	9.0
5	407168	R45175	Hs.117183	gb:yg40f01.s1 Soares infant brain 1NIB Homo s	9.0
	445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	8.9
	409269 433527	AA576953 AW235613	Hs.22972 Hs.133020	Homo sapiens cDNA FLJ13352 fis, clone OVARC10 ESTs	8.9 8.9
	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	8.8
10	423020	AA383092	Hs.1608	replication protein A3 (14kD)	8.7
	425665	AK001050	Hs.159066	ESTs	8.6
	443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT2RP30 ESTs	8.6 8.6
	449433 453878	A1572095 AW954440	Hs.9012 Hs.19025	ESTs	8.6
15	450505	NM_004572	Hs.25051	plakophilin 2	8.6
	407001	U12471	Hs.247954	Human thrombospondin-1 gene, partial cds	8.5
	414315	Z24878	11. 450474	gb:HSB65D052 STRATAGENE Human skeletal muscle	8.5
	425492 435181	AL021918 AA669339	Hs.158174 Hs.28838	zinc finger protein 184 (Kruppel-like) KIAA1571 protein	8.5 8.5
20	436396	AI683487	Hs.299112	Homo sapiens cDNA FLJ11441 fis, clone HEMBA10	8.5
	418384	AW149266	Hs.25130	ESTs	8.4
	453370	AI470523	Hs.182356	ESTs, Moderately similar to translation initi	. 8.4
	409041	AB033025	Hs.50081	KIAA1199 protein ESTs	8.4 8.4
25	447078 448674	AW885727 W31178	Hs.301570 Hs.154140	ESTs	8.3
	433393	AF038564	Hs.98074	atrophin-1 interacting prolein 4	8.3
	433496	AF064254	Hs.49765	VERY-LONG-CHAIN ACYL-COA SYNTHETASE	8.3
	421155	H87879	Hs.102267	lysyl oxidase	8.2
30	438394 400298	BE379623 AA032279	Hs.27693 Hs.61635	CGI-124 protein STEAP1	8.2 8.1
30	409092	AI735283	Hs.172608	ESTs	8.1
	440250	AA876179	Hs.134650	ESTs	8.1
	409143	AW025980	Hs.138965	ESTs	8.1
35	407771 419088	AL138272 Al538323	Hs.62713 Hs.77496	ESTs ESTs	8.1 8.1
55	431725	X65724	Hs.2839	Nomie disease (pseudoglioma)	7.9
	431750	AA514986	Hs.283705	ESTs	7.9
	435635	AF220050	Hs.181385	uncharacterized hematopolatic stem/progenitor	7.9
40	441826 417728	AW503603 AW138437	Hs.129915 Hs.24790	phosphotriesterase related KIAA1573 protein	7.9 7.8
40	418845	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alpha)	7.8
	421039	NM_003478	Hs.101299	cultin 5	7.8
	446999	AA151520	Hs.279525	hypothetical protein PRO2605	7.8
45	429609 415139	AF002246	Hs.210863	cell adhesion molecule with homology to L1CAM ESTs	7.8 7.7
7,5	450192	AW975942 AA263143	Hs.48524 Hs.24596	RAD51-interacting protein	7.7
	423992	AW898292	Hs.137206	Homo sapiens mRNA; cDNA DKFZp564H1663 (from c	7.7
	436211	AK001581	Hs.80961	polymerase (DNA directed), gamma	7.7
50	450101	AV649989 AA037145	Hs.24385 Hs.172865	Human hbc647 mRNA sequence cleavage stimulation factor, 3' pre-RNA, subu	7.5 7.5
50	426921 433330	AW207084	Hs.132816	ESTs	7.5
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDNA clo	7.5
	427660	A1741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone CAE066	7.5
55	422095	A1868872	Hs.288966	ceruloplasmin (ferroxidase) ESTs	7.5 7.5
55	436476 412170	AA326108 D16532	Hs.53631 Hs.73729	very low density lipoprotein receptor	7.4
	428954	AF100781	Hs.194678	WNT1 inducible signaling pathway protein 3	7.4
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	7.4
60	439262	AA832333	Hs.124399	ESTs EST-	7.4 7.3
oo	435420 422892	Al928513 AA988176	Hs.59203 Hs.121553	ESTs hypothetical protein FLJ20641	7.3
	457030	Al301740	Hs.1733B1	dihydropyrimidinase-like 2	7.3
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	7.2
65	409916	BE313625	Hs.57435	solute carrier family 11 (proton-coupled diva	7,2 7.2
05	418007 420900	M13509 AL045633	Hs.83169 Hs.442 <del>6</del> 9	Matrix metalioprotease 1 (interstitial collag ESTs	7.2
	424001	W67883	Hs.137476	KIAA1051 protein	7.2
	400301	X03635	Hs.1657	Estrogen receptor 1	7.1
70	400238	A17220E0	Un 440000	0 ESTs	7.1 7.1
, 0	413573 428071	AI733859 AF212848	Hs.149089 Hs.182339	transcription factor ESE-3B	7.1
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	7.1
	453062	AW207538	Hs.61603	ESTs	7.1
75	456965	AW131888	Hs.172792 Hs.209122	ESTs, Wealdy similar to hypothetical protein	7.1 7.1
, ,	442500 446142	A1819068 A1754693	Hs.145968	ESTs .	7.1
	417791	AW965339	Hs.111471	ESTs	7.0
	418524	AA300576	Hs.85769	acidic 82 kDa prolein mRNA	7.0
80	451797	AW663858 AM 015368	Hs.56120	ESTs	7.0 7.0
00	452909 453616	NM_015368 NM_003462	Hs.30985 Hs.33846	pannexin 1 dynein, axonemal, light intermediate polypept	7.0
	436281	AW411194	Hs.120051	ESTs	7.0
	449897	AW819642	Hs.24135	transmembrane protein vezatin; hypothetical p	6.9
	414142	AW368397	Hs.150042	, ESTs	6.9

	448776	BE302464	Hs.30057	transporter similar to yeast MRS2	6.9
	419423	D26488	Hs.90315	KIAA0007 protein	6.9
	420908	AL049974	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (from d	6.8
_	452971	A1873878	Hs.91789	ESTs	5.8
5	413597	AW302885	Hs.117183	ESTs ·	6.8
	415138	C18356	Hs.78045	fissue factor pathway Inhibitor 2 TFP12	6.8
	437478	AL390172	Hs.118811	ESTs	6.7
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	6.7
10	421184	NM_003616	Hs.102456	survival of motor neuron protein interacting	6.7
10	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	6.6
	446608	N75217	Hs.257846	ESTs	6.6
	438167	R28363	Hs.24285	ESTs	6.6
	445459	Al478629	Hs.158465	ESTs	6.6
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae, h	- 6.6
15	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	6.6
	410292	AA843087	Hs.124194	ESTs	8.5
	415716	N59294	Hs.301141	Horno sapiens cDNA FLJ11689 fis, clone HEMBA10	6.5
	424770	AA425562		gb:zw46e05.r1 Soares_total_fetus_Nb2HF8_9w Ho	6.5
	438122	Al620270	Hs.129837	ESTs	6.5
20	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cONA clo	6.5
	444743	AA045648	Hs.11817	nudix (nucleoside diphosphate linked moiety X	6.5
	450638	AK001826	Hs.25245	hypothetical protein FLJ11269	6.5
	418203	X54942	Hs.83758	CDC28 protein kinase 2	6.5
	439901	N73885	Hs.124169	ESTs	6.5
25	428758	AA433988	Hs.98502	Homo sapiens cDNA FLJ14303 fis, clone PLACE20	6.4
	404552	•		0	6.4
	404599			0	6.4
	419503	AA243642	Hs.137422	ESTs	6.4
	420149	AA255920	Hs.88095	ESTs	6.4
30	440411	N30256	Hs.156971	ESTs, Weakly similar to Weak similarity with	6.4
	449108	Al140683	Hs.98328	ESTs	6.4
	452097	AB002364	Hs.27916	ADAM-TS3; a disintegrin-like and metallopr	6.4
	453619	H87648	Hs.33922	H.sapiens novel gene from PAC 117P20, chromos	6.4
	410273	BE326877	Hs.281523	ESTs	6.3
35	434486	AA678816	Hs.117142	ESTs	6.3
55	454036	AA374756	Hs.93560	ESTs, Weakly similar to unnamed protein produ	6.3
	403381	777014100	115.55500	0	6.2
	421308	AA687322	Hs.192843	ESTs	6.2
	419346	Al830417	16.152045	gb:wh94d12.x1 NCI_CGAP_CLL1 Homo sapiens cDNA	6.2
40	446140	AA356170	Hs.26750	Homo sapiens cDNA: FLJ21908 fis, clone HEP038	6.2
-10	453047	AW023798	Hs.286025	ESTs	6.2
	442573	H93366	Hs.7567	Branched chain aminotransferase 1, cytosolic,	6.1
	410102	AW248508	Hs.279727	ESTs;	6.1
	410004	A1298027	Hs.299115	ESTs	6.1
45	413335	AI613318	Hs.48442	ESTs	6.1
73	424945	Al221919	Hs.173438		6.1
	427510			hypothetical protein FLJ10582	
	451229	Z47542	Hs.179312 Hs.48473	small nuclear RNA activating complex, polypep ESTs	6.1 6.1
	452641	AW967707 AW952893	Hs.237825		6.1
50	433172	AB037841	Hs.102652	signal recognition particle 72kD hypothetical protein ASH1	6.1
50	425465	L18964	Hs.1904		6.1
	437117	AL049256	Hs.122593	protein kinase C; iota ESTs	6.0
	423440	R25234	Hs.143434		
	430510	AW162916	Hs.241576	contactin 1	6.0 6.0
55				hypothetical protein PRO2577	
J.J	433252 434699	AB040957	Hs.151343	KIAA1524 protein	6.0 6.0
	436954	AA643687	Hs.149425	Homo saplens cDNA FLJ11980 fis, clone HEMBB10	5.9
	436032	AA740151 AA150797	Hs.130425 Hs.109276	ESTs Latexin protein	, 5.9
	424590	AW966399	Hs.46821	hypothetical protein FLJ20086	5.9
60	444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-bindi	5.9
50	418379	AA218940	Hs.137516	fidgetin-like 1	5.9
	438081	H49546	Hs.298964	ESTs	5.8
		NM_004272	Hs.9192	Homer, neuronal immediate early gene, 18	5.8
	443270 450459		Hs.299254	ESTs	5.8
65	433612	Al697193 AF078164	Hs.61188		5.8
03	449048			Homo sapiens Ku70-binding protein (KUB3) mRNA	
		Z45051 AW015242	Hs.22920	similar to S68401 (cattle) glucose induced ge	5.8 5.7
	417251		Hs.99488	ESTs; Weakly similar to ORF YKR074w [S.cerevi	5.7 5.7
	429181 454933	AW979104 BE141714	Hs.294009	ESTs gb:QV0-HT0101-061099-032-c04 HT0101 Homo sapi	5.7 5.7
70			Un 1000E0		
	456553 430371	AA721325 D87466	Hs.189058 Hs.240112	ESTs, Weakly similar to cAMP-regulated guanin KIAA0276 protein	5.7 5.7
		D49441			5.7
	425371 424513	BE385864	Hs.155981 Hs.149894	mesothetin mitochondrial translational initiation factor	5.6
	432015			ESTs	5.6
75		AL157504 AM76621	Hs.159115 Hs.71367	ESTs, Moderately similar to ALU7_HUMAN ALU SU	5.6
, ,	438109 407137	AI076621		v-erb-b2 avian erythroblastic leukemia viral	5.6
	407137	T97307	Hs.199067		
	407945 416565	X69208	Hs.606	ATPase, Cu++ transporting, alpha polypeptide	5.6 5.6
	416565	AW000960	Hs.44970	ESTs	5.6 5.5
80	417830	AW504786	Hs.132808	epithelial cell transforming sequence 2 oncog	5.5
00	419752	AA249573	Hs.152618	ESTs .	5.5
	422093	AF151852	Hs.111449	CGI-94 protein fucose-1-phosphate guanylyttransferase	5.5 5.5
	424583	AF017445	Hs.150926	nuclear cap binding protein subunit 2, 20kD	5.5 5.5
	430388	AA356923 AM093022	Hs.240770	Homo saptens cDNA FLJ 11980 fis, clone HEMBB10	5.5
	452534	AW083022	Hs.149425	. The control of the control of the control of the control of	3.3

				COT-	
	453279	AW893940	Hs.59698	ESTs zinc finger protein	5.5 5.5
	424188 453884	AW954552 AA355925	Hs.142634 Hs.36232	KIAA0186 gene product	5.5
	424641	AB001106	Hs.151413	glia maturation factor, beta	5.5
5	444478	W07318	Hs.240	M-phase phosphoprotein 1	5.5
-	427975	AI536065	Hs.122460	ESTs	5.5
	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic; stratum comeum)	5.5
	442914	AW188551	Hs.99519	Homo sapiens cDNA FLJ14007 fis, clone Y79AA10	5.5
	417995	AW974175	Hs.188751	ESTs	5.4
10	418946	AI798841	Hs.132103	ESTs	5.4
	419963	AA743276	Hs.301052	ESTs	5.4
	420362	U79734	Hs.97206	huntinglin interacting protein 1	5.4
	422670 432837	AA371612 AA310693	Hs.115351 Hs.279512	ESTs HSPC072 protein	5.4 5.4
15	447020	T27308	Hs.16986	hypothetical protein FLJ11046	5.4
13	458027	L49054	Hs.85195	ESTs, Highly similar to t(3;5)(q25.1;p34) fus	5.4
	425217	AU076696	Hs.155174	CDC5 (cell division cycle 5, S. pombe, homoto	5.4
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	5.4
00	450434	AA166950	Hs.18645	ESTs, Weakly similar to partial CDS (C.elegan	5.4
20	438279	AA805166	Hs.165165	ESTs, Moderately similar to ALU8_HUMAN ALU SU	5.4
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	5.3
	420328	Y19062	Hs.96870	staufen (Drosophila, RNA-binding protein) hom	5.3 5.3
	436586 435793	A1308862 AB037734	Hs.167028 Hs.4993	ESTs :	5.3
25	422306	BE044325	Hs.227280	Homo sapiens mRNA for Lsm5 protein	5.3
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	5.2
	453293	AA382267	Hs.10653	ESTs	5.2
	429944	R13949	Hs.226440	Homo sapiens clone 24881 mRNA sequence	5.2
~~	434891	AA814309	Hs.123583	ESTs	5.2
30	415263	AA948033	Hs.130853	ESTs	5.2
	409506	NM_006153	Hs.54589	NCK adaptor protein 1	5.2
	412848	AA121514	Hs.70832	ESTS	5.2 5.2
	421246 431548	AW582962 A1834273	Hs.300961 Hs.9711	ESTs, Highly similar to AF151805 1 CGI-47 pro Homo saplens cDNA FLJ13018 fis, clone NT2RP30	5.2
35	412719	AW016610	Hs.129911	ESTs	5.2
J <b>J</b>	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncogene h	5.1
	424078	AB006625	Hs.139033	paternally expressed gene 3	5.1
	433558	AA833757	Hs.201769	ESTs	5.1
40	434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone LNG070	5.1
40	453911	AW503857	Hs.4007	Sarcolemmal-associated protein	5.1
	415539	AI733881	Hs.72472	BMPR-lb; bone morphogenetic protein receptor	5.1
	442717	R88362	Hs.180591	ESTs, Weakly similar to R06F6.5b [C.elegans]	5.1 5.0
	432358 409731	Al093491 AA125985	Hs.72830 Hs.56145	ESTs thymosin, beta, identified in neuroblastoma c	5.0
45	419699	AA248998	Hs.31246	ESTs	5.0
1,5	420313	AB023230	Hs.96427	KIAA1013 protein	5.0
	422505	AL120862	Hs.124165	ESTs; (HSA)PAP protein (programmed cell deat	5.0
	425733	F13287	Hs.159388	Homo sapiens clone 23578 mRNA sequence	5.0
60	434160	BE551196	Hs.114275	ESTs	5.0
50	435094	Al560129	Hs.277523	EST	5.0
	436812	AW298067	LI- 200044	gb:UI-H-BW0-ajp-g-09-0-UI.s1 NCI_CGAP_Sub6 Ho	5.0 4.9
	432415 406117	T16971	Hs.289014	ESTs 0	4.9
	438018	AK001160	Hs.5999	hypothetical protein FLJ 10298	4.9
55	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (from cl	4.9
	448621	AI097144	Hs.5250	ESTs, Weakly similar to BACR37P7.g [D.melanog	4.9
	453001	AW131636	Hs.191260	ESTs	4.9
	410561	BE540255	Hs.6994	Homo sapiens cONA: FLJ22044 fis, clone HEP091	4.9
<b>60</b>	418811	AK001407	Hs.88663	hypothetical protein FLJ10545	4.9
60	436754	AI061288	Hs.133437	ESTs, Moderately similar to gonadotropin indu	4.8
	437212 447312	Al765021	Hs.210775 Hs.36908	ESTs	4.8 4.8
	409732	AI434345 NM_016122	Hs.56148	activating transcription factor 1 NY-REN-58 antigen	4.8
	434690	AI867679	Hs.148410	ESTs	4.8
65	444172	BE147740	Hs.104558	ESTs	4.8
	424539	L02911	Hs.150402	activin A receptor, type I	4.8
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	4.8
	405076	AL390179	Hs.137011	Homo saplens mRNA; cDNA DKFZp547P134 (from cl	4.8
70	420179	N74530	Hs.21168	ESTs	4.7
70	450375 419247	AA009647 S65791	Hs.8850 Hs.89764	a disintegrin and metalloproteinase domain 12 fragile X mental retardation 1	4.7 4.7
	420850	BE139590	Hs.122406	ESTs	4.7
	425420	BE536911	Hs.234545	ESTs ·	4.7
_	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	4.7
75	419131	AA406293	Hs.301622	ESTs	4.7
	422278	AF072873	Hs.114218	ESTs	4.7
	451684	AF216751	Hs.26813	CDA14	4.6
	400296	AA305627	Hs.139336	ATP-binding cassette; sub-family C (CFTR/MRP)	4.6
80	408425	AW058674	Hs.44787	Homo sapiens mRNA; cDNA DKFZp43400227 (from c	4.6
ov	417168 429486	AL133117 AF155827	Hs.81376 Hs.203963	Homo sapiens mRNA; cDNA DKFZp586L1121 (from c hypothetical protein FLJ10339	4.6 4.6
	442917	AA314907	Hs.85950	ESTs	4.6
	443268	AI800271	Hs.129445	hypothetical protein FLJ12496	4.6
	452795	AW392555	Hs.18878	hypothetical protein FLJ21620	4.6

	457300	AW297436	Hs.158849	Homo sapiens cDNA: FLJ21663 fis, clone COL088	4.6
	459551	AI472808		gb:tj70e07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Hom	4.6
	421977	W94197	Hs.110165	ribosomal protein L26 homolog	4.6
_	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member), pro	4.6
5	449722	BE280074	Hs.23960	cyclin B1	4.6
-	431589	AA305688	Hs.267695	UDP-GaltbetaGlcNAc beta 1,3-galactosyltransfe	4.5
	425178	H16097	Hs.161027	ESTs	4.5
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain 9	4.5
	436556		Hs.7572		4.5
10		Al364997	115.1312	ESTs	
10	400534	41 447404	11- 00740	O	4.5
	417845	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DXFZp586F1822 (from c	4.5
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE; Human selenium d	4.5
	448305	AA625207	Hs.264915	Homo sapiens cDNA FLJ12908 fis, clone NT2RP20	4.5
	441006	AW605267	Hs.7627	CGI-60 protein	4.5
15	414569	AF109298	Hs.118258	Prostate cancer associated protein 1	4.5
	447924	AI817226	Hs.170337	ESTs	4.5
	425506	NM_003666	Hs.158205	basic teucine zipper nuclear factor 1 (JEM-1)	4.5
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppressor	4.4
	432842	AW674093	Hs.279525	hypothetical protein PRO2605	4.4
20	413472	BE242870	Hs.75379		4.4
20				solute carrier family 1 (glial high affinity	
	414699	AI815523	Hs.76930	synuclein, alpha (non A4 component of amyloid	4.4
	412733	AA984472	Hs.74554	KIAA0080 protein	4.4
	419790	U79250	Hs.93201	glycerol-3-phosphate dehydrogenase 2 (mitocho	4.4
05	433377	AI752713	Hs.43845	ESTs .	4.4
·25	449535	W15267	Hs.23672	low density lipoprotein receptor-related prot	4.4
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	4.4
	443881	R64512	Hs.237146	Homo sapiens cDNA FLJ14234 fis, clone NT2RP40	4.4
	423025	AA831267	Hs.12244	Homo sapiens cDNA: FLJ23581 fis, clone LNG136	4.4
	408521	Al970672	Hs.46638	chromosome 11 open reading frame 8; fetal br	4.3
30	416241				4.3
30		N52639	Hs.32683	ESTs	
	432005	AA524190	Hs.120777	ESTs, Weakly similar to ELL2_HUMAN RNA POLYME	4.3
	435532	AW291488	Hs.117305	ESTs	4.3
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	4.3
	454193	BE141183		gb:MR0-HT0071-191199-001-b04 HT0071 Homo sapl	4.3
35	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (melanom	4.3
	406069			0	4.3
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone LNG055	4.3
	418413	R95735	Hs.117753	ESTs, Weakly similar to antigen of the monod	4.3
40	452028	AK001859	Hs.27595	hypothelical protein FLJ10997	4.3
40	418693	AJ750878	Hs.87409	thrombospondin 1	4.3
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-induc	4.2
	409763	AL043212		gb:DKFZp434H0623_r1 434 (synonym: htes3) Homo	4.2
	455601	AJ368680	Hs.816	SRY (sex determining region Y)-box 2, partial	4.2
	408908	BE296227	Hs.48915	serine/threonine kinase 15	4.2
45	413582	AW295647	Hs.71331	Homo sapiens cDNA: FLJ21971 fis, clone HEP057	4.2
	423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	4.2
	425024	R39235	Hs.12407	ESTs	4.2
	447153	AA805202	Hs.173912	eukaryotic translation initiation factor 4A,	4.2
50	447406	BE618060	Hs.282882	ESTs	4.2
<i>5</i> 0	449347	AV649748	Hs.295901	ESTs	4.2
	414279	AW021691	Hs.3804	DKFZP564C1940 protein	4.2
	428856	AA436735	Hs.183171	Homo sapiens cDNA: FLJ22002 fis, clone HEP066	4.2
	407872	AB039723	Hs.40735	frizzled (Drosophila) homolog 3	4.2
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phosphate),	4.2
55	436406	AW105723	Hs.125346	ESTs	4.2
	438209	AL120659	Hs.6111	KIAA0307 gene product	4.2
	443653	AA137043	Hs.9663	programmed cell death 6-interacting protein	4.1
	454556	AW807073	11- 450 400	gb:MR4-ST0062-031199-018-d06 ST0062 Homo sapi	4.1
60	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP20	4.1
60	412593	Y07558	Hs.74088	early growth response 3	4.1
	416566	NM_003914	Hs.79378	cyclin A1	4.1
	426342	AF093419	Hs.169378	multiple PDZ domain protein	4.1
	428417	AK001699	Hs.184227	F-box only protein 21	4.1
	429317	AA831552	Hs.268016	solute carrier family 5 (mosito) transporter	4.1
65	446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ12534 fis, clone NT2RM40	4.1
	422988	AW673847	Hs.97321	ESTs	4.0
				==:-	
	434657	AA641876	Hs.191840	ESTs	4.0
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1, 64k	4.0
70	443271	BE568568	Hs.195704	ESTs	4.0
70	421437	AW821252	Hs.104336	ESTs	4.0
	401644			0	4.0
	405095			0	4.0
	418417	R77182		gb:yi65e02.r1 Soares placenta Nb2HP Homo sapi	4.0
	420807	AA280627	Hs.57846	ESTs	4.0
75	429529	AA454190	Hs.193811	ESTs, Moderately similar to reduced expressio	4.0
	457726	AJ217477	Hs.194591	ESTs	4.0
	431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic protein type	4.0
	453403	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fis, clone PLACE10	4.0
QΛ	442768	AL048534	Hs.48458	ESTs, Wealdy similar to ALUS_HUMAN ALU SUBFAM	4.0
80	413430	R22479	Hs.24650	Homo sapiens cDNA FLJ13047 fis, clone NT2RP30	4.0
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	4.0
	425692	D90041	Hs.155956	NAT1; arylamine N-acetyltransferase	4.0
	407792	AI077715	Hs.39384	putative secreted ligand homologous to fpx1	4.0
	408353	BE439838	Hs.44298	hypothetical protein	4.0

	421175	Al879099	Hs.102397	GIOT-3 for gonadotropin inducible transcripti	3.9
	420324	AF163474	Hs.96744	DKFZP586D0823 protein, Prostate androgen-regu	3.9
	417531	NM_003157	Hs.1087	serine/threonine kinase 2	3.9
_	458924	BE242158	Hs.24427	DKFZP56601646 protein	3.9
5	400195			0	3.9
	401480			0	3.9
	410360	AW663690		gb:hj21g03.x1 NCI_CGAP_Li8 Homo sapiens cDNA	3.9
	410908	AA121686	Hs.10592	ESTs	3.9
	420159	Al572490	Hs.99785	ESTs	3.9
10	422805	AA436989	Hs.121017	H2A histone family; member A	3.9
	424639	AI917494	Hs.131329	ESTs	3.9
	428555	NM_002214	Hs.184908	integrin, beta 8	3.9
	431699	NM_001173	Hs.267831	Homo sapiens cDNA FLJ12952 fis, clone NT2RP20	3.9
	433703	AA210863	Hs.3532	nemo-like kinase	3.9
15	437144	AL049466	Hs.7859	ESTs	3.9
	452728	Al915676	Hs.239708	ESTs	3.9
	430447	W17064	Hs.241451	SWUSNF related, matrix associated, actin dep	3.9
	440594	AW445167	Hs.126036	ESTs	3.9
	408938	AA059013	Hs.22607	ESTs	3.9
20	427051	BE178110	Hs.173374	ESTs	3.9
	447568	AF155655	Hs.18885	CGI-116 protein	3.9
	457211	AW972565	Hs.32399	ESTs, Weakly similar to Similar to Ena-VASP I	3.9
	443475	AI066470	Hs.134482	ESTs	3.9
	433447	U29195	Hs.3281	neuronal pentraxin II	3.9
25	428093	AW594506	Hs.104830	ESTs	3.8
	437938	AI950087		ESTs; Weakly similar to Gag-Pol polyprotein [	3.8
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfotransf	3.8
	429250	H56585	Hs.198308	tryptophan rich basic protein	3.8
	441859	AW194364	Hs.128022	ESTs, Wealty similar to FIG1 MOUSE FIG-1 PROT	3.8
30	437700	AA766060	Hs.122848	ESTs	3.8
	439560	BE565647	Hs.74899	hypothetical protein FLJ12820	3.8
	409564	AA045857	Hs.54943	fracture callus 1 (rat) homolog	3.8
	429474	AA453441	Hs.31511	ESTs	3.8
~ ~	431965	BE175190		gb:QV2-HT0577-010500-165-g04 HT0577 Homo sapi	3.8
35	454018	AW016892	Hs.241652	ESTs ·	3.8
	426320	W47595	Hs.169300	transforming growth factor, beta 2	3.8
	439635	AA477288	Hs.94891	Homo saplens cDNA: FLJ22729 fis, done HSI156	3.8
	417517	AF001176	Hs.82238	POP4 (processing of precursor, S. cerevisiae	3.8
40	446402	Al681145	Hs.160724	ESTs	3.8
40	450236	AW162998	Hs.24684	KIAA1376 protein	3.8
	410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar ataxi	3.8
	400268			0 .	3.8
	418217	Al910647	Hs.13442	ESTs	3.8
4.5	421928	AF013758	Hs.109643	polyadenylate binding protein-interacting pro	3.8
45	417300	Al765227	Hs.55610	solute carrier family 30 (zinc transporter),.	3.8
	414136	AA812434	Hs.178227	ESTs	3.8
	453945	NM_005171	Hs.36908	activating transcription factor 1	3.7
	400240			0	3.7
50	407877	AW016811	Hs.234478	Homo sapiens cDNA: FLJ22648 fis, clone HSI073	3.7
50	450581	AF081513	Hs.25195	endometrial bleeding associated factor (left-	3.7
	418223	NM_014733	Hs.83790	KIAA0305 gene product	3.7
	411704	Al499220	Hs.71573	hypothetical protein FLJ10074	3.7
•	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta-5-de	3.7
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	3.7
55	402820			0	3.7
	408090	BE173621	Hs.292478	ESTs	3.7
	416421	AA134006	Hs.79306	eukaryotic translation initiation factor 4E	3.7
	418282	AA215535	Hs.98133	ESTs	3.7
60	418454	AA315308		gb:EST187095 Colon carcinoma (HCC) cell line	3.7
60	418668	AW407987	Hs.87150	Human clone A9A2BR11 (CAC)n/(GTG)n repeal-con	3.7
	422290	AA495854	Hs.48827	hypothetical protein FLJ12085	3.7
	432824	AK001783	Hs.279012	hypothetical protein FLJ10921	3.7
	439907	AA853978	Hs.124577	ESTs	3.7
65	447479	AB037834	Hs.18685	Homo sapiens mRNA for KIAA1413 protein, parti	3.7
65	451073	A1758905	Hs.206063	ESTs	3.7
	450377	AB033091	Hs.24936	ESTs	3.7
	414343	AL036166	Hs.75914	coated vesicle membrane protein	3.7
	448807	Al571940	Hs.7549	ESTs	3.7
70	442821	BE391929	Hs.8752	Putative type II membrane protein	3.7
70	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	3.7
	418068	AW971155	Hs.293902	ESTs, Weakly similar to prolyl 4-hydroxylase	3.7
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-associated	3.7
	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	3.7
75	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PLACE10	3.7
75	411402	BE297855	Hs.69855	NRAS-related gene	. 3.7
	450447	AF212223	Hs.25010	hypothetical protein P15-2	3.6
	414706	AW340125	Hs.76989	KIAA0097 gene product	3.6
	434228	Z42047	Hs.283978	ESTs; KIAA0738 gene product	3.6
QΛ	434164	AW207019	Hs.148135	ESTs	3.6
80	409533	AW969543	Hs.21291	mitogen-activated protein kinase kinase kinas	3.6
	402222	•		. 0	·3.6 3.6
	404915			0	3.6
	404996	AVAIRE 1100		0 . gb:IL3-CT0220-150200-071-H05 CT0220 Homo sapi	3.6
	411560	AW851186		-	0.0
				170	

	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fis, done NT2RP40	3.6
	426010	AA136563	Hs.1975	Homo sapiens cDNA: FLJ21007 fis, clone CAE038	3.6
	427038	NM_014633	Hs.173288	KIAA0155 gene product	3.6
	439255	BE164500	110.110200	gb:RC4-HT0469-230300-014-e10 HT0469 Homo sapi	3.6
5	458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone HEP024	3.6
-	415115	AA214228		hypothetical protein	3.6
			Hs.127751	DKFZP566F084 protein	3.6
	453468	W00712	Hs.32990		
	441205	AW137827	Hs.176904	ESTs	3.6
10	452693	T79153	Hs.48589	zinc finger protein 228 .	3.6
10	417389	BE260964	Hs.82045	Midkine (neurite growth-promoting factor 2)	3.6
	448105	AW591433	Hs.170675	ESTs, Weakly similar to TMS2_HUMAN TRANSMEMBR	3.6
	451522	BE565817	Hs.26498	hypothetical protein FLJ21657	3.6
	440048	AA897461	Hs.158469	ESTs, Weakly similar to envelope protein [H.s	3.5
-	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)-like	3.5
15	452030	AL137578	Hs.27607	Homo sapiens mRNA; cDNA DKFZp564N2464 (from c	3.5
10	400666	712101010	110.21007	0	3.5
		H87863	Hs.151380	ESTs	3.5
	422646				3.5
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, with Glu	
20	408730	AV660717	Hs.47144	DKFZP586N0819 protein	3.5
20	401517			0	3.5
	413775	AW409934	Hs.75528	nucleolar GTPase	3.5
	417177	NM_004458	Hs.81452	fatty-acid-Coenzyme A ligase, long-chain 4	3.5
	427943	AW959075		gb:EST371145 MAGE resequences, MAGE Homo sapl	3.5
	439107	AL046134	Hs.27895	ESTs	3.5
25	447268	Al370413	Hs.36563	Homo sapiens cDNA: FLJ22418 fis, clone HRC085	3.5
	412604	AW978324	Hs.47144	DKFZP586N0819 protein	3.5
	427134	AA398409	Hs.173561	EST	3.5
	430273	AI311127	Hs.125522	ESTs	3.5
					3.5
20	435671	AW137159	Hs.146151	ESTs	
30	433037	NM_014158	Hs.279938	HSPC067 protein	3.5
	453745	AA952989	Hs.63908	Homo sapiens HSPC316 mRNA, partial cds	3.5
	400531	AF151064	Hs.36069	hypothetical protein	3.5
	433345	AI681545	Hs.152982	EST cluster (not in UniGene)	3.4
	406400	AA343629	Hs.104570	kallikrein 8 (neuropsin/ovasin)	3.4
35	407596	R86913		gb:yq30f05.r1 Soares fetal liver spleen 1NFLS	3.4
	453779	N35187	Hs.43388	ESTs	3.4
	444858	Al199738	Hs.208275	ESTs, Weakly similar to unnamed protein produ	3.4
	447688	N87079	Hs.19236	NADH dehydrogenase (ubiquinone) 1 beta subcom	3.4
	424856	AA347746	Hs.9521	ESTs, Weakly similar to KIAA1015 protein [H.s	3.4
40					3.4
40	407864	AF069291	Hs.40539	chromosome 8 open reading frame 1	3.4
	404108			0	
	403729			0	3.4
	404232			0	3.4
	423687	AA329633	Hs.133011	ESTs, Highly similar to Z117_HUMAN ZINC FINGE	3.4
45	428372	AK000684	Hs.183887	hypothetical protein FLJ22104	3.4
	439741	BE379646	Hs.6904	Homo sapiens mRNA full length insert cDNA clo	3.4
	441447	AA934077	Hs.126980	ESTs	3.4
	448358	R44433	Hs.106614	Human DNA sequence from done RP4-534K7 on ch	3.4
	450926	AI744361	Hs.205591	ESTs, Weakly similar to zinc finger protein P	3.4
50	458477	NM_000314	Hs.10712	phosphatase and tensin homolog (mutated in mu	3.4
50					3.4
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cys-X-C	
	452822	X85689	Hs.288617	Homo sapiens cDNA: FLJ22621 fis, clone HSI056	3.4
	441111	AI806867	Hs.126594	ESTs	3.4
	447519	U46258	Hs.23448	ESTs	. 3.4
55	446913	AA430650	Hs.16529	transmembrane 4 superfamily member (tetraspan	3.4
	449581	Al989517	Hs.181605	ESTs	3.4
	456132	BE219771	Hs.237146	Homo sapiens cDNA FLJ14234 fis, clone NT2RP40	3.4
	448186	AA262105	Hs.4094	Homo sapiens cDNA FLJ14208 fis, clone NT2RP30	3.4
	422611	AA158177	Hs.118722	fucosyltransferase 8 (alpha (1,6) fucosyltran	3.4
60	441433	AA933809	Hs.42746	ESTs	3.4
-55				transforming growth factor, beta 1	3.4
	417837	AL079905	Hs.1103	NIF3 (Ngg1 interacting factor 3, S.pombe homo	3.4
	450516	AA902656	Hs.21943		
	407796	AA195509	Hs.272239	lymphocyte activation-associated protein	3.3
65	419200	AW966405	Hs.288856	prefoldin 5	3.3
65	423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (from c	3.3
	445679	A1343868	Hs.58800	Homo sapiens cDNA FLJ12488 fis, clone NT2RM20	3.3
	435014	BE560898	Hs.10026 ·	ribosomal protein L17 isolog	3.3
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin, bone	3.3
	439170	AA332365	Hs.165539	ESTs	3.3
70	429830	AI537278	Hs.225841	DKFZP434D193 protein	3.3
. •	428943	AW086180	Hs.37636	ESTs, Weakly similar to KIAA1392 protein [H.s	3.3
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	3.3
				vaccinia related kinase 1	3.3
	408805	H69912	Hs.48269		3.3
75	441134	W29092	Hs.7678	cellular retinoic acid-binding protein 1	
75	408532	A)453137	Hs.63176	ESTs	3.3
	409517	X90780	Hs.54668	troponin 1, cardiac	3.3
	414304	AI621276	Hs.165998	DKFZP564M2423 protein	3.3
	436427	Al344378	Hs.143399	ESTs	3.3
	436662	AI582393	Hs.126695	ESTs	3.3
80	440304	BE159984	Hs.125395	ESTs	3.3
	447385	F12863	, ~	gb:HSC3FE081 normalized infant brain cDNA Hom	3.3
			Lie 12024		3.3
	451177	A1969716	Hs.13034	ESTS	3.3
	428949	AA442153	Hs.104744	ESTs, Weakly similar to AF208855 1 BM-013 [H.	
	451743	AW074266	Hs.23071	, ESTs	3.3

	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, long f	3.3
	446351	AW444551	Hs.258532	ESTS .	3.3
	435102	AW899053	Hs.76917	F-box only protein 8	3.3
5	418216	AA662240	Hs.283099	AF15q14 protein	3.3
)	401508	*******	11- 00004	University of the Ft 192442 September 1101000	3.3 3.3
	437108 416530	AA434054 U62801	Hs.80624	Homo sapiens cDNA: FLJ23442 fis, clone HSI009	3.3
	443171	BE281128	Hs.79361 Hs.9030	kalīikrein 6 (neurosin, zyme) TONDU	3.3
	458627	AW088642	Hs.97984	ESTs; Weakly similar to WASP-family protein	3.3
10	412078	X69699	Hs.73149	paired box gene 8	3.3
10	414080	AA135257	Hs.47783	ESTs, Weakly similar to T12540 hypothetical p	3.3
	401197	74100201	113.47705	0	3.3
	422134	AW179019	Hs.112110	ESTs	3.3
	409044	Al129586	Hs.33033	ESTs	3.3
15	416198	H27332	Hs.99598	ESTs	3.2
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-conjugat	3.2
	436525	AA721428	Hs.26145	Homo sapiens cDNA FLJ14127 fis, clone MAMMA10	3.2
	409142	AL136877	Hs.50758	chromosome-associated polypeptide C	3.2
	428819	AL135623	Hs.193914	KIAA0575 gene product	3.2
20	428728	NM_016625	Hs.191381	ESTs; Weakly similar to hypothetical protein	3.2
	421261	AA500853	Hs.98133	ESTs	3.2
	446219	A1287344	Hs.149827	ESTs	3.2
	457574	H88717	Hs.27774	ESTs, Highly similar to AF161349 1 HSPC086 [H	3.2
~ ~	409172	Z99399	Hs.118145	ESTs	3.2
25	419388	T67012	Hs.75323	prohibitin	3.2
	434187	AA627098	Hs.99103	ESTs, Weakly similar to I38428 T-complex prot	3.2
	445060	AA830811	Hs.88808	ESTs	3.2
	448254	A1829900	Hs.22929	ESŢs .	3.2
20	452943	BE247449	Hs.31082	hypothetical protein FLJ 10525	3.2
30	411393	AW797437	Hs.69771	B-factor, properdin	3.2
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37kD)	3.2
	408418	AW963897	Hs.44743	KIAA1435 protein	3.2
	442025	AW887434	Hs.11810	ESTs, Weakly similar to CD4.2 [C.elegans]	3.2
35	417006	AW673606	Hs.80758	aspartyl-tRNA synthetase	3.2
33	407881	AW072003	Hs.40958	heparan sulfate (glucosamine) 3-O-sulfotransf	3.2
	444755	AA431791	Hs.183001	ESTs	3.2
	402829	AE454070	Hs.26706	0	3.2 3.2
	451593	AF151879		CGI-121 protein	
40	419926 434551	AW900992	Hs.93796	DKFZP586D2223 protein ESTs, Highly similar to XPB_HUMAN DNA-REPAIR	3.2 3.2
70	445929	BE387162 Al089660	Hs.280858 Hs.7838	makorin, ring finger protein, 1	3.2
	409365	AA702376	Hs.226440	Homo sapiens clone 24881 mRNA sequence	3.2
	418836	A1655499	Hs.161712	ESTs	3.2
	441020	W79283	Hs.35962	ESTs	3.1
45	422363		Hs.115474	replication factor C (activator 1) 3 (38kD)	3.1
	413010	AA393273	Hs.75133	transcription factor 6-like 1 (mitochondrial	3.1
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	3.1
	410486	AW235094	Hs.193424	ESTs, Weakly similar to KIAA1064 protein [H.s	3.1
	434540	NM_016045	Hs.5184	TH1 drosophila homolog	3.1
50	409178	BE393948	Hs.50915	kallikrein 5	3.1
	439480	AL038511	Hs.125316	ESTs	3.1
	417848	AA206581	Hs.39457	ESTs	3.1
	446293	Al420213	Hs.149722	ESTs	3.1
	408108	AI580492	Hs.42743	hypothetical protein	3.1
55	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer, nonpo	3.1
	410519	AW612264	Hs.131705	ESTs	3.1
	421987	A1133161	Hs.286131	CGI-101 protein	3.1
	440046	AW402306	Hs.6877	hypothetical protein FLJ 10483	3.1
60	453931	AL121278	Hs.25144	ESTs	3.1
UU	454423	AW603985	Hs.179662	nucleosome assembly protein 1-like 1	3.1
	459089 419725	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp56401763 (from c	3.1 3.1
	418735	N48769	Hs.44609	ESTs .	
	414245 410909	BE148072 AW898161	Hs.75850 Hs.53112	WAS protein family, member 1 ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	3.1 3.1
65	434926	BE543269	Hs.50252	Homo sapiens HSPC283 mRNA, partial cds	3.1
05	409239	AA740875	Hs.44307	ESTs .	3.1
	429017	AA463605	Hs.238995	ESTS	3.1
	447072	D61594	Hs.17279	tyrosylprolein sulfotransferase 1	3.1
	426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteogenic prot	3.1
70	448133	AA723157	Hs.73769	folate receptor 1 (adult)	3.1
. •	418792	AB037805	Hs.88442	KIAA1384 protein	3.1
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S. cere	3.1
	402077			0	3.1
	440671	AW297920	Hs.130054	ESTs	3.1
75	419890	X17360	Hs.278255	homeo box D4	3.1
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	3.1
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. cerevi	3.1
	431221	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B; yeast)	3.1
00	443584	A1807036	Hs.101619	ESTs	3.1
80	445525	BE149866	Hs.14831	ESTs	3.1
	410441	BE298210		gb:601118016F1 NIH_MGC_17 Homo sapiens cDNA c	3.1
	422634	NM_016010	Hs.118821	CGI-62 protein	3.0
	420022	AA256253	Hs.120817	ESTs	3.0
	453912	AL121031	Hs.32556	KIAA0379 protein	3.0

PCT/US02/19297 WO 02/102235

CDP-diacylglycerol synthase (phosphatidate cy

456844

AI264155

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Hs.152981
          414941
                     C14865
                                   Hs.182159
                                                                                                              3.0
3.0
3.0
          407807
                     AL031427
                                                  Human DNA sequence from clone 167A19 on chrom
                                   Hs.40094
          414725
                     AA769791
                                    Hs.120355
                                                  Homo sapiens cDNA FLJ13148 fis, clone NT2RP30
  5
          444420
                     A1148157
                                    Hs.146766
                                                  FSTs
                                                                                                               3.0
          431742
                     NM 016652
                                                  CGI-201 protein
                                   Hs.268281
          412519
                     AA196241
                                   Hs.73980
                                                  troponin T1, skeletal, slow
                                                                                                               3.0
                                                                                                              3.0
3,0
3.0
          418348
                     AI537167
                                    Hs.96322
                                                  Homo sapiens cDNA: FLJ23560 fis, clone LNG098
          444261
                     AA298958
                                    Hs.10724
                                                  MDS023 protein
10
          457465
                     AW301344
                                   Hs.195969
                                                  FSTs
                                                                                                               3.0
                                                  Homo sapiens two pore potassium channel KT3.3
          443933
                     AI091631
                                   Hs.135501
                                                                                                               3.0
                     AI368158
                                   Hs.128864
                                                  ESTs
          442150
                                                                                                               3.0
          414883
                     AA926960
                                   Hs.77550
                                                  CDC28 protein kinase 1
          442879
                     AF032922
                                    Hs.8813
                                                  syntaxin binding protein 3
                                                                                                               3.0
15
          437949
                     U78519
                                    Hs.41654
                                                  ESTs
                                                                                                              3.0
          403515
                                                                                                               3.0
          403864
                                                                                                               3.0
                     AW207285
                                   Hs.98279
                                                  ESTs
          407785
                                                                                                               3.0
          426199
                     AA371865
                                   Hs.97090
                                                  ESTs
20
          426324
                     AW291787
                                    Hs.200933
                                                                                                               3.0
                                                  peroxisomal membrane protein 3 (35kD, Zellweg vacuolar protein sorting 41 (yeast homolog)
          427738
                     NM_000318
                                   Hs.180612
                                                                                                               3.0
                                                                                                               3.0
          427R37
                     1187309
                                    Hs 180941
                                                                                                               3.0
                     AF124250
                                                  breast cancer anti-estrogen resistance 3
          439430
                                    Hs.6564
          442039
                     AW276240
                                    Hs.128352
                                                  ESTs, Weakly similar to p80 [R.norvegicus]
                                                                                                               3.0
25
                                                   down-regulator of transcription 1, TBP-bindin
                                                                                                              3.0
3.0
          446978
                     NM_001938
                                    Hs.16697
                                                  toll-like receptor 3
          452431
                     U88879
                                    Hs.29499
                     T17431
                                                  DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide
                                                                                                               3.0
                                    Hs.65412
          452841
                                    Hs.225597
                                                                                                               3.0
          432114
                     AL036021
                                                  ESTs
                                    Hs.31704
                                                  ESTs, Weakly similar to KIAA0227 [H.sapiens]
                                                                                                               3.0
          445640
                     AW969626
30
          442607
                     AA507576
                                    Hs.288361
                                                  KIAA0741 gene product
                                                                                                               3.0
                                                  I factor (complement)
          453920
                     AI133148
                                    Hs.36602
                                                                                                               3.0
                                                                                                               3.0
          430000
                     AW205931
                                   Hs.99598
                                                  ESTs
                                                                                                               3.0
                     A1688663
                                   Hs.116586
          429164
                                                  ESTs
                     AI240665
                                   Hs.8895
                                                  ESTs
          453331
35
                                                  H.sapiens gene from PAC 426l6, similar to syn
                     BE614599
                                   Hs.106823
                                                                                                               3.0
          448663
          425776
                     U25128
                                    Hs.159499
                                                  parathyroid hormone receptor 2
                                                                                                               3.0
          401714
                                                                                                               3.0
                                                                                                               3.0
          400903
          428428
                     AL037544
                                   Hs.184298
                                                  cyclin-dependent kinase 7 (homolog of Xenopus
                                                                                                               3.0
40
                     AJ525743
                                    Hs.160603
                                                                                                               3.0
          443761
                                                  ESTs
          451640
                     AA195601
                                    Hs.26771
                                                  Human DNA sequence from clone 747H23 on chrom
                                                                                                               3.0
          442580
                     A1733682
                                   Hs.130239
                                                  FSTs
                                                                                                               3.0
          TABLE 10B
45
          Pkey: Unique Eos probeset identifier number
          CAT number: Gene cluster number
          Accession: Genbank accession numbers
                      CAT Number
          Pkey
50
          407596
                      1003489_1
                                         R86913 R86901 H25352 R01370 H43764 AW044451 W21298
          409763
                      115392_1
                                         AL043212 AA077575 AA077655 R19502 BE545457 Al638421 R14093
           410360
                      1197225_-2
                                         BE298210 AIG72315 AW086489 BE298417 AA455921 AA902537 BE327124 R14963 AA085210 AW274273 AI333584 AI369742 AI039658 AI885095 AI476470 AI287650 AI885299 AI985381 AW592624 AW340136 AI266556 AA456390 AI310815 AA484951
          410441
                      120358_1
55
          411560
                      1249443_1
                                         AW851186 AW996967 BE143456
           414315
                      143512_1
                                         Z24878 AA494098 F13654 AA494040 AA143127
           418417
                      1750818_1
                                         R77182 R77197 R80484
                                         AA315308 AA223392 BE538098 BE087173
           418454
                      175699_1
                                         AJ830417 AA236612
          419346
                      184129 1
60
           424770
                      243504_1
                                         AA425562 Al880208 AA346646 N22655 AW811775 AW811786
                                         AW959075 W06838 AA417863
           427943
                      284802_1
           431965
                      33959_2
                                         BE175190 BE003348
           436812
                      427323_1
                                         AW298057 AA731645 AA810101 AW194180 AI690573 AW978773
                                         AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598
           437938
                      44573 2
65
                                         AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444
                                         N92578 F13493 AA927794 Al560251 AW874068 AL 134043 AW235363 AA663345 AW008282 AA488954 AA283144 Al890387 Al950344
                                         AT741346 A1689062 AA282915 AW102898 A1872193 A1763273 AW173586 AW150329 A1653832 A1762688 AA988777 AA488892 A1356394
AW103813 A1539642 AA642789 AA856975 AW505512 A1961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209
AW856538 AA180009 AA337499 AW961101 AA251669 AA251874 A1819225 AW205862 A1683338 A1858509 AW276905 A1633006 AA972584
70
                                          AA908741 AW072629 AW513996 AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701
                                         AW613456 Al373032 Al564269 F00531 H83488 W37181 W78802 R66056 Al002839 R67840 AA300207 AW959581 T63226 F04005 .
                                          BE164500 AA832198 BE164502
           439255
                      470321_1
           447385
                      719912_1
                                         F12863 Al377223 T75099
                                         BE141183 AW178167 AW178162 AW178166 AW178172 AW845893 AW178159 AW178222 AW178213 AW178215 AW178090 AW178091
           454193
                      1050256_1
 75
                                          AW178161 AW178207 AW178210 AW178214 AW178212 BE140918 BE140917 AW178135 AW178205 AW178209 AW178223 AW178220
                                          AW178206 AW178203 AW178165 AW178168 AW178160 AW178136 AW845878 AW178131 AW178138 AW178105 AW845894 AW178129
                                          AW845810 AW84582B AW178216 AW178112 AW178211 AW178224 BE140915 AW178221 AW178130 AW178134 AW178196 AW178108
                                          AW178133 AW178164 AW178218 AW178171 AW178157 AW178158 AW178103 BE141189 AW178170 AW845816 BE141586 AW178156
                                          AW178104 AW178163 AW178093 AW178208 AW178137 AW178140 AW178219 BE141592 AW845901 BE141580 AW178155 BE141598
 80
                                          BE140957
AW807073 AW807055 AW807067 AW807276 AW807030 AW807363 AW845892 AW807091 AW807275 AW807284 AW807287 AW845891
           454556
                      1223878 1
                                          AW807195 AW807271
                                          BE141714 AW845993 AW845989
           454933
                      1245515_1
```

PCT/US02/19297 WO 02/102235

TABLE 10C:

5

Pkey: Unique number corresponding to an Eos probeset

Ref. Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402-489-495

Strand: Indicates DNA strand from which exons were predicted

Nt\_position: Indicates nucleotide positions of predicted exons

Nt\_position 278637-279292 17982-18115,20297-20456 Strand 400534 400666 6981826 8118496 Minus 10 Pius 59112-59228 400903 2911732 Plus 401197 9719705 Plus 176341-176452 166120-166347,166451-166557,169651-169832 110779-110983 29278-29770 401480 7321503 Plus 401508 7534110 Minus 15 401517 7677912 Plus 82655-83959 8576138 Plus 401644 401714 6715702 Plus 95484-96681 65014-65195 3261-3834,3939-4269 402077 B117414 Plus 402222 9958106 Plus 20 110326-110491 82274-82443 402408 9796239 Minus 402820 402829 6456853 Minus 8918414 101532-101852,102006-102263 Plus Minus 403381 9438267 26009-26178 403515 7656757 Minus 173358-179553 25 37662-37909-, 51753-51890,79290-79445 403729 7543752 Minus 7709019 8247074 403864 Minus 404108 63603-64942 Minus 404232 71800-71956 8218045 Minus 404552 404567 404599 404915 7243881 19854-20010 30 7249169 Minus 101320-101501 8705107 7341766 110443-110733 100915-101087 Ptus Minus 404996 6007890 Plus 37999-38145,38652-38998,39727-39872,40557-40674,42351-42450

138877-139066

68880-69374 54304-54584

Table 11A lists about 222 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were 40 selected as for Table 10A, except that the ratio was greater than or equal to 2.0, and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. ig, fn3, egf, 7tm domains, signal sequences, transmembrane domains). Predicted protein domains are noted.

TABLE 11A: ABOUT 222 UP-REGULATED GENES ENCODING EXTRACELLULAR/CELL SURFACE PROTEINS, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES Pkey: Primekey

> ratio 30.0 25.2 22.7 19.0 17.4 15.1 14.1 13.8 13.6 11.0 10.8

8.9 8.8 8.5 8.4 8.1 7.9 7.8 7.4 7.2 7.1 7.0 6.8 6.6 6.4 5.8 5.7

5.5 5.4

45 Ex. Accn: Exemplar Accession

405095

406069

406117

35

8072599

9117732

9142932

Plus

Plus

Ptus

UG ID: UniGene ID

Title: UniGene title

PFAM domains: predicted protein structural domains

ratio: ratio tumor vs normal tissue 50

Dυ						
	Pkey	Ex. Accn	UGID	Title	PFAM domains	
	400292	AA250737	Hs.72472	BMPR-lb; bone morphogenetic pro	pkinase, Activin_recp	
	400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Strom	SS,hemopexin,Peptidas	
	427585	D31152	Hs.179729	collagen; type X; alpha 1 (Schmid m	C1g,Collagen	
55	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular m	tsp_1	
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	TM	
	443646	AI085198	Hs.298699	ESTs	TSPN,vwc,tsp_1,EGF	
	436209	AW850417	Hs.254020	ESTs, Moderately similar to unname	TM	
	418601	AA279490	Hs.86368	calmegin	SS.catreticutin	
60	428532	AF157326	Hs.184786	TBP-interacting protein	TM	
	427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) rec	TM,neur_chan	
	432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamin	TM,Glycos_transf_2,Ri	
	404567	NM_015902	Hs.278428	progestin induced protein (DD5)	TM.HECT.zl-UBR1	
	445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	SS.MAM.EGF	
65	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	TM,MSP_domain	
	407001	U12471	Hs.247954	Human thrombospondin-1 gene, par	TSPN,vwc,tsp_1,EGF	
	453370	AJ470523	Hs.182356	ESTs, Moderately similar to translat	ABC_tran,ABC_membr	
	400298	AA032279	Hs.61635	STEAP1	TM	
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	SS,Cys_knot	
70	429609	AF002246	Hs.210863	cell adhesion molecule with homolo	TM.fn3.lg	
	412170	D16532 .	Hs.73729	very low density lipoprotein recepto	TM.ldl recept_a.ldl_rec	
	428954	AF100781	Hs.194678	WNT1 inducible signaling pathway	SS,IGFBP,Cys_knot,tsp	
	418007	M13509	Hs.83169	Matrix metalloprotease 1 (interstitia	SS,hemopexin,Peptidas	
	424001	W67883	Hs.137476	KIAA1051 protein	Pep_M12B_propep,Rep	
75	456965	AW131888	Hs.172792	ESTs, Weakly similar to hypothetica	TM	
	446142	AI754693	Hs.145968	ESTs	Cadherin_C_term.cadhe	
	415138	C18356	Hs.78045	tissue factor pathway Inhibitor 2 TFP	Kunitz BPTI, G-gamma	
	438167	R28363	Hs.24286	ESTs	7tm 1	
	452097	AB002364	Hs.27916	ADAM-TS3; a disintegrin-like and	Pep_M128_propep,Rep	
80	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose in	SS	
	425371	D49441	Hs.155981	mesolhelin	SS	
	407945	X69208	Hs.606	ATPase, Cu++ transporting, alpha p	TMLE1-E2_ATPase.Hy	
	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic; stratum c	SS, trypsin	
	420362	U79734	Hs.97206	huntingtin interacting protein 1	TM,ENTH,I_LWEQ	
		V. U. UT		, manager and according process.		•

	413384	NM_000401	Hs.75334	exostoses (multiple) 2	TM	5.3
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	Collagen, TSPN	5.2
	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral	TGF-bela,TGFb_propep	5.1
5	415539	AI733881	Hs.72472	BMPR-lb; bone morphogenetic pro	pkinase,Activin_recp	5.1 4.9
5	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	TM Activia consultings	4.8
	424539 450375	L02911 AA009647	Hs.150402	activin A receptor, type I a disintegrin and metalloproteinase d	Activin_recp,pkinase disintegrin,Reprolysin,P	4.7
	450575 451684		Hs.8850	CDA14	TM	4.6
	400296	AF216751	Hs.26813	ATP-binding cassette; sub-family C	TM_ABC_tran_ABC_m	4.6
10	429597	AA305627 NM_003816	Hs.139336 Hs.2442	a disintegrin and metalloproteinase d	TM	4.5
10	400534	AP000541	ris.2442	predicted exons	TM, KRAB, zf-C2H2	4.5
	425506	NM_003666	Hs.158205	basic leucine zipper nuclear factor 1	TM,Folate_carrier	4.5
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high aff	TM,SDF	4.4
	449535	W15267	Hs.23672	low density lipoprotein receptor-rela	SS,ldi_recept_b,ldi_rece	4.4
15	452028	AK001859	Hs.27595	hypothetical protein FLJ10997	Zn_carbOpept,Propep_M	4.3
15	418693	AI750878	Hs.87409	thrombospondin 1	EGF,TSPN,tsp_1,tsp_3,	4.3
	410361	BE391804	Hs.62661	guanylate binding protein 1, interfer	TMGBP	4.2
	407872	AB039723	Hs.40735	frizzled (Drosophila) homolog 3	Frizzled,Fz,7tm_2	4.2
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium pho	TM,Na_Pi_cotrans	4.2
20	412494	AL133900	Hs.792	ADP-ribosylation factor domain pro	arf,zf-B_box,zf-C3HC4	4.0
	405095	NM_014479	Hs.145296	disintegrin protease	Reprolysin, disintegrin	4.0
	431130	NM_006103	Hs.2719	epididymls-specific; whey-acidic pro	SS,wap	4.0
	407792	AI077715	Hs.39384	putative secreted ligand homologous	SS	4.0
	408829	NM_006042	Hs.48384	heparan suffate (glucosamine) 3-0-s	TM	3.8
25	450581	AF081513	Hs.25195	endometrial bleeding associated fact	SS,TGF-beta,TGFb_pro	3.7
	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3,	TM,Sterol_desat	3.7
	450447	AF212223	Hs.25010	hypothetical protein P15-2	TM,ANF_receptor,guan	3.6
	414706	AW340125	Hs.76989	KIAA0097 gene product	TM	3.6
	417389	BE260964	Hs.82045	Midkine (neurite growth-promoting	TM,PTN_MK	3.6
30	400666	X07820	Hs.2258	Matrix Metalloproteinase 10 (Strom	SS,hemopexin,Peptidas	3.5
	406400	AA343629	Hs.104570	kallikrein 8 (neuropsin/ovasin)	SS,trypsin	3.4
	407864	AF069291	Hs.40539	chromosome 8 open reading frame 1	TM,FHA,BRCT	3.4
	452822	X85689	Hs.288617	Homo sapiens cDNA: FLJ22621 fis.	EGF,fn3,pkinase	3.4
	446913	AA430650	Hs.16529	transmembrane 4 superfamily memb	TM,transmembrane4	3.4
35	422611	AA158177	Hs.118722	fucosyltransferase 8 (alpha (1,6) fuc	SS	3.4
	423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZ	cadherin,Cadherin_C_te	3.3
	435102	AW899053	Hs.76917	F-box only protein 8	TM,Sec7	3.3
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	SS,TM,trypsin	3.3
40	401197	•		predicted exons	arf,Ets	3.3
40	436525	AA721428	Hs.26145	Homo sapiens cDNA FLJ14127 fis,	TM	3.2
	452943	BE247449	Hs.31082	hypothetical protein FLI10525	TM	3.2
	411393	AW797437	Hs.69771	B-factor, properdin	SS,sushi,trypsin,vwa,fib	3.2
	407881	AW072003	Hs.4096B	heparan sulfate (glucosamine) 3-0-s	SS	3.2
15	418835	A1655499	Hs.161712	ESTs	pkinase,Activin_recp	3.2
45	409178	BE393948	Hs.50915	kallikrein 5	SS,trypsin	3.1
	421987	AI133161	Hs.286131	CGI-101 protein	TM	3.1
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	SS	3.1
	426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteo	SS,TGFb_propeptide,T	3.1
50	448133	AA723157	Hs.73769	folate receptor 1 (adult)	TM	3.1
50	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprot	SS.Peptidase_M10,hem	3.1
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosp	TM, Cytidylyltrans	3.0
	414725	AA769791	Hs.120355	Homo sapiens cDNA FLJ13148 fis,	SPRY,7tm_1	3.0
	407785	AW207285	Hs.98279	ESTs	Sema,ig	3.0
55	427738	NM_000318	Hs.180612	peroxisomal membrane protein 3 (35	TM,zf-C3HC4	3.0
22	452431	U88879	Hs.29499	toll-like receptor 3	TM,TIR,LRRCT	3.0 3.0
	453920	AI133148	Hs.36602	I factor (complement)	ldl_recept_a,trypsin,SRC	3.0
	453331	Al240665	Hs.8895	ESTs	disintegrin,Reprolysin,P	3.0
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	TM,7tm_2	3.0
60	428428	AL037544	Hs.184298	cyclin-dependent kinase 7 (homolog	TM,pkinase TM,LRRCT,LRRNT,LR	2.9
UU	407910	AA650274	Hs.41296	fibronectin leucine rich transmembra diubiquitin	TM,ubiquilin,7tm_3,AN	29
	408380	AF123050	Hs.44532	a disintegrin and metalloproteinase d	disintegrin, Reprolysin	29
	407783 420757	AW995872	Hs.172028	androgen receptor (dihydrotestostero	TM_Androgen_recep,ho	2.9
		X78592	Hs.99915	wingless-type MMTV integration sit	cadherin,Cadherin_C_te	2.9
65	424406 428549	D54120 AA430064	Hs.146409 Hs.220929	ESTs, Moderately similar to ARF-fa	at	29
05	419452		Hs.90572	PTK7 protein tyrosine kinase 7	TM,pkinase,lg	29
	452281	U33635 T93500	Hs.28792	ESTs	TGFb_propeptide,TGF-	29
	420440	NM_002407	Hs.97644	mammaglobin 2	SS.Uteroglobin	2.9
	418848	AI820961	Hs.193465	ESTs	pkinase,Activin_recp	2.9
70	421991	NM_014918	Hs.110488	KIAA0990 protein	SS	2.9
, 0	433190	M26901	Hs.3210	renin	SS,asp	2.9
	424538	NM_005095	Hs.150390	zinc finger protein 262	TM	2.8
	433002	AF048730	Hs.279906	cyclin T1	SS	2.8
	444342	NM_014398	Hs.10887	similar to lysosome-associated mem	TM,Lamp	2.8
75	430598	AK001764	Hs.247112	hypothetical protein FLJ 10902	TM	2.8
	428450	NM_014791	Hs.184339	KIAA0175 gene product	TM,pkinase,KA1	2.8
	450171	AL133661	Hs.24583	hypothetical protein DKFZp434C03	TM	2.8
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate tran	TM,GATase_2,SIS	2.8
	430016	NM_004736	Hs.227656	xenotropic and polytropic retrovirus	TM	2.8
80	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	Collagen, COLFI, TSPN	2.8
	424894	H83520	Hs.153678	reproduction 8	SS,UBX	2.8
	430651	AA961694	Hs.105187	kinesin protein 9 gene	SS	2.7
	414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-	TM	2.7
	448595	AB014544	Hs.21572	. KIAA0644 gene product	TM,LRRCT,LRR	2.7
				-	177	
					111	

	452835	AK001269	Hs.30738	ESTs	TM	2.7
	403019	AAB34626	Hs.66718	RAD54 (S.cerevisiae)-like	SS.Anti proliferat	2.7
	420281	A1623693	Hs.191533	ESTs	Cation_efflux	2.7
_	434815	AF155582	Hs.46744	core1 UDP-galactose:N-acetylgalact	SS	2.6
5	432201	AI538613	Hs.135657	TMPRSS3a mRNA for serine protea	trefoil, trypsin	2.6
	430450	R23553	Hs.241489	hypothetical protein	SS	26
	448402	BE244226	Hs.21094	RAB18, member RAS ancogene fam	ras,arf	2.6
	421802	BE261458	Hs.108408	CGI-78 protein	TM TM 7km 4	2.6
10	452355	N54926	Hs.29202	G protein-coupled receptor 34 gb:EST22d11 WATM1 Homo saple	TM,7tm_1 ank,death,RHD,TIG	2.6 2.6
10	417742 451346	R64719 NM_006338	Hs.26312	glioma amplified on chromosome 1	TMJg,LRR,LRRNT,LR	2.6
	433147	AF091434	Hs.43080	platelet derived growth factor C	TM,PDGF,CUB	26
	420079	NM_014051	Hs.94896	PTD011 protein	SS,TM,	2.6
	419918	X80700	Hs.93728	pre-B-cell leukemia transcription fac	homeobox,ig,Acyltransf	2.5
15	432350	NM_005865	Hs.274407	protease, serine, 16 (thymus)	SS	2.5
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte gro	pkinase,Sema,Ptexin_re	2.5
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	SS,TIR,ig	2.5
	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	TM COCIA IN	2.5
20	433929	A1375499	Hs.27379	ESTs	EGF,ld_recept_a,ldl_re	2.5 2.5
20	443562 414386	AF118838 X00442	Hs.9599 Hs.75990	solute carrier family 25, member 13 haptoglobin	TM,mito_carr sushi,trypsin	2.5 2.5
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltr	AIRS,formyl_transf,GA	2.5
	449207	AL044222	Hs.23255	nucleoporin 155kD	TM	2.5
	416107	AA173846	Hs.79015	antigen identified by monoclonal ant	TMJg	2.4
25	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	TMPH	24
	414812	X72755	Hs.77367	monokine induced by gamma interfe	SS,IL8	2.4
	406137	R42764	Hs.3248	mutS (E. coli) homolog 6	TM,MutS_C,MutS_N,P	2.4
	450710	AW953381	Hs.18627	ESTs, Weakly similar to G01447 GP	TM.	24
20	430291	AV660345	Hs.238126	CGI-49 protein	TM.	24
30	425184	BE278288	Hs.155048	Lutheran blood group (Auberger b a	ig TM	2.4 2.4
	451418 412277	BE387790 BE277592	Hs.26369 Hs.73799	ESTs guanine nucleotide binding protein (	TM,G-alpha	24
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A	SS,IL8	24
	451806	NM_003729	Hs.27076	RNA 3-terminal phosphate cyclase	TMRCT	23
35	416224	NM_002902	Hs.79088	reticulocalbin 2, EF-hand calcium bi	SS,efhand	2.3
	452268	NM_003512	Hs.28777	H2A histone family, member L	histone, Calc_CGRP_IA4	2.3
	451668	Z43948	Hs.26789	ASPIC (acidic secreted protein in ca	SS,TM,	2.3
	400880	M84349	Hs.119663	CD59 antigen	SS,UPAR_LY6	2.3
40	421340	F07783	Hs.1369	decay accelerating factor for comple	SS,sushi	23
40	443986	AI381750	Hs.283437	HTGN29 protein	TM TM Outlands	2.3 2.3
	443037 440516	AW500305 S42303	Hs.8906 Hs.161	syntaxin 7	TM,Syntaxin HNH,cadherin,Cadherin	2.3
	404877	AI394145	Hs.18048	cadherin 2, type 1, N-cadherin (neur melanoma antigen MAGE-10	TM,MAGE	23
	440704	M69241	Hs.162	insulin-like growth factor binding pr	SS,thyroglobulin_1,IGF	2.3
45	437952	D63209	Hs.5944	solute carrier family 11 (proton-coup	TM	23
	418624	AI734080	Hs.104211	ESTs	Sema,lg	2.2
	410434	AF051152	Hs.63668	toll-like receptor 2	SS,TIR,LRRCT,LRR	2.2
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatina	SS,fn2,hemopexin,Pepti	2.2
50	431457	NM_012211	Hs.256297	integrin, alpha 11	TM,FG-GAP,vwa	2.2
50	407907	AI752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5	SS,Lysyl_hydro	2.2 2.2
	400898 400303	AF220030 AA242758	Hs.125300 Hs.79136	Homo sapiens tripartite motif protein Human breast cancer, estrogen regul	SPRY,7tm_1 SS,TM,	2.2
	411789	AF245505	Hs.72157	Homo saziens mRNA; cDNA DKFZ	ig,LRRCT	2.2
	414809	A1434699	Hs.77356	transferrin receptor (p90, CD71)	TM.PA.Ribosomal_S2	2.2
55	401131	NM_001651	Hs.298023	Homo sapiens aquaporin 5 (AQP5),	TM,MIP	2.2
	400277	Y00281	Hs.2280	Human mRNA for ribophorin I	TM	2.1
	409317	U20165	Hs.53250	bone morphogenetic protein recepto	TM,pkinase .	2.1
	409956	AW103364	Hs.727	H.saplens activin beta-A subunit (ex	TGF-beta,TGFb_propep	2.1
60	451253	H48299	Hs.26126	claudin 10	TM,PMP22_Claudin	2.1
OU	429638	Al916662	Hs.211577	Kinectin 1 (kinesin receptor)	TM .	21
	409267 418414	NM_012453 J04977	Hs.52515 Hs.84981	transducin (beta)-like 2 X-ray repair complementing defectiv	TM,WD40 SS	21 21
	449057	AB037784	Hs.22941	ESTs	TM	2.1
	417666	AI345001	Hs.82380	menage a trois 1 (CAK assembly fac	zf-C3HC4	2.1
65	428485	NM_002950	Hs.2280	ribophorin I	TM	2.1
	445798	NM_012421	Hs.13321	rearranged L-myc fusion sequence	TM,zf-C2H2	2.1
	430057	AW450303	Hs.2534	bone marphogenetic protein recepto	TM,Activin_recp,pkina	2.1
	425189	H16622		gb:ym26c07.r1 Soares infant brain 1	RasGEF,PH,fibrinogen_	21
70	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycopro	SS,Glyco_hydro_18	2.1
70	421343	BE246444	Hs.283685	hypothetical protein FLJ20396	. TM	21 21
	425627 426261	AF019612 AW242243	Hs.297007 Hs.168670	ESTs	TM,Peptidase_M50 E1-E2_ATPase,Cation_	21
	431638	NM_000916	Hs.2820	peroxisomal farnesylated protein oxytocin receptor	TM,7tm_1	21
	456546	AI690321	Hs.203845	ESTs, Weakly similar to TWIK-rela	TM	21
75	421685	AF189723	Hs.106778	calcium transport ATPase ATP2C1	TME1-E2_ATPase,Hy	21
	424099	AF071202	Hs.139336	ATP-binding cassette; sub-family C	TM,ABC_tran,ABC_m	21
	424800	AL035588	Hs.153203	MyoD family inhibitor	TM	21
	410007	AW950887	Hs.57813	zine ribbon domain containing, 1	TFIIS	2.1
00	436135	D85390	Hs.5057	carboxypeptidase D	SS,Zn_carbOpept	2.1
80	420633	NM_014581	Hs.99526	odorant-binding protein 2B	TM,lipocalin	2.1
	420162	BE378432	Hs.95577	cyclin-dependent kinase 4	pkinase,ank,ArfGap,PH	21
	426156 442711	BE244537 AF151073	Hs.167382 Hs.8645	natriuretic peptide receptor A/guany hypothetical protein	TM,ANF_receptor,guan TM	2.0 2.0
	411872	AW327356	Hs.90918	chromosome 11 open reading frame	TM	2.0
					178	

	427801	AW979155	Hs.234433	hypothetical protein PRO1068	TM_Aa_trans	2.0
	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	TM	2.0
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplas	TM,ER_lumen_recept,i	2.0 2.0
5	431846 404210	BE019924 U02478	Hs.271580 Hs.100469	Uroplakin 1B Hizman AF-6 mRNA	TM,transmembrane4 TM,RA,DIL,PDZ,FHA	20
•	435640	AF220053	Hs.54960	uncharacterized hematopoietic stem/	TM,SET,zf-CXXC,PHD	2.0
	447906	AL050062	Hs.19999	DKFZP566K023 protein	SS	2.0
	412666	AL080116	Hs.74420	origin recognition complex, subunit	TM	2.0 2.0
10	417181 423945	L10123 AA410943	·Hs.1071 Hs.72472	surfactant protein A binding protein BMPR-lb; bone morphogenetic pro	TM TM_pkinase,Activin_rec	20
10	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	SS,typsin	2.0
	448350	L14561	Hs.78546	Homo sapiens clone 24411 mRNA s	TM,E1-E2_ATPase,Hy	2.0
	401093	Al955244	Hs.121520	HYPOTHETICAL 16.4 kDa PROTE	TMLRRCT	2.0
15	415664 448165	NM_004939 NM_005591	Hs.78580 Hs.202379	DEAD/H (Asp-Gtu-Ala-Asp/His) bo melotic recombination (S. cerevisiae	DEAD,helicase_C,SPRY DNA_repair,Glyco_tran	20 20
13	416391	Al878927	Hs.79284	mesoderm specific transcript (mouse	TM,abhydrolase	20
	422926	NM_016102	Hs.121748	ring finger protein 16	SPRY,zf-C3HC4,zf-B_	2.0
	446849	AU076617	Hs.16251	cleavage and polyadenylation specif	TM	2.0
20	427617 411678	D42063 Al907114	Hs.179825 Hs.71465	RAN binding protein 2-like 1 squalene epoxidase	TM,Ran_BP1,zf-RanBP TM,Monooxygenase	2.0 2.0
20	432554	AJ479813	Hs.278411	NCK-associated protein 1	TM	2.0
	TABLE 11			1		
25		ique Eos probese ber: Gene cluste				
23		: Genbank acce		~*		
	Pkey	CAT Number	Accession	4000 D40 454		
30	417742 425189	1696282_1 247825_1		4680 R12451 17322 AA351959		
50	423109	24/023_1	110022 KI	17322 AA331535		
	TABLE 11	IC:		•		
	Pkey: Uni	ique number con	responding to a	an Eos probeset	on 1. m	to the subtraction of the Park
35				oers in this column are Genbank identifier ( , et al. (1999) <u>Nature</u> 402:489-495	G) numbers. "Dunnam I. et al." rete	rs to the publication entitled "The DNA sequence of
33				exons were predicted		
				ns of predicted exons		
	-		011	Ab fit		
40	Pkey 400534	Ref 6981826	Strand Minus	Nt_position 278637-279292		
	401197	9719705	Plus	176341-176452		
	Table 134	liete about 57 au	anae un maula	fermon of hereamon senses assess of hat	adult liceupe that are likely to porode	a cither enzymes or amteins amenable to modulation b
45	Table 12A small mol	lists about 57 gr ecules. These w	enes up-regula ere selected a:	ted in ovarian cancer compared to normal s for Table 10A, except that the ratio was o	adult lissues that are likely to encode reater than or equal to 2.0, and the p	e either enzymes or proteins amenable to modulation by predicted protein contained a structural domain that is
45	small mol	ecules. These w	ere selected a	s for Table 10A, except that the ratio was g	reater than or equal to 2.0, and the p	e either enzymes or proteins amenable to modulation by predicted protein contained a structural domain that is ters). Predicted protein domains are noted.
45	small moli indicative	ecules. These w of enzymatic fun	ere selected as ction or of bein	s for Table 10A, except that the ratio was g ig modulated by small molecules (e.g., pkir	reater than or equal to 2.0, and the p lase, peptidase, isomerase, transpor	oredicted protein contained a structural domain that is ters). Predicted protein domains are noted.
	small moli indicative TABLE 12	ecules. These w of enzymatic fun 2A: ABOUT 57 Ui	ere selected as ction or of bein	s for Table 10A, except that the ratio was g ig modulated by small molecules (e.g., pkir	reater than or equal to 2.0, and the p lase, peptidase, isomerase, transpor	predicted protein contained a structural domain that is
45 50	small mole indicative TABLE 12 Pkey: Pri	ecules. These w of enzymatic fun 2A: ABOUT 57 Ui	ere selected a ction or of bein P-REGULATE	s for Table 10A, except that the ratio was g ig modulated by small molecules (e.g., pkir	reater than or equal to 2.0, and the p lase, peptidase, isomerase, transpor	oredicted protein contained a structural domain that is ters). Predicted protein domains are noted.
	small mole indicative TABLE 12 Pkey: Pri Ex. Accn: UG ID: U	ecules. These w of enzymatic fun 2A: ABOUT 57 Ui mekey Exemptar Acces niGene ID	ere selected a ction or of bein P-REGULATE	s for Table 10A, except that the ratio was g ig modulated by small molecules (e.g., pkir	reater than or equal to 2.0, and the p lase, peptidase, isomerase, transpor	oredicted protein contained a structural domain that is ters). Predicted protein domains are noted.
	small mole indicative TABLE 12 Pkey: Pri Ex. Accn: UG ID: U Title: Uni	ecules. These woof enzymatic fun A: ABOUT 57 Ui mekey Exemplar Acces niGene ID Gene title	ere selected at ction or of bein P-REGULATEI ssion	s for Table 10A, except that the ratio was g g modulated by small molecules (e.g., pkir D GENES ENCODING EXTRACELLULAR	reater than or equal to 2.0, and the p lase, peptidase, isomerase, transpor	oredicted protein contained a structural domain that is ters). Predicted protein domains are noted.
50	small molindicative  TABLE 12  Pkey: Pri Ex. Accn: UG ID: U Title: Uni PFAM doi	ecules. These woof enzymatic fun  A: ABOUT 57 Un  A: ABOUT 57	ere selected at ction or of bein P-REGULATEI ssion I structural dom	s for Table 10A, except that the ratio was g g modulated by small molecules (e.g., pkir D GENES ENCODING EXTRACELLULAR	reater than or equal to 2.0, and the p lase, peptidase, isomerase, transpor	oredicted protein contained a structural domain that is ters). Predicted protein domains are noted.
	small molindicative  TABLE 12  Pkey: Pri Ex. Accn: UG ID: U Title: Uni PFAM doi	ecules. These woof enzymatic fun A: ABOUT 57 Ui mekey Exemplar Acces niGene ID Gene title	ere selected at ction or of bein P-REGULATEI ssion I structural dom at	s for Table 10A, except that the ratio was g g modulated by small molecules (e.g., pkir D GENES ENCODING EXTRACELLULAR	realer than or equal to 2.0, and the p ase, peptidase, isomerase, transpor CELL SURFACE PROTEINS, OVAI	predicted protein contained a structural domain that is ters). Predicted protein domains are noted. RIAN CANCER VERSUS NORMAL ADULT TISSUES
50	small molindicative  TABLE 12 Pkey: Pri Ex. Accn: UG ID: U Title: Uni PFAM do: ratio: ratio	ecules. These woof enzymatic fun A: ABOUT 57 Uitmekey Exemplar Access niGene till Gene title mains: predicted to turnor vs. norm Ex. Accn	ere selected at ction or of bein P-REGULATEI ssion I structural dom at UGID	s for Table 10A, except that the ratio was g g modulated by small molecules (e.g., pkir D GENES ENCODING EXTRACELLULAR nains	reater than or equal to 2.0, and the p ase, peptidase, isomerase, transpor ICELL SURFACE PROTEINS, OVAI PFAM domains	predicted protein contained a structural domain that is ters). Predicted protein domains are noted.  RIAN CANCER VERSUS NORMAL ADULT TISSUES  ratio
50	small molindicative  TABLE 12 Pkey: Pri Ex. Accn: UG ID: U Title: Uni PFAM dor ratio: ratio  Pkey 400292	ecules. These wo of enzymatic fun 2A: ABOUT 57 Ui mekey Exemplar Access niGene ID Gene fite mains: predicted to turnor vs. norm Ex. Accn AA250737	ere selected at ction or of bein P-REGULATED ssion I structural dom at UG ID Hs.72472	s for Table 10A, except that the ratio was g g modulated by small molecules (e.g., pkir D GENES ENCODING EXTRACELLULAR nains  Title BMPR-lb; bone morphogenetic pro	reater than or equal to 2.0, and the p ase, peptidase, isomerase, transpor CELL SURFACE PROTEINS, OVAI PFAM domains pkinase, Activin_recp	predicted protein contained a structural domain that is ters). Predicted protein domains are noted.  RIAN CANCER VERSUS NORMAL ADULT TISSUES  ratio 30.0
50 55	small molindicative  TABLE 12 Pkey: Pri Ex. Accn: UG ID: U Title: Uni PFAM dor ratio: ratio Pkey 400292 400289	ecules. These woof enzymatic fun A: ABOUT 57 Uimekey Exemplar Access niGene till Gene title mains: predicted to turnor vs. norm Ex. Accn	ere selected at ction or of bein P-REGULATEI ssion  I structural domat  UG ID Hs.72472 Hs.2258	s for Table 10A, except that the ratio was g g modulated by small molecules (e.g., pkir D GENES ENCODING EXTRACELLULAR nains  Title BMPR-lb; bone morphogenetic pro Matrix Metalloproteinase 10 (Strom	reater than or equal to 2.0, and the passe, peptidase, isomerase, transport/CELL SURFACE PROTEINS, OVAF  PFAM domains pkinase, Activin_recp SS, Peptidase_M10	redicted protein contained a structural domain that is ters). Predicted protein domains are noted.  RIAN CANCER VERSUS NORMAL ADULT TISSUES  ratio 30.0 25.2
50	small molindicative  TABLE 12 Pkey: Pri Ex. Accn: UG ID: U Title: Uni PFAM dor ratio: ratio  Pkey 400292	ecules. These wo of enzymatic fun Az: ABOUT 57 Un mekey Exemptar Acces niGene ID Gene fitte mains: predicted to turnor vs. norm Ex. Accı AA250737 X07820	ere selected at ction or of bein P-REGULATED ssion I structural dom at UG ID Hs.72472	s for Table 10A, except that the ratio was g g modulated by small molecules (e.g., pkir D GENES ENCODING EXTRACELLULAR nains  Title BMPR-lb; bone morphogenetic pro Matrix Metalloproteinase 10 (Strom	reater than or equal to 2.0, and the p ase, peptidase, isomerase, transpor CELL SURFACE PROTEINS, OVAI PFAM domains pkinase, Activin_recp	redicted protein contained a structural domain that is ters). Predicted protein domains are noted.  RIAN CANCER VERSUS NORMAL ADULT TISSUES  ratio 30.0 25.2 18.7 16.2
50 55	small moli indicative  TABLE 12 Pkey: Prii Ex. Accn: UG für. UT itile: Uni PFAM doi ratio: ratio  Pkey 400292 400289 426427 424905 433159	ecules. These wo of enzymatic fun A: ABOUT 57 Ui mekey Exemplar Access nicene ID Gene file mains: predicted to turnor vs. norm Ex. Accn AA250737 X07820 M86699 NM_002497 AB035898	ere selected at ction or of bein P-REGULATEI siston  I structural domat  UG ID Hs.72472 Hs.2258 Hs.169840 Hs.153704 Hs.150587	s for Table 10A, except that the ratio was g g modulated by small molecules (e.g., pkir D GENES ENCODING EXTRACELLULAR hains  Title  BMPR-lb; bone morphogenetic pro Matrix Metalloproteinase 10 (Strom TTK protein kinase  NIMA (never in mitusis gene a)-rela kinesin-like protein 2	reater than or equal to 2.0, and the plase, peptidase, isomerase, transport CELL SURFACE PROTEINS, OVAF PFAM domains pkinase, Activin_recp SS, Peptidase_M10 pkinase pkinase kinesin	redicted protein contained a structural domain that is ters). Predicted protein domains are noted.  RIAN CANCER VERSUS NORMAL ADULT TISSUES  ratio 30.0 25.2 18.7 16.2 11.5
50 55	small mole indicative TABLE 12 Pkey: Pri Ex. Acci: UG ID: U Title: Uni PFAM do ratio: ratii Pkey 400292 400293 426427 424905 433159 453370	ecules. These wo of enzymatic fun Az: ABOUT 57 Uimekey Exemplar Access niGene fite mains: predicted to turnor vs. norm Ex. Acci AA250737 X07820 M86699 NM_002497 AB035898 AI470523	ere selected action or of bein P-REGULATEI ssion I structural dom at UG ID Hs.72472 Hs.2258 Hs.169840 Hs.153704 Hs.150587 Hs.182356	s for Table 10A, except that the ratio was g g modulated by small molecules (e.g., pkir D GENES ENCODING EXTRACELLULAR nains  Title  BMPR-lb; bone morphogenetic pro Matrix Metalloproteinase 10 (Strom TTK protein kinase NIMA (never in mitosis gene a)-rela kinesin-like protein 2  ESTs, Moderately similar to translat	reater than or equal to 2.0, and the passe, peptidase, isomerase, transport/CELL SURFACE PROTEINS, OVAF  PFAM domains pkinase, Activin_recp SS, Peptidase_M10 pkinase pkinase kinase kinase kinase kinase kinase kinase kinase	redicted protein contained a structural domain that is ters). Predicted protein domains are noted.  RIAN CANCER VERSUS NORMAL ADULT TISSUES  ratio 30.0 25.2 18.7 16.2 11.5 8.4
50 55 60	small moli indicative  TABLE 12 Pkey: Pri Ex. Accn: UG 10: UT ille: Uni PFAM doi ratio: ratio: ratio: Pkey 400292 400289 426427 424905 433159 453370 418007	ecules. These wo of enzymatic fun Az: ABOUT 57 Ui- mekey Exemplar Access niGene 10 Gene 6tite mains: predicted to turnor vs. norm Ex. Accn AA250737 X07820 M86699 NM_002497 AB035898 AI470523 M13509	ere selected at ction or of bein P-REGULATEI ssion  I structural domata  UG ID HS.72472 HS.2258 HS.153704 HS.153704 HS.150587 HS.182356 HS.83169	s for Table 10A, except that the ratio was g g modulated by small molecules (e.g., pkir D GENES ENCODING EXTRACELLULAR nains  Title BMPR-lb; bone morphogenetic pro Matrix Metalloproteinase 10 (Strom TTK protein kinase NIMA (never in mitosis gene a)-rela kinesin-like protein 2 ESTs, Moderately similar to translat Matrix metalloprotease 1 (intersitiia	reater than or equal to 2.0, and the passe, peptidase, isomerase, transporticeLL SURFACE PROTEINS, OVAFORD PRAM domains pkinase, Activin_recp SS, ,Peptidase_M10 pkinase pkinase kinesin ABC_tran SS, ,Peptidase_M10	radio a structural domain that is ters). Predicted protein domains are noted.  RIAN CANCER VERSUS NORMAL ADULT TISSUES  ratio 30.0 25.2 18.7 16.2 11.5 8.4 7.2
50 55	small mole indicative TABLE 12 Pkey: Pri Ex. Acci: UG ID: U Title: Uni PFAM do ratio: ratii Pkey 400292 400293 426427 424905 433159 453370	ecules. These wo of enzymatic fun Az: ABOUT 57 Uimekey Exemplar Access niGene fite mains: predicted to turnor vs. norm Ex. Acci AA250737 X07820 M86699 NM_002497 AB035898 AI470523	ere selected action or of bein P-REGULATEI ssion I structural dom at UG ID Hs.72472 Hs.2258 Hs.169840 Hs.153704 Hs.150587 Hs.182356	s for Table 10A, except that the ratio was g g modulated by small molecules (e.g., pkir D GENES ENCODING EXTRACELLULAR nains  Title  BMPR-lb; bone morphogenetic pro Matrix Metalloproteinase 10 (Strom TTK protein kinase NIMA (never in mitosis gene a)-rela kinesin-like protein 2  ESTs, Moderately similar to translat	reater than or equal to 2.0, and the passe, peptidase, isomerase, transport/CELL SURFACE PROTEINS, OVAF  PFAM domains pkinase, Activin_recp SS, Peptidase_M10 pkinase pkinase kinesin ABC_tran SS, Peptidase_M10 SK_Sno,pkinase_C SH2,SH3	redicted protein contained a structural domain that is ters). Predicted protein domains are noted.  RIAN CANCER VERSUS NORMAL ADULT TISSUES  ratio 30.0 25.2 18.7 16.2 11.5 8.4 7.2 6.1 5.2
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50 55 60 65 70	small mole indicative  TABLE 12 Pkey: Pri Ex. Acc; Pri UG ID: U Title: Uni IPFAM do ratio: ra	ecules. These wo of enzymatic fun variants f	ere selected at ction or of bein ction or of bein p-REGULATEI ssion  I structural domatal  UG ID Hs.72472 Hs.2258 Hs.169840 Hs.150587 Hs.182356 Hs.83169 Hs.1904 Hs.54589 Hs.72472 Hs.150587 Hs.182356 Hs.267831 Hs.74899 Hs.272672 Hs.150336 Hs.267831 Hs.74899 Hs.272672 Hs.169771 Hs.183001 Hs.161712 Hs.169771 Hs.183001 Hs.161712 Hs.165072 Hs.26602 Hs.26602 Hs.266322 Hs.96572	s for Table 10A, except that the ratio was g g modulated by small molecules (e.g., pkin D GENES ENCODING EXTRACELLULAR D GENES ENCODING ENCOD	reater than or equal to 2.0, and the passe, peptidase, isomerase, transpor ICELL SURFACE PROTEINS, OVAI PFAM domains pkinase, Activin_recp SS, Peptidase_M10 pkinase pkinase kinesin ABC_tran RhogAp, Peptidase_C SH2, SH3 pkinase Activin_recp Activin_recp, pkinase TM_ABC_tran RhogAp, FF, ras C2, PI-PLC-Y, PI-PLC-X ANF_receptor, pkinase SS, Peptidase_M10 EGF, fn3, pkinase SS, TM, trypsin SS, sushi, trypsin, waa, fn3, AAA pkinase, Activin_recp SS, trypsin SS, Peptidase_M10, ig kl_recept_a, trypsin, SRCR pkinase TM, pkinase, pkinase SS, Peptidase_M10, ig kl_recept_a, trypsin, SRCR pkinase	ratio 30.0 25.2 18.7 16.2 11.5 8.4 7.2 6.1 5.2 5.1 4.8 4.6 3.9 3.8 3.6 3.5 3.4 3.3 3.2 3.2 3.2 3.2 3.1 3.1 3.0 2.9 2.9
50 55 60 65 70	small mole indicative  TABLE 12 Pkey: Prii Ex. Accr. U Title: Urai PFAM dor ratio: rat	ecules. These w of enzymatic fun  A: ABOUT 57 Ui mekey Exemplar Acces niGene 10 Gene fitle mains: predicted o turnor vs. norm  Ex. Accn AA250737 X07820 M86699 NM_002497 AB035898 AI470523 M13509 L18964 NM_006153 AI733881 L02911 AA305627 NM_001173 BE565647 AF212223 X07820 X85689 U62801 AW1797437 AAA31791 AA3155499 BE393948 M31126 AI133148 AA923729	ere selected at ction or of bein p-REGULATEI ssion  P-REGULATEI ssion  I structural domate structural	s for Table 10A, except that the ratio was g g modulated by small molecules (e.g., pkin D GENES ENCODING EXTRACELLULAR D GENES ENCODING ENCOD	reater than or equal to 2.0, and the passe, peptidase, isomerase, transport CELL SURFACE PROTEINS, OVAFORD PROMISES, Peptidase_M10 pkinase, Activin_recp SS, Peptidase_M10 pkinase pkinase kinesin ABC_tran SS, Peptidase_M10 SK_SNo, pkinase_C SH2, SH3 pkinase, Activin_recp, pkinase TM_ABC_tran RhoGAP,FF.ras C2,PLPLC-Y,PLPLC-X ANF_receptor, pkinase SS, Peptidase_M10 EGF_fn3, pkinase SS,TM_trypsin SS,sushi, trypsin, waa_fn3, AAA pkinase, Activin_recp SS, trypsin SS, Peptidase_M10, ig bl_recept_a, trypsin, SRCR pkinase	ratio 30.0 25.2 18.7 16.2 11.5 8.4 7.2 6.1 5.2 5.1 4.8 4.6 3.9 3.8 3.6 3.5 3.4 3.3 3.2 3.2 3.2 3.2 3.1 3.1 3.0 2.9
50 55 60 65 70	small mole indicative  TABLE 12 Pkey: Pri Ex. Acc; Pri UG ID: UT IIIle: Uni PFAM do ratio: ratio ratio:	ecules. These wo of enzymatic fun of enz	ere selected at ction or of bein p-REGULATEI ssion  I structural domat str	s for Table 10A, except that the ratio was g g modulated by small molecules (e.g., pkin D GENES ENCODING EXTRACELLULAR D GENES ENCODING EXTRACELLULAR D GENES ENCODING EXTRACELLULAR D GENES ENCODING EXTRACELLULAR D GENES D G GENES D GENES D G G G GENES D G G G G G G G G G G G G G G G G G G	reater than or equal to 2.0, and the passe, peptidase, isomerase, transpor ICELL SURFACE PROTEINS, OVAI PFAM domains pkinase, Activin_recp SS, Peptidase_M10 pkinase kinase kinase kinase kinase SS, Peptidase_M10 Ski_Sno,pkinase_C SH2,SH3 pkinase, Activin_recp kinase TM_ABC_tran RhoGAP,FF.ras C2,Pi-Pi_C-Y,Pi-Pi_C-X ANF_receplor, pkinase SS, TM_trypsin SS_sushi_trypsin, wa_fn3, AAA pkinase, Activin_recp SS, typsin SS_sushi_trypsin, wa_fn3, AAA pkinase, Activin_recp St. TM_trypsin SS_sushi_trypsin, sRCR pkinase TM_pkinase_Activin_recp St. TM_trypsin_sRCR pkinase TM_pkinase_Activin_recp TM_pkinase_Activin_recp TM_pkinase_Activin_recp	ratio 30.0 25.2 18.7 16.2 11.5 8.4 7.2 6.1 5.2 5.1 4.8 4.6 3.9 3.8 3.6 3.5 3.4 3.3 3.2 3.2 3.2 3.2 3.2 3.2 3.2 3.2 3.2

PCT/US02/19297 WO 02/102235

	401323	AL158037		predicted exon	lactamase_B	2.7
	444798	BE242144	Hs.12013	ATP-binding cassette, sub-family E	SH3,pkinase ,ABC_tran	2.7
	432201	AI538613	Hs.135657	TMPRSS3a mRNA for serine protea	trefoil, trypsin	26
	448402	BE244226	Hs.21094	RAB18, member RAS oncogene fam	ras.arf	26
5	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte gro	pkinase,Sema	25
-	453448	AL036710	Hs.209527	ESTs	CNH,pkinase	2.5
	414386	X00442	Hs.75990	haptoglobin	sushi,trypsin	2.5
	421270	H56037 ·	Hs.108146	ESTs	RhoGAP	2.4
	414695	BE439915	Hs.76913	proteasome (prosome, macropain) su	proteasome	2.4
10	431341	AA307211	Hs.251531	proteasome (prosome, macropain) su	proteasome	2.4
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (4	AAA Viral_helicase1	2.2
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatina	SS,fn2, Peptidase_M10	2.2
	416517	AA775987	Hs.79357	proteasome (prosome, macropain) 26 ·	AAA	2.2
	417601	NM_014735	Hs.82292	KIAA0215 gene product	PHD	2.1
15	400509	M97639	Hs.155585	receptor tyrosine kinase-like orphan	pro_isomerase	2.1
	430057	AW450303	Hs.2534	bone morphogenetic protein recepto	Activin_recp,pkinase	2.1
	421841	AA908197	Hs.108850	KIAA0936 protein	TPR pkinase	2.1
	453078	AF053551	Hs.31584	metaxin 2	pro_isomerase	2.1
	424099	AF071202	Hs.139336	ATP-binding cassette; sub-family C	TM_ABC_tran	2.1
20	411190	AA306342	Hs.69171	protein kinase C-like 2	pkinase,pkinase_C,HR1	2.1
	407740	AA295547	Hs.62666	ESTs	p450	2.1
	420162	BE378432	Hs.95577	cyclin-dependent kinase 4	pkinase,ank,ArfGap ,ras	2.1
	420490	H69894	Hs.193041	ESTs	PI3Ka,PI3_PI4_kinase	2.1
	426156	BE244537	Hs.167382	natriuretic peptide receptor Alguany	TM_ANF_receptor ,pkinase	2.0
25	423945	AA410943	Hs.72472	BMPR-lb; bone morphogenetic pro	TM,pkinase,Activin_recp	2.0
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	SS,trypsin	2.0
	447298	BE617527	Hs.180450	ribosomal protein S24	PI3Ka, PI4_kinase	2.0
	427617	D42063	Hs.179825	RAN binding protein 2-like 1	TPR,pro_jsomerase	2.0
	453546	AF042385	Hs.33251	peptidylprolyl isomerase E (cycloph	pro_isomerase,rm	. 20
30						
	TADIE 1	20				

40

TABLE 12C:
Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
Strand: Indicates DNA strand from which exons were predicted

35 Nt\_position: Indicates nucleotide positions of predicted exons

> Pkey 401323 Ref Strand 9212516 Plus Nt\_position 213509-214450

Table 13A lists about 1086 genes up-regulated in ovarian cancer compared to normal ovaries. These were selected as for Table 10A, except that the ratio was greater than or equal to 10, and the denominator was the median value for various non-malignant ovary specimens.

45 TABLE 13A: About 1086 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY

Pkey: Primekey
Ex. Acon: Exemplay Accession
UG ID: UniGene ID
Title: UniGene title

50 ratio: ration tumor vs. normal ovary

	Pkey	Ex. Acon	UGID	Title	ratio
	439706	AW872527	Hs.59761	ESTs	109.2
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin, bone	107.8
55	422095	· Al868872	Hs.288966	ceruloplasmin (ferroxidase)	104.4
	447111	AI017574	Hs.17409	cysteine-rich protein 1 (Intestinal)	88.3
	431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic protein type	82.8
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (antil	81.9
	413859	AW992356	Hs.8364	ESTs	73.9
60	446291	BE397753	Hs.14623	Interferon, gamma-inducible protein 30	72.7
	426050	AF017307	Hs.166096	E74-like factor 3 (ets domain transcription f	68.1
	411469	T09997	Hs.70327	cysteine-rich protein 2	66.6
	429504	X99133	Hs.204238	tipocalin 2 (oncogene 24p3)	65.7
	416971	R34657	Hs.80658	uncoupling protein 2 (mitochondrial, proton c	64.9
65	450273	AW296454	Hs.24743	hypothetical protein FLJ20171	62.5
	446441	AK001782	Hs.15093	hypothetical protein	60.7
	428758	AA433988	Hs.98502	Homo sapiens cDNA FLJ14303 fis, clone PLACE20	59.7
	441406	Z45957	Hs.7837	Homo sapiens cDNA FLJ10457 fis, clone NT2RP10	57.8
	441859	AW194364	Hs.128022	ESTs, Weakly similar to FIG1 MOUSE FIG-1 PROT	56. <b>7</b>
70	448406	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076	55.7
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264	55.2
	418068	AW971155	Hs.293902	ESTs, Wealdy similar to prolyl 4-hydroxylase	54.8
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin, uteri	53.4
	412636	NM_004415	Hs.74316	desmoplakin (DPI, DPII)	51.4
75	430634	Al860651	Hs.26685	ESTs	50.7
	439318	AW837046	Hs.6527	G protein-coupled receptor 56	50.7
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (versican)	50.6
	407786	AA687538	Hs.38972	tetraspan 1	50.4
	426836	N41720	Hs.172684	vesicle-associated membrane protein 8 (endobr	49.7
80	417308	H60720	Hs.81892	KIAA0101 gene product	48.9
	436876	Al124756	Hs.5337	isocitrate dehydrogenase 2 (NADP+), milochond	48.4
	439180	Al393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia viral	47.1
•	428289	M26301	Hs.2253	complement component 2	46.3
	405484			. 0	46.1

	425371	D49441	Hs.155981	mesothelin	45.7
	403912			0	45.0
	443021	AA368546	Hs.8904	lg superfamily protein	44.6
•	427697	T18997	Hs.180372	BCL2-like 1	44.3
5	428227	AA321649	Hs.2248	INTERFERON-GAMMA INDUCED PROTEIN	44.0
	404678			0	43.9
	400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin 2)	43.8
	451035	AU076785	Hs.430	plastin 1 (l isoform)	43.8
• •	440848	BE314650	Hs.7476	ATPase, H+ transporting, lysosomal (vacuolar	42.8
10	436278	BE396290	Hs.5097	synaptogyrin 2	42.4
	413936	AF113676	Hs.75621	serine (or cysteine) proteinase inhibitor, cl	42.1
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgranulin	42.1
	428411	AW291464	Hs.10338	ESTs	41.8
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgranulin	41.5
15	412477	AA150864	Hs.790	microsomal glutathione S-transferase 1	40.7
	417130	AW276858	Hs.81256	S100 calcium-binding protein A4 (calcium prot	40.1
	424673	AA345051	Hs.294092	ESTs ·	39.8
	416530	U62801	Hs.79361	kallikreln 6 (neurosin, zyme)	39.7
~~	443162	T49951	Hs.9029	ESTs; Highly similar to KERATIN; TYPE I CYTO	39.5
20	413719	BE439580	Hs.75498	smail inducible cytokine subfamily A (Cys-Cys	39.3
	424687	J05070	Hs.151738	matrix metalloproleinase 9 (gelatinase B, 92k	38.9
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprotein-39	38.5
	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member), pro	38.1
~ ~	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic acid	37.9
25	415511	AI732617	Hs.182362	ESTs	37.7
	409453	AI885516	Hs.95612	ESTs	37.7
	445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	37.3
	442432	BE093589	Hs.38178	Homo sapiens cDNA: FLJ23468 fis, clone HSI116	37.3
~~	408243	Y00787	Hs.624	interleukin 8	37.3
30	419092	J05581	Hs.89603	mucin 1, transmembrane	36.7
	444172	BE147740	Hs.104558	ESTs	36.0
	412115	AK001763	Hs.73239	hypothetical protein FLJ10901	35.8
	420440	NM_002407	Hs.97644	mammaglobin 2	35.7
	414386	X00442	Hs.75990	haptoglobin	35.3
35	423225	AA852604	Hs.125359	Thy-1 cell surface antigen	35.1
	440598	H13032	Hs.103378	ESTs, Weakly similar to DRR1 [H.sapiens]	35.0
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	34.9
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	34.8
40	445919	T53519	Hs.290357	ESTs	34.7
40	416854	H40164	Hs.80296	Purkinje cell protein 4	34.4
	414186	U33446	Hs.75799	protease, serine, 8 (prostasin)	34.2
	434371	AA631362		gb:np86b01.s1 NCI_CGAP_Thy1 Homo sapiens cDNA	33.9
	421937	A1878857	Hs.109706	HN1 protein	33.9
	449722	BE280074	Hs.23960	cydin B1	33.8
45	400965			0	33.7
	452203	X57522	Hs.158164	ATP-binding cassette, sub-family B (MDR/TAP),	33.5
	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncogene h	33.5
	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, importin a	33.4
	408901	AK001330	Hs.48855	hypothetical protein FLJ 10468	33.3
50	438461	AW075485	Hs.286049	phosphoserine aminotransferase	33.3
	422963	M79141	Hs.13234	ESTs	33.3
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia viral	33.2
	431836	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	32.8
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phosphate),	32.5
55	431211	M86849	Hs.5566	Homo sapiens connexin 26 (GJB2) mRNA, complet	32.5
	436552	NM_014038	Hs.5216	HSPC028 protein	32.5
	442533	AA161224	Hs.8372	ubiquinol-cytochrome c reductase (6.4kD) subu	32.5
	406400	AA343629	Hs.104570	kallikrein 8 (neuropsin/ovasin)	32.4
<b>C</b> 0	450353	Al244661	Hs.103296	ESTs	32.4
60	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKALP)	32.4
	433412	AV653729	Hs.8185	CGI-44 protein; sulfide dehydrogenase like (y	32.3
	441020	W79283	Hs.35962	ESTs	32.2
	432201	AI538613	Hs.135657	TMPRSS3a mRNA for serine protease (ECHOS1) (T	32.0
	424125	M31669	Hs.1735	inhibin, beta 8 (activin AB beta polypeptide)	31.9
65	453309	AI791809	Hs.32949	defensin, beta 1	31.8
	408380	AF123050	Hs.44532	diubiquitin	31.7
	419329	AY007220	Hs.288998	S100-type calcium binding protein A14	31.6
	409231	AA446644	Hs.692	GA733-2; epithelial glycoprotein (EGP) (KSA)	31.6
70	423961	D13666	Hs.136348	Homo sapiens mRNA for osteoblast specific fac	31.2
70	413840	Al301558	Hs.290801	ESTs	30.8
	440943	AW082298	Hs.146161	ESTs, Weakly similar to KIAA0859 protein [H.s	30.8
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone COL013	30.4
	410132	NM_003480	Hs.58882	Microfibril-associated glycoprotein-2	30.2
75	418203	X54942	Hs.83758	CDC28 protein kinase 2	30.1
75	412719	AW016610	Hs.129911	ESTs	30.0
	407862	BE548267	Hs.50724	Homo sapiens cDNA FLJ10934 fis, clone OVARC10	30.0
	431563	AI027643	Hs.120912	ESTs	29.9
	431743	AW972642	Hs.293055	ESTs	29.8
00	443295	AI049783	Hs.241284	ESTs	29.7
80	413745	AW247252	Hs.75514	nucleoside phosphorylase	29.7
	441028	AI333660	Hs.17558	ESTs	29.6
	442315	AA173992	Hs.7956	ESTs	29.6
	452838	U65011	Hs.30743	Preferentially expressed antigen in melanoma	29.5
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to M	29.5

	ASSSEA	DE440449	Un nove	cional congnition particle 10kD	20.4
	432280 420158	BE440142 AI791905	Hs.2943 Hs.95549	signal recognition particle 19kD hypothetical protein	29.4 29.3
	445033	AV652402	Hs.155145	ESTs	29.2
_	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	29.1
5	432706	NM_013230	Hs.286124	CD24	29.0
	422163	AF027208	Hs.297332	prominin (mouse)-like 1	28.7
	447035	NM_004753	Hs.17144	short-chain dehydrogenase/reductase 1	28.6 28.2
	443958 422956	BE241880 BE545072	Hs.10029 Hs.122579	cathepsin C ESTs	28.1
10	450377	AB033091	Hs.24936	ESTs	28.0
	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	28.0
	444725	AW952022	Hs.234174	Homo sapiens cDNA FLJ13819 fis, clone THYRO10	27.8
	430250	NM_016929	Hs.283021	chloride intracellular channel 5	27.7
15	416305	AU076628 L20688	Hs.79187 Hs.83656	coxsackie virus and adenovirus receptor  Pho CDP dissociation inhibitor (CDI) hata	27.6 27.5
13	418174 417233	W25005	Hs.24395	Rho GDP dissociation inhibitor (GDI) beta small inducible cytokine subfamily B (Cys-X-C	27.4
	417866	AW057903	Hs.82772	collagen, type XI, alpha 1	27.3
	427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3A	27.2
20	442993	BE018682	Hs.44343	ESTs	27.2
20	407137	T97307	Hs.199067	v-erb-b2 avian erythroblastic leukemia viral	27.0
•	419356 433662	AI656166 W07162	Hs.7331 Hs.150826	ESTs	27.0 26.7
	422576	BE548555	Hs.118554	CATX-8 protein CGI-83 protein	26.4
	423271	W47225	Hs.126256	interleukin 1, beta	26.3
25	443715	Al583187	Hs.9700	cyclin E1	26.1
	420186	NM_015925	Hs.95697	liver-specific bHLH-Zip transcription factor	26.0
	419551	AW582256	Hs.91011	anterior gradient 2 (Xenepus taevis) homolog	25.9
	443672 416889	AA323362 AW250318	Hs.9667 Hs.80395	butyrobetzine (gamma), 2-oxoglutarate dioxyge mal, T-cell differentiation protein	25.8 25.3
30	408474	AA188823	Hs.83196	Homo sapiens cDNA: FLJ23597 fis, clone LNG152	25.3
-	411825	AK000334	Hs.72289	hypothetical protein FLJ20327	25.3
	400881			0	25.2
	440594	AW445167	Hs.126036	ESTs	25.1
35	414586	AA306160	Hs.76506	lymphocyte cytosolic protein 1 (L-plastin)	25.1 25.1
33	411925 417869	AW014588 BE076254	Hs.72925 Hs.82793	chromosome 11 open reading frame 13 proteasome (prosome, macropain) subunit, beta	25.0
	433447	U29195	Hs.3281	neuronal pentraxin II	25.0
	450858	C18458	Hs.25597	elongation of very long chain fatty acids (FE	24.8
40	410619	BE512730	Hs.65114	keratin 18	24.8
40	434094	AA305599	Hs.238205	hypothetical protein PRO2013	24.6
	421924	BE514514	Hs.109606	coronin, actin-binding protein, 1A	24.6 24.5
	446859 421451	Al494299 AA291377	Hs.16297 Hs.50831	COX17 (yeast) homolog, cytochrome c oxidase a ESTs	24.3
	433929	Al375499	Hs.27379	ESTs	24.3
45	438930	AW843633	Hs.81256	S100 catcium-binding protein A4 (calcium prot	24.2
	444212	AW503976	Hs.10649	basement membrane-induced gene	24.2
	441633	AW958544	Hs.112242	ESTs	24.2
	441134 417715	W29092 AW969587	Hs.7678 Hs.86366	cellular retinoic acid-binding protein 1 ESTs	24.2 24.1
50	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolog 1	24.1
•	416984	H38765	Hs.80706	diaphorase (NADH/NADPH) (cytochrome b-5 reduc	24.1
	430125	U46418	Hs.233950	serine protease inhibitor, Kunitz type 1	23.9
	434078	AW880709	Hs.283683 ~	EST	23.8
55	408669	Al493591	Hs.78146	platelet/endothelial cell adhesion molecule (	23.8
55	439413 - 449034	A1598252 A1624049	Hs.37810 Hs.277523	ESTs gb:ts41a09x1 NCI_CGAP_Ut1 Homo sapiens cDNA	23.7 23.7
	420344	BE463721	Hs.97101	Putative G protein-coupled receptor GPCR150	23.6
	431243	U46455	Hs.252189	syndecan 4 (amphiglycan, ryudocan)	23.6
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated prot	23.5
60	451267	AI033894	Hs.117865	solute carrier family 17 (anion/sugar transpo	23.4
	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	23.4 23.4
	419693 431103	. AA133749 M57399	Hs.92323 Hs.44	FXYD domain-containing ion transport regulato pleiotrophin (heparin binding growth factor 8	23.4
	451110	Al955040	Hs.301584	ESTs	23.3
65	426295	AW367283	Hs.75839	zinc finger protein 6 (CMPX1)	23.2
	448517	AA082750	Hs.42194	hypothetical protein FLJ22649 similar to sign	23.1
	424670	W61215	Hs.116651	epithelial V-like antigen 1	23.1
	417847	AI521558	Hs.288312	Homo sapiens cDNA: FLJ22316 fis, clone HRC052	23.1 23.1
70	449027 424969	AJ271216 AW950928	Hs.22880 Hs.153998	dipeptidytpeptidase III creatine kinase, mitochondrial 1 (ubiquitous)	23.1
. •	433159	AB035898	Hs.150587	kinesin-like protein 2	23.0
	411393	AW797437	Hs.69771	B-factor, properdin	23.0
	434815	AF155582	Hs.46744	core1 UDP-galactose:N-acetylgalactosamine-alp	22.8
75	427585	D31152	Hs.179729	collagen; type X; alpha 1 (Schmid metaphyseal	22.7
75	445721 448258	H92136	Hs.13144 He 85015	HSPC160 protein ESTs, Weakly similar to A4P_HUMAN INTESTINAL	22.6 22.6
	448258 456844	BE386983 Al264155	Hs.85015 Hs.152981	CDP-diacylglycerol synthase (phosphatidate cy	22.6
	452698	NM_001295	Hs.301921	ESTs	22.5
00	418693	AI750878	Hs.87409	thrombospondin 1	22.4
80	414880	AW247305	Hs.119140	eukaryotic translation initiation factor 5A	22.4
	401519			0	22.3 22.3
	402496 420324	AF163474	Hs.96744	0 DKFZP586D0823 protein, Prostate androgen-regu	22.3
	403022	N IOMIN	11000177	0	22.2
				100	

					<b></b>
	434042	A1589941	Hs.8254	hypothetical protein PRO0899	22.1 22.1
•	419080 406545	AW150835 AB018249	Hs.18878 Hs.10458	hypothetical protein FLJ21620 small inducible cytokine subfamily A (Cys-Cys	22.1
	447362	AW176120	Hs.9061	ESTs	22.0
5	429547	AW009166	Hs.99376	ESTs	22.0
-	427954	J03060	Hs.247551	metaxin 1	22.0
	423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (from c	22.0
	428392	H10233	Hs.2265	secretory granule, neuroendocrine protein 1 (	21.9
10	444107	T46839	Rs.10319	UDP glycosyltransferase 2 family, polypeptide	21.7
10	414421-	Al521130	Hs.55567	ESTs, Weakly similar to LAK-4p [H.sapiens]	21.5
	412589	R28660	Hs.24305	ESTS	21.5 21.5
	446525 416847	AW967069 L43821	Hs.211556 Hs.80261	Homo sapiens cDNA: FLJ23378 fis, clone HEP162 enhancer of filamentation 1 (cas-like docking	21.5
	436972	AA284679	Hs.25640	claudin 3	21.5
15	428698	AA852773	Hs.297939	ESTs; Weakly similar to neogenin [H.sapiens]	21.5
	421340	F07783	Hs.1369	decay accelerating factor for complement (CO5	21.4
	413966	AA133935	Hs.173704	ESTs	21.4
	448243	AW369771	Hs.77496	ESTs	21.3
20	421928	AF013758	Hs.109643	polyadenylate binding protein-interacting pro	21.3
20	403399			0	21.3
	435793	AB037734	Hs.4993	ESTs	21.3 21.2
	432629	AW860548	Hs.280658	ESTs ESTs	21.2
	449057 437575	AB037784 AW954355	Hs.22941 Hs.36529	ESTs ·	21.2
25	401131	A11337000	113.30323	0	21.0
23	407207	T03651	Hs.179661	tubulin, bela polypeptide	20.8
	444783	AK001468	Hs.62180	ESTs	20.8
•	426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	20.8
	447343	AA256641	Hs.236894	ESTs; Highly similar to LOW-DENSITY LIPOPROTE	20.7
30	409041	AB033025	Hs.50081	KIAA1199 protein	20.6
	421305	BE397354	Hs.289721	diptheria toxin resistance protein required f	20.6
	411704	Al499220	Hs.71573	hypothetical protein FLJ10074	20.5
	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related oncog	20.5
35	432827	Z68128	Hs.3109	Rho GTPase activating protein 4	20.4 20.4
33	410174	AA305007 BE278288	Hs.59461	DKFZP434C245 protein Lutheran blood group (Auberger b antigen incl	20.4
	425184 452322	BE566343	Hs.155048 Hs.28988	glutaredoxin (thioltransferase)	20.3
	447526	AL048753	Hs.340	small inducible cytokine A2 (monocyte chemota	20.2
	447335	BE617695	Hs.286192	protein phosphatase 1, regulatory (inhibitor)	20.2
40	424867	AI024860	Hs.153591	Not56 (D. melanogaster)-like protein	20.1
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activating e	20.1
	429083	Y09397	Hs.227817	BCL2-related protein A1	20.0
	410173	AA706017	Hs.119944	ESTs	19.8
4.5	433047	M86135	Hs.279946	methionine-tRNA synthetase	19.8
45	419088	Al538323	Hs.77496	ESTs	19.7
	403381	1105500	U- 50000	O	19.6
	409162	H25530	Hs.50868	solute carrier family 22 (organic cation tran	19.5 19.4
	426150 449292	NM_003658 Al990292	Hs.167218 Hs.225457	BarH-like homeobox 2 ESTs	19.4
50	425207	AB014551	Hs.155120	rho/rac guanine nucleotide exchange factor (G	19.4
50	419950	AK001645	Hs.93871	hypothetical protein FLJ10783	19.3
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-conjugat	19.3
	445930	AF055009	Hs.13456	Homo sapiens clone 24747 mRNA sequence	19.2
	446608	N75217	Hs.257846	ESTs	19.1
55	425222	M85430	Hs.155191	villin 2 (ezrin)	19.1
	428309	M97815	Hs.183650	cellular retinoic acid-binding protein 2	19.1
	420005	AW271106	Hs.133294	ESTs	19.1
	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular matrix p	19.0 -
60	407142 430122	AA412535 NM_013342	Hs.55235 Hs.233765	sphingomyelin phosphodiesterase 2, neutral me TCF3 (E2A) fusion partner (in childhood Leuke	19.0 18.9
UU	446293	Al420213	Hs.149722	ESTs	18.9
	444825	AW167613	Hs.248	mitogen-activated protein kinase kinase kinas	18.9
	407634	AW016569	Hs.301280	UDP-GlcNAc:betaGal beta-1,3-N-acetyiglucosami	18.9
	445200	AA084460	Hs.12409	somatostatin	18.9
65	418917	X02994	Hs.1217	adenosine dearninase	18.8
	435777	AW419202	Hs.286192	protein phosphatase 1, regulatory (inhibitor)	18.8
	431049	AA846576	Hs.103267	hypothetical protein FLJ22548 stralar to gene	18.7
	426427	M86699	Hs.169840	TTK protein kinase	18.7
70	436281	AW411194	Hs.120051	ESTs	18.6
70	425907	AA365752	Hs.155965	ESTs	18.6
	459720	AIAME120E	Un 12561	ESTs ESTs Worldy similar to d 137E 16 5 (H expires)	18.6 18.5
	421242 457715	AW161386 AA642402	Hs.13561 Hs.59142	ESTs, Wealtly similar to dJ37E16.5 [H.sapiens] ESTs	18.5
	457715 451668	Z43948	Hs.26789	ASPIC (acidic secreted protein in cartilage)A	18.4
75	437142	A1791617	Hs.145068	ESTs	18.4
	418588	BE387040	Hs.182476	ESTs. Weakly similar to similar to alpha/beta	18.3
	433068	NM_006456	Hs.288215	sialyltransferase	18.3
	419854	AW664873	Hs.87836	Homo sapiens PAC done RP5-1087M19 from 7q11.	18.3
00	444726	NM_006147	Hs.11801	interferon regulatory factor 6	18.3
80	423011	NM_000683	Hs.299847	ESTs, Highly similar to A2AD_HUMAN ALPHA-2C-2	18.2
	451428	AW083384	Hs.11067	ESTs, Weakly similar to K02E10.2 [C.elegans]	18.2
	424865	AF011333	Hs.153563	lymphocyte antigen 75	18.2 18.1
	418742	AW451197	Hs.113418	ESTs ESTs; hypothetical protein SBBI48	18.1
	446627	AI973016	Hs.15725	CO.19' HARDERGE BLOCKIL GOOD-O	10.1

	404005	41200774	11-00004	ESTs	40 4
	424885 402926	AI333771	Hs.82204	0	18.1 18.0
	405452			Ŏ	18.0
	428541	AA431367	Hs.234546	GMPR2 for guanosine monophosphale reductase i	18.0
5	454390	AB020713	Hs.56966	KIAA0906 protein	18.0
_	441784	AJ522132	Hs.28700	ESTs	18.0
	418758	AW959311	Hs.87019	ESTs	17.9
	408621	A1970672	Hs.46638	chromosome 11 open reading frame 8; fetal br	17.9
10	426201	AW182614	Hs.128499	ESTs	17.8
10	410442	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta polype	17.8
	456423	AW748920	11- 4504	gb:CM2-BT0306-171199-034-g02 BT0306 Homo sapi	17.8 17.8
	422867 448110	L32137 AA626937	Hs.1584 Hs.181551	cartilage oligomeric matrix protein ESTs	17.7
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	17.7
15	405224	74,000,00	12.101012	0	17.7
10	447630	AI660149	Hs.44865	lymphoid enhancer-binding factor 1	17.7
	407663	NM_016429	Hs.37482	COPZ2 for nonclathrin coat protein zeta-COP	17.7
	427490	Z95152	Hs.178695	mitogen-activated protein kinase 13	17.6
	414812	X72755	Hs.77367	monokine induced by gamma interferon	17.6
20	427691	AW194426	Hs.20726	ESTs	17.6
	420650	AA455706	Hs.44581	heat shock protein hsp70-related protein	17.5
	439841	AF038961	Hs.6710	mannose-P-dotichol utilization defect 1	17.5
	425810	AI923627	Hs.31903	ESTs	17.5
25	425397	J04088	Hs.156346	topolsomerase (DNA) II alpha (170kD)	17.5 17.4
25	456098 428579	AW747800	Hs.55016	hypothetical protein FLJ21935	17.4
	410361	NM_005756 BE391804	Hs.184942 Hs.62661	G protein-coupled receptor 64 guanylate binding protein 1, interferon-induc	17.4
	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	17.4
	411734	AW374954	Hs.71779	Homo sapiens DNA from chromosome 19, cosmid F	17.3
30	405295	. 11101 7007		0	17.3
	408340	AB037762	Hs.44268	myelin gene expression factor 2	17.3
	456068	AJ677897	Hs.76640	RGC32 protein	17.3
	448571	AA486794	Hs.66915 *	ESTs, Weakly similar to 16.7Kd protein [H.sap	17.2
	441829	AL117482	Hs.7978	DKFZP434C131 protein	17.2
35	418004	U37519	Hs.87539	aldehyde dehydrogenase 8	17.2
	412078	X69699	Hs.73149	paired box gene 8	17.2
	414658	X58528	Hs.76781	ATP-binding cassette, sub-family D (ALD), mem	17.1
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (melanom	17.0
40	426805	AB032945	Hs.172506	myosin VB	17.0
40	410247	AF181721	Hs.61345	RU2S	17.0
	434516	AA807814	Hs.70582	ESTs, Moderately similar to AF144056 1 apopto	16.9 16.9
	428153 417793	AW513143 AW405434	Hs.98367 Hs.82575	hypothetical protein FLJ22252 similar to SRY- small nuclear ribonucleoprotein polypeptide B	16.9
	454163	AW175997	115.02373	gb;QV0-BT0078-190899-005-E02 BT0078 Homo sapi	16.9
45	415402	AA164687	Hs.297889	ESTs	16.9
	420309	AW043637	Hs.21766	ESTs	16.9
	419201	M22324	Hs.1239	alanyl (membrane) aminopeptidase (aminopeptid	16.9
	444391	AL137597	Hs.11114	hypothetical protein dJ1181N3.1	16.9
	457705	AW974668		gb:EST386757 MAGE resequences, MAGM Homo sapi	16.8
50	412723	AA648459	Hs.179912	ESTs	16.8
	435774	R88056	Hs.4992	tumor suppressing subtransferable candidate 1	16.8
	408753	Al337192	Hs.47438	SH3 domain binding glutamic acid-rich protein	16.8
	447783	AF054178	Hs.19561	NADH dehydrogenase (ubiquinone) 1 alpha subco	16.8
55	418085	R40328	Hs.258822	ESTs ESTs, Weakly similar to SP49_HUMAN SPLICEOSOM	16.7 16.7
55	452472	AW957300 BE243971	Hs.294142 Hs.50649	quinone oxidoreductase homolog	16.7
	409112 410250	AI082777	Hs.61384	KIAA1445 protein	16.7
	446219	Al287344	Hs.149827	ESTs	16.6
	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (eplthelial)	16.6
60	425812	AA364128	Hs.245633	ESTs	16.6
-	411742	AW247593	Hs.71819	eukaryotic translation initiation factor 4E b	16.6
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	16.6
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolo	16.6
CE	440667	BE076969	Hs.7337	hypothetical protein FLJ10936	16.6
65	430375	AW371048	Hs.93758	H4 histone family, member H	16.6
	419607	R52557	Hs.91579	Homo sapiens clone 23783 mRNA sequence	16.6
	410328	BE080190	Hs.62275	CGI-141 protein	16.5 16.5
	405426	ASSONA	Hs.278562	0 elautin 7	16.5
70	432636 434725	AA340864 AK000796	Hs.4104	claudin 7 hypothetical protein	16.5
70	414683	S78296	Hs.76888	internexin neuronal intermediate filament pro	16.5
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	16.5
	449944	AF290512	Hs.58215	Homo sapiens rhotekin mRNA, partial cds	16.4
	400666			0	16.4
75	421536	BE250690	Hs.105509	CTL2 gene	16.4
	436032	AA150797	Hs.109276	latexin protein	16.4
	418196	AI745649	Hs.26549	ESTs, Weakly similar to T00066 hypothetical p	16.4
	452323	W44356	Hs.292812	ESTs, Weakly similar to C43H8.1 [C.elegans]	16.4
00	407699	AAB25974	Hs.32646	Homo sapiens cDNA: FLJ21901 fis, clone HEP034	16.4
80	414617	Al339520	Hs.20524	ESTs, Moderately similar to hexokinase I (H.s	16.3
	408204	AA454501	Hs.43666	protein tyrosine phosphatase type IVA, member	16.3
	452650	AW270150	Hs.254516	ESTs	16.3
	432906	BE265489	Hs.3123	tethal giant larvae (Drosophila) homolog 2	16.3 16.3
	402408			. 0	10.0

					40.0
	408805	H59912	Hs.48269	vaccinia related kinase 1	16.3
	447155	AA100605	Hs.121557	ESTs, Weakly similar to AF251041 1 SGC32445 p	16.3
	405699			0	16.2
~	406893	M22406		gb:Human intestinal mucin mRNA, partial cds,	16.2
5	418629	BE247550	Hs.86859	growth factor receptor-bound protein 7 (GRB7)	16.2
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related kinase	16.2
	424243	AI949359	Hs.301837	ESTs, Highly similar to cis Golgi-localized c	16.2
	418462	BE001596	Hs.85266	integrin, beta 4	16.1
• •	457205	Al905780	Hs.198272	NADH dehydrogenase (ubiquinone) 1 beta subcom	16.1
10	428188	M98447	Hs.22	transglutaminase 1 (K polypeptide epidermal t	16.1
	449845	AW971183	Hs.60054	ESTs	16.1
	406429			0	16.1
	407375	AA091354		gb:10815.seq.F Human fetal heart, Lambda ZAP	16.1
	448377	AJ494514	Hs.171380	ESTs	16.1
15	431156	NM_002220	Hs.2722	inositol 1,4,5-trisphosphate 3-kinase A	16.0
10	450043	AA885699	Hs.24332	CGI-26 protein	16.0
	403121	741000000	IBLETOVE	0	16.0
	400214			Ö .	15.9
	453252	R02436	Hs.215725	ESTs	15.9
20		NM_006176	Hs.26944	neurogranin (protein kinase C substrate, RC3)	15.9
20	451734				15.9
	416855	AA188763	Hs.36793	Homo sapiens cDNA: FLJ23188 fis, clone LNG120	15.9
	424474	AA308883	Hs.148680	calcyon; D1 dopamine receptor-interacting pro	15.9
	423685	BE350494	Hs.49753	Homo sapiens mRNA for KIAA1561 protein, parti	15.9
25	428187	AI687303	Hs.285529	ESTs	
25	438817	Al023799	Hs.163242	ESTs	15.9
	425692	D90041	Hs.155956	NAT1; arylamine N-acetyltransferase	15.9
	421674	T10707	Hs.296355	neuronal PAS domain protein 2	15.9
	439999	AA115811	Hs.6838	ras homolog gene family, member E	15.9
20	411351	W02919	Hs.283476	peroxisomal acyl-CoA thioesterase	15.9
30	413027	NM_002885	Hs.75151	RAP1, GTPase activating protein 1	15.9
	453884	AA355925	Hs.36232	KIAA0186 gene product	15.8
	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase C-bet	15.8
	422748	AA316266	Hs.129349	ESTs	15.8
	414591	A1888490	Hs.55902	ESTs	15.8
35	421877	AW250380	Hs.109059	mitochandrial ribosomal protein L12	15.8
	404780			0	15.8
	401192			Ò	15.8
	447519	U46258	Hs.23448	ESTs	15.8
	434262	AF121858	Hs.12169	sorting nexin 8	15.7
40	451253	H48299	Hs.26126	claudin 10	15.7
• •	435499	R89344	Hs.14148	ESTs	15.7
	422424	Al186431	Hs.116577 ·	prostate differentiation factor; placental bo	15.7
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP20	15.7
	424562	Al420859	Hs.150557	basic transcription element binding protein 1	15.7
45	443247	BE614387	Hs.47378	ESTs	15.7 ·
	430696	AA531276	Hs.59509	ESTs	15.6
	437044	AL035864	Hs.69517	ESTs, highly similar to differentially expres	15.6
	428237	AF175206	Hs.183125	killer cell lectin-like receptor F1	15.6
	440048	AA897461	Hs.158469	ESTs, Weakly similar to envelope protein [H.s	15.6
50	414922	D00723	Hs.77631	glycine cleavage system protein H (aminomethy	15.6
50	422030	X51416	Hs.110849	estrogen-related receptor alpha	15.6
	408716	Al567839	Hs.151714	ESTs	15.5
				6-phosphofructo-2-kinase/fructose-2,6-biphosp	15.5
	410258	X52638	Hs.739		15.5
55	410530	M25809 D61594	Hs.64173	ESTs, Highly similar to VAB1_HUMAN VACUOLAR A	15.5
55	447072		Hs.17279	tyrosylprotein sulfotransferase 1	
	409015	BE389387	Hs.49767	NADH dehydrogenase (ubiquinone) Fe-S protein	15.5 15.5
	447549	Al871120 -	Hs.231265	ESTs .	
	449704	AK000733	Hs.23900	GTPase activating protein	15.4
60	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIIb, recept	15.4
UU	421630	NM_001956	Hs.1407	endothelin 2	15.4
	433018	A1669760	Hs.188881	ESTs	15.4
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	15.3
	407014	U38268		gb:Human cytochrome b pseudogene, partial cds	15.2
15	429311	AF080157	Hs.198998	conserved helix-loop-helix ubiquitous kinase	15.2
65	431842	NM_005764	Hs.271473	epithelial protein up-regulated in carcinoma,	15.2
	406907	Z25427	•	gb:H.sapiens protein-serine/threonine kinase	15.2
	458495	Al202029	Hs.148593	ESTs	15.2
	420551	AL137692	Hs.98790	Homo sapiens mRNA; cDNA DKFZp434P182 (from cl	15.1
70	448443	AW167128	Hs.231934	ESTs	15.1
70	443646	A1085198	Hs.298699	ESTs	15.1
	431538	AL137547	Hs.259619	Homo sapiens mRNA; cDNA DKFZp434B1120 (from c	15.1
	436687	AA868643	Hs.120461	ESTs	15.1
	420917	AW135716	Hs.117330	ESTs	15.0
7.	428575	M19684	Hs.184929	serine (or cysteine) proteinase inhibitor, cl	15.0
75	403482			0	15.0
	421499	A1271438	Hs.105022	Homo sapiens PAC clone RP4-701016 from 7q33-q	15.0
	401047			0	14.9
	417749	U09196	Hs.82520	polymerase (DNA-directed), delta 4	14.9
	416693	AJ373204	Hs.79531	Homo sapiens TTF-I interacting peptide 20 mRN	14.9
80	428474	AB023182	Hs.184523	KIAA0965 protein	14.9
	428862	NM_000346	Hs.2316	SRY (sex-determining region Y)-box 9 (campome	14.9
	430271	T06199	Hs.237506	heat shock cognate 40	14.9
	414328	Z21666	Hs.75900	aconitase 2, mitochondrial	14.9
	415314	N88802	Hs.5422	glycoprotein M6B	14.8

	453735	AI066629	Hs.125073	ESTs	14.8
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT2RP20	14.8
	423575	C18863	Hs.163443	ESTs	14.8
	438081	H49546	Hs.298964	ESTs	14.8
5	403485			0	14.8
	452114	N22687	Hs.8236	ESTs	14.8
	426559	AB001914	Hs.170414	paired basic amino acid cleaving system 4	14.8
	412869	AA290712	Hs.82407	Homo sapiens HSPC296 mRNA, partial cds	14.8
_	452101	T60298		gb:yb87f12.r1 Stratagene liver (937224) Homo	14.7
10	420505	AW967984	Hs.291612	ESTs	14.7
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolog	14.7
	433336	AF017986	Hs.31386	ESTs; Highly similar to FRIZZLED PROTEIN PRE	14.7
	428977	AK001404	Hs.194698	cyclin B2	14.7
	429785	H82114	Hs.301769	ESTs	14.7
15	402424			0	14.7
	424971	AA479005	Hs.154036	tumor suppressing subtransferable candidate 3	14.7
	433037	NM_014158	Hs.279938	HSPC067 protein	14.6
	421670	BE207318	Hs.106674	BRCA1 associated protein-1 (ubiquitin carboxy	14.6
	438598	AI805943	Hs.5723	Homo sapiens cDNA: FLJ23439 fis, clone HSI001	14.6
20	453370	Al470523	Hs.182356	ESTs, Moderately similar to translation initi	14.6
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone HEP091	14.6
	402287			0	14.6
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	14.6
	442047	AA974598	Hs.150324	ESTs	14.5
25	428582	BE336699	Hs.185055	BENE protein	14.5
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	14.5
	406851	AA609784	Hs.180255	major histocompatibility complex, class II, D	14.5
	457316	Al123657	Hs.127264	ESTs	14.5
	420453	AL157500	Hs.97840	Homo sapiens mRNA; cDNA DKFZp434G015 (from cl	14.5
30	436406	AW105723	Hs.125346	ESTs	14.5
	420736	AI263022	Hs.82204	ESTs	14.5
	419743	AW408762	Hs.127478	ESTs	14.5
	429113	D28235	Hs.196384	Prostaglandin-endoperoxide synthase 2 (COX-2)	14.5
	450256	AA286887	Hs.24724	MFH-amplified sequences with leucine-rich tan	14.5
35	424906	A1566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3' untr	14.5
	. 427414	F11750	Hs.6647	Homo sapiens cDNA FLJ13088 fis, clone NT2RP30	14.4
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-activat	14.4
	418738	AW388633	Hs.6682	solute carrier family 7, member 11	14.3
	429414	AI783656	Hs.202095	empty spiracles (Drosophila) homolog 2	14.3
40	424669	AA417181	Hs.120858	Homo saptens cDNA FLJ13945 fis, clone Y79AA10	14.3
	408989	AW361666	Hs.49500	KIAA0746 protein	14.3
	406788	AI911841	Hs.5184	TH1 drosophila homolog	14.3
	417861	AA334551	Hs.82767	sperm specific antigen 2	14.3
	402104			0	14.3
45	416368	R88849		gb:ym96a06.r1 Soares adult brain N2b4HB55Y Ho	14.2
	405802			Ò	14.2
	448357	N20169	Hs.108923	ESTs	14.2
	444261	AA298958	Hs.10724	MDS023 protein	14.2
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, with Glu	14.2
50	425163	D10040	Hs.154890	fatty-acid-Coenzyme A ligase, long-chain 2	14.1
	402520			0	14.1
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain 9	14.1
	430044	AA464510	Hs.152812	EST cluster (not in UniGene)	14.1
	429663	M68874	Hs.211587	Human phosphatidylcholine 2-acylhydrolase (cP	14.1
55	427036	AA397625	Hs.163913	ESTs	. 14.1
	444381	BE387335	Hs.283713	ESTs	14.1
	432090	AW972855	Hs.292853	ESTs	14.0
	406778	H06273	Hs.101651	Homo sapiens mRNA; cDNA DKFZp434C107 (from cl	14.0
-	404961	AW972195	Hs.284236	aldo-keto reductase family 7, member A3 (alla	14.0
60	452313	Y00486	Hs.28914	adenine phosphoribosyltransferase	14.0
	452355	N54926	Hs.29202	G protein-coupled receptor 34	14.0
	429942	Al338993	Hs.134535	ESTs	14.0
	403165			0	13.9
	442150	Al368158	Hs.128864	ESTs	13.9
65 ·	439709	AW401433	Hs.6649	hypothetical protein FLJ20128	13.9
	456799	AC004923	Hs.135187	Homo sapiens clone CDABP0025 mRNA sequence	13.9
	427356	AW023482	Hs.97849	ESTs	13.9
	448982	A1638164	Hs.225520	ESTs	13.9
70	432025	BE407132	Hs.111286	hypothetical protein FLJ22512	13.8
70	427505	AA361562	Hs.178761	26S proteasome-associated pad1 homolog	13.8
	402965			0	13.8
•	418601	AA279490	Hs.86368	calmegin	13.8
	436954	AA740151	Hs.130425	ESTs	13.8
75	405024			0	13.8
75	453976	BE463830	Hs.163714	ESTs	13.8
	431921	N46466	Hs.58879	ESTs	13.8
	401735			0	13.8
	445496	AB007860	Hs.12802	development and differentiation enhancing fac	13.8
οΛ	425007	AA456483	Hs.172081	phosphodiesterase 4D, cAMP-specific (dunce (D	13.7
80	409463	Al458165	Hs.17296	ESTs	13.7
	430193	AI826653	Hs.102928	Homo sapiens cDNA FLJ13479 fis, clone PLACE10	13.7
	458869	A1637934	Hs.224978	ESTs	13.7
	426769	AA075596	Hs.172153	glutathione peroxidase 3 (plasma)	13.7
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	13.7

	439901	N73885	Hs.124169	ESTs	13.7
	431374	BE258532	Hs.251871	CTP synthase	13.7
	432861	- AA339526	Hs.279593	HSPC171 protein	13.7
5	441172 410001	A1279652 AB041036	Hs.132879	ESTs kaffikrein 11; serine protease (TLSP)	13.7 13.7
5	430315	NM_004293	Hs.57771 Hs.239147	guarine deaminase	13.6
	422769	AA938905	Hs.289112	CGI-43 protein	13.6
	402389	74 000000	110-200112	0	13.6
	448977	X91809	Hs.22698	regulator of G-protein signatting 19	13.6
10	459648			gb:IL3-CT0220-150200-070-B02 CT0220 Homo sapi	13.6
	452972	M31732	Hs.31210	B-cell CLL/lymphoma 3	13.6
	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	13.6
	448585	AB020676	Hs.21543	KIAA0869 protein	13.6
15	428385	AF112213	Hs.184062	putative Rab5-interacting protein	13.6 13.6
13	434699 447238	AA643687 AW451676	Hs.149425 Hs.158564	Homo sapiens cDNA FLJ11980 fis, clone HEMBB10 ESTs	13.6
	437108	AA434054	Hs.80624	Homo sapiens cDNA: FLJ23442 fis, clone HSI009	13.6
	425749	AW328587	Hs.159448	surfeit 2	13.5
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	13.5
20	413753	U17760	Hs.301103	Laminin, beta 3 (nicein (125kD), kalinin (140	13.5
	419034	NM_002110	Hs.89555	hemopoietic cell kinase	13.5
	448361	H82028	Hs.238707	Homo sapiens cDNA: FLJ22457 fis, clone HRC099	13.5
	412754	AW160375	Hs.74565	amyloid beta (A4) precursor-like protein 1	13.5 13.5
25	419081 407732	AJ798863 AW138839	Hs.87191 Hs.24210	ESTs :	13.5
23	423329	AF054910	Hs.127111	tektin 2 (testicular)	13.5
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced, 68k	13.4
	439636	AF086467		gb:Homo sapiens full length insert cDNA clone	13.4
	417605	AF006609	Hs.82294	regulator of G-protein signalling 3	13.4
30	445861	BE293423	Hs.11809	single ig it-1R-related molecule	13.4
	447350	AI375572	Hs.172634	ESTs; HER4 (c-erb-B4)	13.4
	451807	W52854	Hs.27099	DKFZP564J0863 protein	13.4
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, long f	13.4 13.4
35	422443 412504	NM_014707 Z44496	Hs.116753 Hs.26039	histone deacetylase 7B Homo sapiens cDNA FLJ13937 fis, clone Y79AA10	13.4
55	453344	BE349075	Hs.44571	ESTs	13.4
	402885	02043010	15.44071	0	13.4
	438712	AW978161	Hs.169877	ESTs	13.4
	421774	AL050374	Hs.108169	DKFZP586C1619 protein	13.3
40	425638	NM_012337	Hs.158450	nasopharyngeal epithelium specific protein 1	13.3
	401897			0	13.3
	425601	AW629485	Hs.293352	ESTs	13.3
	450779	AW204145	Hs.156044	ESTs Markharimina to wantered protein produ	13.3 13.3
45	444858 442619	AJ199738 AA447492	Hs.208275 Hs.20183	ESTs, Weakly similar to unnamed protein produ ESTs, Weakly similar to AF164793 1 protein x	13.3
73	434263	N34895	Hs.44648	ESTs	13.3
	426059	BE292842	Hs.166120	interferon regulatory factor 7	13.3
	407467	D55638		gb:Human B-ceil PABL (pseudoautosomal boundar	13.3
	412560	R24601	Hs.108300	CCR4-NOT transcription complex, subunit 3	13.2
50	442986	Al025990	Hs.285520	ESTs	13.2
	420317	AB006628	Hs.96485	KIAA0290 protein	13.2
	443211	AI128388	Hs.143655	ESTS	13.2 13.2
	434361 423493	AF129755 AI815965	Hs.117772 Hs.129683	ESTs ubiquitin-conjugating enzyma E2D 1 (homologou	13.2
55	414183	AW957446	Hs.301711	ESTs	13.2
55	447778	BE620592	Hs.71190	ESTs	13.2
	435106	AA100847	Hs.193380	ESTs, Highly similar to AF174600 1 F-box prot	13.1
	439490	AW249197	Hs.100043	ESTs, Weakly similar to PSF_HUMAN PTB-ASSOCIA	· 13.1
<b>C</b> C	409606	AW444594	Hs.2387	transglutaminase 4 (prostate)	13.1
60	421308	AA687322	Hs.192843	ESTs	13.1
	414950	C15407	11- 70000	gb:C15407 Clontech human aorta polyA+ mRNA (6	13.1
	416783	AA206186	Hs.79889	monocyte to macrophage differentiation-associ	13.1 13.1
	415927 422605	AL120168 H16646	Hs.78919 Hs.118666	Kell blood group precursor (McLeod phenotype) Human clone 23759 mRNA, partial cds	13.0
65	430427	AA296701	Hs.241413	opticin	13.0
05	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic; stratum comeum)	13.0
	421693	X71490	Hs.106876	ATPase, H+ transporting, lysosomal (vacuolar	13.0
	407727	AW411148	Hs.38044	DKFZP564M082 protein	13.0
70	427706	AW971225	Hs.293800	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	13.0
70	406709	AJ355761	Hs.242463	keralin 8	13.0
•	405353	A18/20 4000	Un 24504	0	13.0 13.0
	453060 459299	AW294092 BE094291	Hs.21594 Hs.155651	ESTs hepatocyte nuclear factor 3, beta	13.0
	459299 447843	AW337186	Hs.224891	ESTs	13.0
75	446576	A1659477	Hs.51820	ESTs, Moderately similar to ALU7_HUMAN ALU SU	13.0
	449700	L02867	Hs.78358	ESTs	13.0
	436476	AA326108	Hs.53631	ESTs	13.0
	432532	AW058459	Hs.162246	ESTs	13.0
00	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	13.0
80	432673	AB028859	Hs.278605	ER-associated DNAJ: ER-associated Hsp40 co-ch	12.9
	414684	AW630023	Hs.76893	3-hydroxybutyrate dehydrogenase (heart, mitoc	12.9 12.9
	447210	AF035269 AW274357	Hs.17752	phosphatidylserine-specific phospholipase A1a Fzr1 protein	12.9
	427923 437395	AL365408	Hs.268384 Hs.10632	hypothetical protein DKFZp762M136	12.9
	401000		1 33. 10002	· in home many are the services	

	441627	AA947552	Hs.58086	ESTs	12.9
	419084	AA496539	Hs.179902	transporter-like protein .	12.9
	423067	AA321355	Hs.285401	ESTs	129
	423070	R55677	Hs.155569	ESTs	12.8
5	441344	BE250144	Hs.41514	ESTs	12.8
•	423527	Al206965	Hs.105861	Homo septens cDNA FLJ13824 fis, clone THYRO10	12.8
	417006	AW673606	Hs.80758	aspartyl-tRNA synthetase	12.8
	453552	AL041941	Hs.154729	3-phosphoinositide dependent protein kinase-1	12.8
	453657	W23237	Hs.296162	ESTs	12.8
10	434414	A1798376	FIS.230 TO2	gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens cDNA	12.7
10			U. 70000		12.7
	456051	T85626	Hs.76239	hypothetical protein FLJ20608	12.7
	451659	BE379761	Hs.14248	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	12.7
	418216	AA662240	Hs.283099	AF15q14 protein	
1.5	423281	AJ271684	Hs.126355	C-type (calcium dependent, carbohydrate-recog	12.7
15	424275	AW673173	Hs.144505	DKFZP566F0546 protein	12.7
	440062	Al350518	Hs.129692	ESTs	12.7
	444371	BE540274	Hs.239	Forkhead box M1	12.7
	412520	AA442324	Hs.795	H2A histone family, member O	12.7
	413349	BE086692		gb:QV1-BT0678-130400-156-g07 BT0678 Homo sapi	12.7
20	414500	W24087	Hs.76285	DKFZP564B167 protein	12.6
	429261	AW176254	Hs.143475	ESTs	12.6
	402238			0	12.6
	400280			0	12.6
	421246	AW582962	Hs.300961	ESTs, Highty similar to AF151805 1 CGI-47 pro	12.6
25	442029	AW956698	Hs.14456	neural precursor cell expressed, developmenta	12.6
	435502	L13266	Hs.105	glutamate receptor, ionotropic, N-methyl D-as	12.6
	409964	AW368226	Hs.67928	ESTs	12.6
		AW382987	Hs.88474	prostaglandin-endoperoxide synthase 1 (prosta	12.5
	418793			Homo sapiens cDNA FLJ12750 fis, clone NT2RP20	12.5
20	452117	A1421760	Hs.77870	1,772	12.5
30	448074	BE621355	Hs.27160	ESTs	
	442655	AW027457	Hs.30323	ESTs	12.5
	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	12.5
	400240			0	12.5
~ ~	413048	M93221	Hs.75182	mannose receptor, C type 1	12.5
35	426215	AW963419	Hs.155223	ESTs	12.5
	430024	AI808780	Hs.227730	integrin, alpha 6	12.5
	445655	AA873830	Hs.167745	B cell linker protein	12.5
	419941	X98654	Hs.93837	phosphatidylinositol transfer protein, membra	12.5
	425280	U31519	Hs.1872	phosphoenolpyruvate carboxykinase 1 (soluble)	12.5
40	427767	AI879283	Hs.180714	cytochrome c oxidase subunit VIa polypeptide	124
	450243	AW119084	Hs.201037	ESTs	12.4
	408930	AA146721	Hs.49005	hypothetical protein	12.4
	418783	T41368	, , , , , ,	gb:ph1d1_19/1TV Outward Alu-primed hncDNA lib	12.4
	452096	BE394901	Hs.226785	ESTs	12.4
45		BE385864	Hs.149894	mitochondrial translational initiation factor	12.4
73	424513				12.4
	422306	BE044325	Hs.227280	Homo sapiens mRNA for Lsm5 protein	12.4
	409031	AA376836	Hs.76728	ESTs	12.4
	435515	N40080	Hs.6879	DC13 protein	
50	429583	NM_006412	Hs.209119	1-acylglycerol-3-phosphate 0-acyltransferase	12.3
50	449643	R05989	Hs.19603	ESTs	12.3
	440313	AL050060	Hs.7158	DKFZP566H073 protein	12.3
	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	12.3
	447357	Al375922	Hs.159367	ESTs	12.3
	405089			0	12.3
55	414972	BE263782	Hs.77695	KIAA0008 gene product	12.3
	435039	AW043921	Hs.130526	ESTs	12.3
	447033	Al357412	Hs.157601	EST - not in UniGene	12.3
	427521	AW973352	Hs.299056	ESTs	12.3
	409377	AA300274	Hs.115659	Homo sapiens cDNA: FLJ23461 fis, clone HSI077	12.3
60	400116			0	12.3
	445806	AL137516	Hs.13323	hypothelical protein FLJ22059	12.2
	457817	AA247751	Hs.79572	cathepsin D (lysosomal aspartyl protease)	12.2
	442410	AW996503	Hs.197680	ESTs	12.2
	445404	A1261687	Hs.145541	ESTs, Weakly similar to JC4974 sodium iodide	12.2
65	403372	AW249152	Hs.44017	SIR2 (silent mating type information regulati	12.2
UJ	427082	AB037858	Hs.173484	hypothetical protein FLJ10337	12.2
					12.2
	433764	AW753676	Hs.39982	ESTs ·	12.2
	400268	1400004	11- 0040	0	12.2
70	433190	M26901	Hs.3210	renin	12.2
70	444863	AW384082	Hs.301323	ESTs	
	434779	AF153815	Hs.50151	potassium inwardly-rectifying channel, subfam	12.2
	451346	NM_006338	Hs.26312	glioma amplified on chromosome 1 protein (leu	12.2
	430262	AA218780	Hs.237323	N-acetylghucosamine-phosphate mutase	12.2
75	421071	Al311238	Hs.104476	ESTs	12.2
75	426773	NM_015556	Hs.172180	KIAA0440 protein	12.1
	409178	BE393948	Hs.50915	kallikrein 5	12.1
	400250			0	12.1
	428450	NM_014791	Hs.184339	KIAA0175 gene product	12.1
	414531	T69387	Hs.76364	allograft inflammatory factor 1	12.1
- 80	448210	AW247775	Hs.7393	hypothetical protein from EUROIMAGE 1987170	12.1
	440081	AA863389	Hs.135643	ESTs	12.1
	413179	N99692	Hs.75227	NADH dehydrogenase (ubiquinone) 1 alpha subco	12.1
	447551	BE066634	Hs.929	myosin, heavy polypeptide 7, cardiac muscle,	12.1
	400517	AF242388	Hs.149585	lengsin	12.1
	400011	272300		- management	

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	401610 454381	A1025000	11- 402422	0 ESTs	12.0 12.0
	443997	Al935093 AW081465	Hs.193428 Hs.299544	ESTs	12.0
_	402944			0	12.0
5	430637	BE160081	Hs.256290	S100 calcium-binding protein A11 (calgizzarin	12.0
	415099	A1492170	Hs.77917	ubiquitin carboxyl-terminal esterase L3 (ubiq	12.0 12.0
	445422 416667	AV653731 AK000526	Hs.282829 Hs.79457	ESTs hypothetical protein FLJ20519	12.0
	442611	BE077155	Hs.177537	ESTs	12.0
10	443271	BE568568	Hs.195704	ESTs	12.0
-	415120	N64464	Hs.34950	ESTs	12.0
	439574	Al469788	Hs.165190	ESTs	12.0 12.0
	405804 412519	AA196241	Hs.73980	0 troponin T1, skeletal, slow .	12.0
15	414135	NM_004419	Hs.2128	dual specificity phosphatase 5	12.0
	447075	AV662037	Hs.124740	ESTs	12.0
	416841	N33878	Hs.249495	heterogeneous nuclear ribonucleoprotein A1	120
	402943	05554050	11- 00000	O and analysis of heaveless relate as hopeful A	11.9 11.9
20	416933 439744	BE561850 AL389994	Hs.80506 Hs.301272	small nuclear ribonucleoprotein polypeptide A ESTs, Weakly similar to homologue of Drosphil	11.9
20	405762	ALD03334	10.001272	0	11.9
	408983	NM_000492	Hs.663	cystic fibrosis transmembrane conductance reg	11.9
	455102	BE005496		gb:CM1-BN0117-110400-183-b09 BN0117 Homo sapi	11.9
25	402840	4141445000	11- 400005	O	11.9 11.9
25	449183 439273	AW445022 AW139099	Hs.196985 Hs.269701	Homo saplens cDNA: FLJ21135 fis, clone CAS072 ESTs	11.9
	450484	BE220675	113.203101	gb:ht98f11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA	11.9
	445431	AF137386	Hs.12701	plasmolipin	11.9
20	401888			0	11.9
30	426037	AW160780	Hs.166071	cyclin-dependent kinase 5	11.9 11.9
	416742 418324	R38544 AW246273	Hs.248420 Hs.84131	ESTs threonyl-IRNA synthetase	11.8
	412870	N22788	Hs.82407	Homo sapiens HSPC296 mRNA, partial cds	11.8
	432680	T47364	Hs.278613	interferon, alpha-inducible protein 27	11.8
35	421478	AI683243	Hs.97258	ESTs	11.8
	426635	BE395109	Hs.129327	ESTs	11.8 11.8
	420523 426227	AA262999 U67058	Hs.42788 Hs.168102	ESTs Hurnan proteinase activated receptor-2 mRNA; 3	11.8
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural arachnod	11.8
40	441816	AI401807	Hs.149997	ESTs	11.8
	424596	AB020639	Hs.151017	estrogen-related receptor gamma	11.8
	400640	A A 7024 E 7	Un 72700	() foliate meaning 1 (adult)	11.8 11.8
	448133 401532	AA723157	Hs.73769	folate receptor 1 (adult) 0	11.8
45	400161			Ŏ	11.8
	442556	AL137761	Hs.8379	Homo sapiens mRNA; cDNA DKFZp586L2424 (from c	11.7
	451002	AA013299	Hs.8018	ESTs, Weakly similar to ALU3_HUMAN ALU SUBFAM	- 11.7
	401879 415989	AI267700	Hs.111128	0 ESTs	11.7 11.7
50	415565	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	11.7
	410616	AW873401	Hs.273599	ESTs	11.7
	449239	T24653	Hs.23360	likely ortholog of yeast ARV1	11.7
	447669	AL049985	Hs.19180	Homo sapiens mRNA; cDNA DKFZp564E122 (from cl	11.7 11.7
55	436877 434560	AA931484 R13052	Hs.121255 Hs.3964	ESTs, Weakly similar to cDNA EST EMBL:D67419 Homo sapiens clone 24877 mRNA sequence	11.7
	448105	AW591433	Hs.170675	ESTs, Weakly similar to TMS2_HUMAN TRANSMEMBR	11.7
	400279			0	11.6
	440497	AA887266	Hs.144979	ESTs .	11.6
60	451260	AW750773	Un 407744	gb:CM0-CN0044-260100-164-h03 CN0044 Homo sapi	11.6
OO	429175 408209	A1953040 NM_004454	Hs.127714 Hs.43697	ets variant gene 5 (ets-related molecule)	11.6
	428856	AA436735	Hs.183171	Homo sapiens cDNA: FLJ22002 fis, clone HEP066	11.6
	420153	N22120	Hs.75277	hypothetical protein FLJ13910	11.6
ĊĖ	428760	Al351459	Hs.192398	ESTs	11.6
65	421401	AW410478	Hs.104019	transforming, acidic coiled-coil containing p	11.6 11.6
	404502 430423	Al190548	Hs.143479	0 ESTs, Weakly similar to hypothetical protein	11.6
	405192			0	11.6
	439092	AA830149		gb:oc44f08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA	11.6
70	401714	4.47.40000	11- 50400	0	11.5 11.5
	439335 406082	AA742697 S47833	Hs.62492 Hs.82927	ESTs, Weakly similar to S59856 collagen alpha adenosine monophosphate deaminase 2 (isoform	11.5
	401010	041000	,	0	11.5
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkinesin6)	11.5
75	409339	AB020586	Hs.54037	ectonucleotide pyrophosphatase/phosphodiester	11.5
	459684	DE05 4000	Un tornen	gb:ao86a08.x1 Schiller meningiorna Homo sapien	11.5 11.5
	451051 415323	BE254309 BE269352	Hs.125262 Hs.949	DKFZP586G1624 protein neutrophil cytosolic factor 2 (65kD, chronic	11.5
	412153	R87934		gb:yo47b10.r1 Soares adult brain N2b4HB55Y Ho	11.5
80	427256	AL042436	Hs.97723	ESTs	11.5
	406708	AI282759	Hs.242463	keratin 8	11.4
	457644	AA770080	Hs.144962 Hs.121483	ESTs, Moderately similar to 159365 ubiquitin chloride channel 1, skeletal muscle (Thomsen	11.4 11.4
	422848 424134	Z25884 AF070637	Hs.140950	hypothetical protein	11.4
				• • • • • • • • • • • • • • • • • • • •	

					44.4
	451931	AK000208	Hs.27267	Homo sapiens cDNA FLJ20201 fis, clone COLF121	11.4
	400438	AF185611	Hs.115352	growth hormone 1	11.4
	412994	D32257	Hs.75113	general transcription factor IIIA	11.4
_	408124	U89337	Hs.42853	cAMP responsive element binding protein-like	11.4
5	452249	BE394412	Hs.61252	ESTs	11.4
	424627	AA344555		gb:EST50715 Gall bladder I Horno sapiens cDNA	11.4
	405626			0	11.4
	436690	AA373970	Hs.183096	ESTs.	11.4
• •	415862	R51034	Hs.144513	ESTs	11.4
10	406755	N80129	Hs.94360	metallothionein 1L	11.4
	433657	A1244368	Hs.8124	PH domain containing protein in retina 1	11.4
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	11.4
	423334	AK000906	Hs.127273	hypothetical protein FLJ10044	11.4
	433053	BE301909	Hs.279952	glutathione S-transferase subunit 13 homolog	11.4
15	428423	AU076517	Hs.184276	solute carrier family 9 (sodium/hydrogen exch	11.3
	442353	BE379594	Hs.49136	ESTs	11.3
	447700	Al420183	Hs.171077	ESTs, Weakly similar to similar to serine/thr	11.3
	402077			0	11.3
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypeptide 1	11.3
20	405145			0	11.3
	428248	Al126772	Hs.40479	ESTs	11.3
	425508	AA991551	Hs.97013	ESTs	11.3
	428340	AF261088	Hs.154721	aconitase 1, soluble	11.3
	431452	Al073641	Hs.152372	ESTs	11.3
25	446651	AA393907	Hs.97179	ESTs .,	11.3
23	443755		Hs.9730	tachykinin 3 (neuromedin K, neurokinin beta)	11.3
		C18397		ESTs, Moderately similar to unnamed protein p	11.3
	436209 401020	AW850417	Hs.254020	Cors, woderately surman to difficulties protestry	11.3
		414047000	Hs.301423	ontainer hinding mentain & (anthroin)	11.2
20	456724	AW247388		calcium binding protein 1 (calibrain)	11.2
30	407227	H94949	Hs.171955	trophinin associated protein (tastin)	11.2
	402066	11045000	11- 404000	0	11.2
	442721	AI015892	Hs.101282	Homo sapiens mRNA; cDNA DKFZp434B102 (from cl	11.2
	401025			0	
25	452423	AA991724	Hs.180535	Homo sapiens cDNA: FLJ22711 fis, done HSI133	11.2
35	431685	AW296135	Hs.267659	vav 3 oncogene	11.2
	425176	AW015644	Hs.301430	ESTs, Moderately similar to TEF1_HUMAN TRANSC	11.2
	435496	AW840171	Hs.265398	ESTs. Weakly similar to transformation-relate	11.2
	409079	W87707	Hs.82065	interlaukin 6 signal transducer (gp130; oncos	11.2
	456995	T89832	Hs.170278	ESTs	11.2
40	419223	X50111	Hs.1244	CD9 antigen (p24)	11.2
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	11.2
	407604	AW191962	Hs.288061	actin, beta	11.2
	437929	T09353	Hs.106642	ESTs, Weakly similar to hypothetical protein	11.1
	415789	H01581		gb:yj33f08.r1 Soares placenta Nb2HP Homo sapi	11.1
45	424447	AL137376	Hs.147368	Homo sapiens mRNA; cDNA DKFZp434J0226 (from c	11.1
	435034	AF282693	Hs.150185	inflammation-related G protein-coupled recept	11.1
	404931			0	11.1
	445979	A1695047	Hs.202395	ESTs	11.1
	446733	AA863360	Hs.26040	ESTs; Highly similar to CYTOCHROME P45 IVA2	11.1
50	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated protein	11.1
•	445258	Al635931	Hs.147613	ESTs	11.1
	417251	AW015242	Hs.99488	ESTs; Wealty similar to ORF YKR074w [S.cerevi	11.1
	421041	N36914	Hs.14691	ESTs	11.1
	425537	AB007913	Hs.158291	KIAA0444 protein	11.1
55	435763	AJ243929	Hs.190419	ESTs	11.1
55	444790 -		Hs.11955	B9 protein	11.1
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	11.1
	433882	U90441	Hs.3622	procollagen-proline, 2-oxoglutarate 4-dioxyge	11,1
	405358	UUV-71	,	0	11.1
60	435814	AW615179	Hs.152870	ESTs	11.0
00	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	11.0
	446772	AW294404	Hs.144515	Homo sapiens cDNA FLJ11672 fis, clone HEMBA10	11.0
	456694	AW016382	Hs.105642	Homo sapiens cDNA: FLJ23271 fis, clone HEP001	11.0
	441128	AA570256	Hs.54628	ESTs	11.0
65				UDP-N-acetyl-alpha-D-galactosamine:polypeptid	11.0
UJ	432677 412576	NM_004482 AA447718	Hs.278611 Hs.107057	ESTs	11.0
				coactivator-associated arginine methyltransfe	11.0
	411122	F00809	Hs.143696		11.0
	427225	AA432391	Hs.258903	Homo sapiens mRNA for KIAA1640 protein, parti	11.0
70	426260	NM_002541	Hs.168669	oxoglutarate dehydrogenase (lipoamide)	11.0
70	444652	BE513613	Hs.11538	actin related protein 2/3 complex, subunit 1A	11.0
	431947	AL359613	Hs.49933	hypothetical protein DKFZp762D1011	11.0
	414432	BE378174	Hs.26506	Homo sapiens clone CDABP0005 mRNA sequence	
	458627	AW088642	Hs.97984	ESTs; Weakly similar to WASP-family protein [	10.9
75	409142	AL136877	Hs.50758	chromosome-associated polypeptide C	10.9
75	447627	AF090922	Hs.285902	CGI-113 protein	10.9
	447656	NM_003726	Hs.19126	src kinase-associated phosphoprotein of 55 kD	10.9
	454227	AW963897	Hs.44743	KIAA1435 protein	10.9
	402927			0	10.9
00	422380	AA309881	Hs.136246	ESTs	10.9
80	455986	BE177736		gb:RC1-HT0598-140300-021-g06 HT0598 Homo sapi	10.9
	410962	BE273749	Hs.752	FK506-binding protein 1A (12kD)	10.9
	450361	BE327108	Hs.202512	ESTs CALLED AND C	10.9
	457484	H57645		gb:yr21e01.r1 Soares fetal liver spleen 1NFLS	10.9
	407903	Al287341	Hs.154029	. bHLH factor Hes4	10.9

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				_	
	403398			0	10.9 10.9
	401405 405570			· ·	10.9
	421240	R72730	Hs.29283	ESTs, Weakly similar to PLK_HUMAN PROTEOGLYCA	10.9
5	403649			0	10.9
	447824	BE620800		gb:601483379T1 NIH_MGC_69 Homo sapiens cDNA c	10.9
	450935	BE514743	Hs.25664	tumor suppressor deteted in oral cancer-relat lysophospholipase-like	10.9 10.9
	439853 · 451852	AL119566 R51928	Hs.6721	obryi71c05.r1 Soares breast 2NbHBst Homo sapi	10.9
10	431218	NM_002145	Hs.2733	homeo box B2	10.9
	457794	AA689292	Hs.246850	ESTs .	10.9
	444374	AA009841	Hs.11039	Homo sapiens cDNA FLJ12798 fis, clone NT2RP20	10.9
	456566 405552	AW235317	Hs.259214	ESTS 0	10.8 10.8
15	405552 439436	BE140845	Hs.57868	ESTs	10.8
10	435310	AA705075	Hs.169536	Rhesus blood group-associated glycoprotein	10.8
	411125	AA151647	Hs.68877	cytochrome b-245, alpha polypeptide	10.8
	415807	H03139	Hs.24683	ESTs	10.8 10.8
20	409430 417033	R21945 H83784	Hs.166975 Hs.40532	splicing factor, arginine/serine-rich 5 ESTs, Weakly similar to PEBP MOUSE PHOSPHATID	10.8
20	418464	R87580	113.40502	gb:ym89h07.r1 Soares adult brain N2b4HB55Y Ho	10.8
	404567			0	10.8
	418384	AW149266	Hs.25130	ESTs	10.8
25	421971	U63127	Hs.110121	SEC7 homolog	10.8 10.8
23	428769 459104	AW207175 R19238	Hs.106771 Hs.282057	ESTs ESTs	10.8
	410896	AW809637	115.202051	qb:MR4-ST0124-261099-015-b07 ST0124 Homo sapi	10.8
	416969	AI815443	Hs.283404	organic cation transporter	10.8
20	408796	AA688292	Hs.118553	ESTs	10.8
30	426298	AW965058	Hs.111583	ESTS	· 10.8 10.8
	421595 408007	AB014520 AW135965	Hs.105958 Hs.246783	Homo sapiens cDNA: FLJ22735 fis, clone HUV001 ESTs	10.8
	400167	, A11100000	113.240700	0	10.7
	445243	Al217439	Hs.109854	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	10.7
35	421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (achondro	10.7
	412241 425827	AW948343		gb:RCO-MT0015-130400-031-c01 MT0015 Homo sapi gb:45b6 Human retina cDNA randomly primed sub	10.7 10.7
	420255	W28316 NM_007289	Hs.1298	membrane metallo-endopeptidase (neutral endop	10.7
	430891	U22492	Hs.248118	G protein-coupled receptor 8	10.7
40	402883			0	10.7
	423811	AW299598	Hs.50895	homeo box C4	10.7 10.7
	447078 414343	AW885727 AL036166	Hs.301570 Hs.75914	ESTs coaled vesicle membrane protein	10.7
	446913	AA430650	Hs.16529	transmembrane 4 superfamily member (tetraspan	10.7
45	452279	AA286844	Hs.61260	hypothetical protein FLJ13164	10.7
	401220			0	10.7
	459259	AJ003294	Ue OCE	gb:AJ003294 Selected chromosome 21 cDNA libra RAP1A, member of RAS oncogene family	10.7 10.7
	414171 448449	AA360328 BE314567	Hs.865 Hs.211440	ESTs	10.7
50	429670	L01087	Hs.211593	protein kinase C, theta	10.7
	446759	R61463	Hs.16165	expressed in activated T/LAK lymphocytes	10.7
	400776	AMEDIEDE	12- 104020	O ESTo	10.7 10.7
	428093 412801	AW594506 AA121055	Hs.104830	ESTs gb:zm22b01.r1 Stratagene pancreas (937208) Ho	10.7
55	440545	AW183201	Hs.190559	ESTs	10.6
-	434540	NM_016045	Hs.5184	TH1 drosophila homolog	10.6
•	414273	BE269057		gb:601184231F1 NiH_MGC_8 Homo sapiens cDNA cl	10.6
	401817	Alakannann	Hs.63489	O amilia turcina abecatatasa nan masatas tu	10.6 10.6
60	410423 430590	AW402432 AW383947	Hs.246381	protein tyrosine phosphatase, non-receptor ty CD68 antigen	10.6
O.O	426680	AA320160	Hs.171811	adenylate kinase 2	10.6
	445413	AA151342	Hs.12677	CGI-147 protein	10.6
	402947			0	10.6
65	457426 424148	AW971119 BE242274	Hs.1741	gb:EST383206 MAGE resequences, MAGL Homo sapi integrin, beta 7	10.6 10.6
05	404944	00242274	165.1741	0	10.6
	405421			Ō	10.6
	416772	AI733872	Hs.79769	protocadherin 1 (cadherin-like 1)	10.6
70	414191	AW250089	Hs.75807 Hs.284171	PDZ and LIM domain 1 (elfin)	10.6 10.6
70	457588 406038	Al571225 Y14443	Hs.88219	KIAA1535 protein zinc finger protein 200	10.6
	404790		10.002.0	0	10.6
	418922	AW956580	Hs.42699	Thrombospondin-1 (Hs.87409)	10.6
75	425940	AB023184	Hs.163990	KIAA0967 protein	10.6
75	448749 418870	AW859679 AF147204	Hs.21902 Hs.89414	Homo sapiens clone 25237 mRNA sequence CXCR4; chemokine CXC receptor 4 (fusin)	10.6 10.5
	417933	X02308	Hs.82962	thymidylate synthetase	10.5
	450538	AW297395	Hs.227052	ESTs	10.5
οΔ	427928	AA417662	Hs.119217	ESTs	10.5
80	432721	AL121478	Hs.3132	steroidogenic acute regulatory protein	10.5 10.5
	429267 439190	AA299290 AW978693	Hs.246857 Hs.293811	ESTs, Highly similar to S71100 protein kinase ESTs	10.5
	408975	AW958693	Hs.49391	hypothetical protein LOC54149	10.5
	415130	W85893	Hs.249867	. ESTs	10.5
				4	

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	105300			Ularra agricus along 24400 - DUA	10.5
	425738 440232	H29630 A1766925	Hs.159408 Hs.112554	Homo sapiens clone 24420 mRNA sequence ESTs	10.5 10.5
	425065	AA371906	Hs.294151	ESTs, Moderately similar to KIAA0544 protein	10.5
_	420829	AW665612	Hs.221969	ESTs	10.5
5	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	10.5 10.5
	407771 444611	AL138272 AK002180	Hs.62713 Hs.11449	ESTs DKFZP564O123 protein	10.5
	444665	BE613126	Hs.47783	ESTs, Weakly similar to T12540 hypothetical p	10.5
10	448030	N30714	Hs.20161	HDCME31P protein	10.5
10	438982	AW979101	Hs.291980	ESTS ESTS	10.5 10.5
	446224 405108	AW450551	Hs.13308	0	10.5
	438233	W52448	Hs.56147	ESTs	10.5
1.5	401799			0	10.5
15	454038	X06374	Hs.37040	platelet-derived growth factor alpha polypept sorbitol dehydrogenase	10.5 10.5
	414222 421828	AL135173 AW891965	Hs.878 Hs.289109	dimethylarginine dimethylaminohydrolase 1	10.5
	422626	AA344932	Hs.118786	metallothionein 2A	10.5
20	449261	AI637592	Hs.224958	ESTs	10.4
20	416218	R21499	Hs.23213	ESTs ESTs; Wealdy similar to D2092.2 [C.elegans]	10.4 10.4
	457848 442577	W26524 AA292998	Hs.125682 Hs.163900	ESTs Tready suring to D2092.2 [C.C.C.C.G.G.G.G.G.G.G.G.G.G.G.G.G.G.G.G	10.4
	406505	AF016272	Hs.115418	cadherin 16, KSP-cadherin	10.4
25	412258	AA376768	Hs.288977	Homo sapiens cDNA: FLJ22622 fis, clone HSI056	10.4
25	429224	AI905780	Hs.198272	NADH dehydrogenase (ubiquinone) 1 beta subcom	10.4 10.4
	447774 403914	BE018118	Hs.19554	chromosome 1 open reading frame 2 0	10.4
	406329			0	10.4
٠.	402423			0	10.4
30	431986	AA536130	Hs.149018	ESTs	10.4 10.4
	423145 414402	BE264548 BE294186	Hs.222190	ESTs, Weakly similar to secretory carrier mem ab:601172959F1 NIH_MGC_17 Homo sapiens cDNA c	10.4
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	10.4
	426095	A1278023	Hs.89986	ESTs	10.4
35	434577	R37316	Hs.179769	Homo sapiens cDNA: FLJ22487 fis, clone HRC109	10.4
	442415 421506	Al005101 BE302796	Hs.129550 Hs.105097	ESTs thymidine kinase 1, soluble	10.3 10.3
	435084	D17516	Hs.301607	adenylate cyclase activating polypeptide 1 (p	10.3
	431724	AA514535	Hs.283704	ESTs	10.3
40	456798	AJ006422	Hs.135183	centaurin-alpha	10.3
	417370	T28651	Hs.82030	tryptophanyl-IRNA synthetase 2-5oligoadenylate synthetase-like	10.3 10.3
	422596 435226	AF063611 AI248938	Hs.118633 Hs.270106	ESTs	10.3
	433192	AB040880	Hs.225594	ESTs, Moderately similar to KIAA1447 protein	10.3
45	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	10.3
	416228	AW505190	Hs.79089	sema domain, immunoglobulin domain (lg), tran	· 10.3 10.3
	453403 447906	BE466639 AL050062	Hs.61779 Hs.19999	Homo sapiens cDNA FLJ13591 fis, clone PLACE10 DKFZP566K023 protein	10.3
	401782	NM_012434	Hs.117865	solute carrier family 17 (anion/sugar transpo	10.3
50	453927	AA082465	Hs.301751	ESTs, Weakly similar to /prediction	10.3
	450737 421633	AW007152 AF121860	Hs.203330 Hs.106260	ESTs sorting nexin 10	10.3 10.3
	409881	AF139799	Hs.202830	ESTs	10.3
-	432883	U48936	Hs.3112	sodium channel, nonvoltage-gated 1, gamma	10.3
55	440099	AL080058	Hs.6909	DKFZP564G202 protein	10.3
	419024	X56411	Hs.1219	alcohol dehydrogenase 4 (class II), pi polype 0	10.3 10.3
	401835 408896	A1610447	Hs.48778 ·	nihan nmtein	10.3
	443120	AW402677	Hs.290801	ESTs	10.3
60	400208			0	10.2
	416908	AA333990	Hs.80424	coagulation factor XIII, A1 polypeptide	10.2 10.2
	400166 434642	W25739	Hs.135287	ESTs	10.2
	424837	BE276113	Hs.153436	N-acetyltransferase, homolog of S. cerevisiae	10.2
65	435075	R51094	Hs.12400	ESTs	10.2
	425912	AL137629	Hs.162189 Hs.155111	serine/threonine kinase with Dbl- and pleckst ESTs	10.2 10.2
	435080 414998	A1831760 NM_002543	Hs.77729	oxidised low density lipoprotein (lectin-like	10.2
	410020	T86315	Hs.728	ribonuclease, RNase A family, 2 (liver, eosin	10.2
70	411410	R20693	Hs.69954	laminin, gamma 3	10.2
	450294	H42587	Hs.238730	ESTs Homo sapiens cDNA FLJ14269 fis, clone PLACE10	10.2 10.2
	421154 414271	AA284333 AK000275	Hs.287631 Hs.75871	protein kinase C binding protein 1	10.2
	400812	- 11 10000010	1-00-0011	0	10.2
75	425843	BE313280	Hs.159627	death associated protein 3	10.2
	449392	Z41698	Hs.26039	Homo sapiens cDNA FLJ13937 fis, clone Y79AA10	10.2
	409089 401383	NM_014781	Hs.50421	KIAA0203 gene product 0	10.2 10.2
	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Drosoph	10.2
80	442912	A1088060	Hs.131450	ESTs	10.2
	400954	D25969	Hs.76325	Homo sapiens cDNA: FLJ23125 fis, clone LNG082	10.2
	401029 416502	BE382701 NM_006159	Hs.25960 Hs.79389	v-myc avian myelocytomatosis viral related on nel (chicken)-like 2	10.2 10.2
	421905	A1660247	Hs.32699	. ESTs, Weakly similar to LIV-1 protein [H.sapi	10.2

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10.2
               405094
                                                                                                                                                                   10.2
                450832
                               AW970602
                                                    Hs.105421
                                                                          ESTs
                                                                          ESTs, Wealty similar to AF151840 1 CGI-82 pro
                                                                                                                                                                   10.2
                440076
                                R32052
                                                    Hs.178617
                                BE536115
                                                    Hs.160983
                                                                                                                                                                   10.2
                447563
   5
                                                                         KIAA1275 protein
                421238
                               AB033101
                                                    Hs.102796
                                                                                                                                                                   10.2
                                                                                                                                                                   10.2
                400882
                                                                          ESTs, Weakly similar to AF220049 1 uncharacte
                                                                                                                                                                   10.1
                               BF539367
                                                    Hs.295953
               415738
               445464
                               AW172389
                                                    Hs.249999
                                                                                                                                                                   10.1
                                                                          ESTs
                                                    Hs.210338
                                                                                                                                                                   10.1
               459042
                               AW272058
10
               414469
                               R51952
                                                    Hs.32587
                                                                          steriod receptor RNA activator 1 (complexes w
                                                                                                                                                                   10.1
                                                                          gb:xx205g05.x1 Soares_fetal_fiver_spleen_1NFLS
ESTs, Weakly similar to p140mDia [M.musculus]
                434732
                               AI078443
                                                                                                                                                                   10.1
                                                    Hs. 174424
                                                                                                                                                                   10.1
                441030
                               AW204139
                               BE616767
                                                                          B-cell CLL/lymphoma 78
                                                    Hs.16269
                                                                                                                                                                   10.1
                446855
                                                                          hypothetical protein
                               AF151074
                                                    Hs.132744
               456785
15
                                                                                                                                                                   10.1
                404182
                                                                          ESTs, Weakly similar to unnamed protein produ
phosphoinositide-3-kinase, catalytic, beta po
Homo saptens cDNA FLJ 13495 fis, clone PLACE10
               410358
                               AW975168
                                                    Hs.13337
                                                                                                                                                                   10.1
                                                    Hs.239818
                430355
                               NM_006219
                                                                                                                                                                   10.1
                                                    Hs.239566
                                                                                                                                                                   10.1
                               R39246
               442152
                                                                          Homo sapiens mRNA; cDNA DKFZp564C2163 (from c
                               AI879252
                                                                                                                                                                   10.1
               436354
                                                    Hs.5151
20
                                                                          conserved gene amplified in osteosarcoma
                                                                                                                                                                   10.1
                426711
                               AA383471
                                                    Hs.180669
                450599
                                AA460865
                                                    Hs.48516
                                                                                                                                                                   10.1
                                                                          gb:PM0-HT0335-180400-008-c08 HT0335 Homo saci
                454393
                               BE153288
                                                                                                                                                                   10.1
                                                                                                                                                                   10.1
                403383
                                                                                                                                                                   10.1
                               U04045
                                                    Hs.78934
                                                                          mutS (E. coli) homolog 2 (colon cancer, nonpo
                415947
25
                               NM_006799
                                                    Hs.72026
                                                                          protease, serine, 21 (testisin)
                                                                                                                                                                   10.1
                411773
                                AW402166
                                                                          Epstein-Barr virus induced gene 2 (lymphocyte
                                                                                                                                                                   10.1
                412116
                                                    Hs.784
                413808
                                J00287
                                                    Hs.182183
                                                                          caldesmon 1
                                                                                                                                                                   10.0
                                                                                                                                                                   10.0
                458572
                               A1223423
                                                    Hs.292794
                                                                          FSTs
                                                                                                                                                                   10.0
                403295
30
                                                                                                                                                                   10.0
                403910
                453400
                               AI991901
                                                    Hs.82590
                                                                          ESTs, Moderately similar to ALU7_HUMAN ALU SU
                                                                                                                                                                   10.0
                406502
                                                                                                                                                                   10.0
                                                                                                                                                                   10.0
                404743
                                                                          gb:601141065F1 NIH_MGC_9 Homo sapiens cDNA d
                412517
                               BE271584
                                                                                                                                                                   10.0
35
                                                                                                                                                                   10.0
                402679
                                                                          gb:CM0-HT0245-031199-085-h05 HT0245 Homo sapi
                455864
                               BE148970
                                                                                                                                                                   10.0
                425734
                                AF056209
                                                    Hs.159396
                                                                          peptidylglycine alpha-amidating monooxygenase
                                                                                                                                                                   10.0
                                                                          Homo sapiens cDNA FLJ12627 fis, clone NT2RM40
                419280
                                W07506
                                                    Hs.283725
                                                                                                                                                                   10.0
                443503
                                AV645438
                                                    Hs.282927
                                                                          ESTs
                                                                                                                                                                   10.0
40
                                AI937547
                                                    Hs.124915
                                                                          Human DNA sequence from clone 380A1 on chromo
                                                                                                                                                                   10.0
                423165
                                                                                                                                                                   10.0
                450206
                                A1796450
                                                    Hs.201600
                                                                          ESTs
                459052
                                AA298812
                                                    Hs.98539
                                                                          ESTs
                                                                                                                                                                   10.0
                456248
                                AL035786
                                                    Hs.82425
                                                                          actin related protein 2/3 complex, subunit 5
                                                                                                                                                                   10.0
                428438
                               NM_001955
AW468397
                                                    Hs.2271
                                                                          Endothelin 1
                                                                                                                                                                   10.0
45
                                                    Hs.100000
                                                                          S100 calcium-binding protein A8 (calgranutin
                                                                                                                                                                   10.0
                456525
                426127
                                1.36983
                                                    Hs.167013
                                                                          dynamin 2
                TABLE 13B:
               Pkey: Unique Eos probeset identifier number
50
                CAT number. Gene cluster number
                Accession: Genbank accession numbers
                                CAT Number
                Pkey
                                                          AW809637 AW809697 AW810554 AW809707 AW809885 AW810000 AW810088 AW809742 AW809816 AW809749 AW809639 AW809722
                410896
                                1226053_1
                                                          AW809836 AW809774 AW810023 AW810013 AW809813 AW809660 AW809728 AW809768 AW809951 AW809657 AW809954
55
                412153
                                1279701 1
                                                          R87934 AW898205 AW896020 AW896035
                                                          AW948343 AW948341 AW902855 AW984737
                412241
                                1284681_1
                412517
                                                          BE271584 AA112511
                                 130281_1
                412801
                                 132825_1
                                                          AA121055 AA330917
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                                                          BE086692 BE087077 BE087072
BE269057 BE513434 BE396654
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                                1363558_1
                                1431911_1
                414273
                414402
                                 1443240_1
                                                          BE294186 BE298975
                                                          C15407 D81769 D61133
                414950
                                 1509777_1
                                                          H01581 H12850 R65905 H13053
R88849 R84573 H50890
                415789
                                 1555357_1
 65
                                1591066_1
                416368
                                                          R87580
                418464
                                 1759038 -2
                                                          T41368 T41369 T41294
                418783
                                 1789791_1
                424627
                                 241724_1
                                                          AA344555 AA344312 AW963070
                425827
                                 256834_1
                                                          W28316 W26507 AA364334
 70
                434371
                                 384839_1
                                                          AA631362 AA631438
                434414
                                                          AI798376 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231
                                38585_1
                                                          AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174
                                                          ATTOTION AND THE AND T
 75
                434732
                                392447_1
                                                          Al078443 AA648102 Al765577 AW974381
                 439092
                                 468554_1
                                                           AA830149 AW978407 M85983 AW503637
                                                           AF086467 W81444 W81445
                 439636
                                 47467_1
  80
                 447824
                                 73861_-1
                                                           BE620800
                                 83645_1
863912 1
                                                          BE220675 AA345621 AA009992
AW750773 AI768154
                 450484
                 451260
                                                           R51928 AI820698 R4B360 AI820694
                                 888359 1
                 451852
                                                           T60298 AI858257 T69667 T67634 T61224 T71537 T68933
                 452101
                                 898742 1
```

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454163
                       1048369_1
                                          AW175997 AW176000 AW175999 AW175994 AW176004 AW175989
                                         BE153283 BE153151 BE152925 AA078302
BE005496 BE005494 AW856324 AW900199
BE148970 BE148975 BE148957 BE148937
BE177736 BE177735 BE177734
           454393
                       115888_1
           455102
                       1253524_1
           455864
                       1377038_1
  5
                       1397521_1
187241_1
           455986
                                          AW748920 AA487506 AA248914 AA780494
           456423
                                         AW971119 AA574265 AA513268
H57645 T19302 AA527038 Z24851 H93171
AW974568 AA661959 AA649572 AA640401 AA640402
           457426
                       336189_1
           457484
                       342113_1
           457705
                       389383 1
10
                                          AJ003294 AJ003315 AJ003293
           459259
                       966269_1
           TABLE 13C:
           Pkey: Unique number corresponding to an Eos probeset
           Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
15
           Strand: Indicates DNA strand from which exons were predicted
           Nt_position: Indicates nucleotide positions of predicted exons
                                                    Nt_position
144324-144429
                                      Strand
20
                        8117686
           400640
                                      Plus
                                                    17982-18115,20297-20456
           400666
                        8118496
                                      Plus
           400776
                         8131651
                                                    103576-103720
                                      Plus
           400812
                         8568711
                                      Plus
                                                    71708-72153
                                                    91446-91603,92123-92265
110431-110708
           400881
400882
                        2842777
2842777
                                      Minus
25
                                      Minus
                         7770576
                                                    173043-173564
           400965
                                      Minus
           401010
                         8117391
                                                    83967-84180
                                      Minus
           401020
                         8117458
                                      Minus
                                                    59085-60227
                                                    179287-179483,181044-181166,181844-182039
4804-5035,5133-5314
           401025
                         8117518
                                      Minus
30
           401047
401131
                         6705887
                                      Minus
                                      Minus
                                                    94802-94987,95804-95887,96323-96487,97596-97826
                         8699812
           401192
                                                    69559-70101
                         9719502
                                      Minus
           401220
                         9929324
                                      Minus
                                                    48079-48279
                                                    155543-157381
69276-69452,69548-69958
           401383
                         6721135
                                      Minus
35
           401405
401519
                         7768126
                                      Minus
                                                    157315-157950
                         6649315
                                      Plus
           401532
                         7798785
                                      Plus
                                                    124414-124950,125050-125418
           401610
                         7705041
                                                     18921-19505
                                      Minus
           401714
                         6715702
                                      Plus
                                                    96484-96681
40
                                                    217235-217356,217621-217873
147802-148251
                                      Plus
Plus
           401735
                         3252819
                         7331447
           401799
           401817
                         7417850
                                      Minus
                                                    45888-46535
           401835
                         7139700
                                      Plus
                                                     142257-142742
           401879
                         8099914
                                      Minus
                                                    101064-102827
189498-190514
45
           401888
                         8516069
                                      Minus
           401897
                         8569218
                                      Plus
                                                    604-767
                                                    135543-136031
           402066
                         6649269
                                      Plus
           402077
                         8117414
                                                    65014-65195
                                      Plus
                                                     122409-122600
           402104
                         8119072
                                      Plus
                                                    24726-24880,26791-27021
40811-42447
50
           402238
                         7690126
                                      Ptus
           402287
                         4559317
                                      Plus
           402389
                                      Minus
                                                    771-972,1571-1683
                         9885999
                                                     110326-110491
            402408
                         9796239
                                       Minus
            402423
                         9796344
                                      Minus
                                                    62487-62664
55
                                                    64925-65073
            402424
                         9796344
                                      Minus
                                                    8615-9103
           402496
                         9797769
                                      Minus
                         7596899
           402520
                                                     171761-171996
                                      Minus
                                                     132079-132216
            402679
                         8113438
                                      Plus
            402840
                         9369121
                                       Minus
                                                     57118-57306
60
            402883
                         9926562
                                       Ptus
                                                     38666-38803,38885-39019,39097-39231,39308-39445
                                                     71919-72049
41261-41443
            402885
                         9926751
                                       Plus
                         R217647
                                       Minus
            402926
                                                     47247-47396
                                       Minus
            402927
                         8217647
                                                     38467-39068
            402943
                         6456831
                                       Ptus
65
            402944
                         9368423
                                       Plus
                                                     110411-110716,111173-111640
                                                     101629-101991
46865-46941,47032-47148
            402947
                         9368458
                                       Minus
            402965
                         9581599
                                       Minus
                                       Plus
Plus
                         3132351
                                                     92097-92864
            403022
                         9180223
                                                     4059-4258
            403121
 70
            403165
                         9838098
                                                     90595-91848
                                       Minus
                                                     22386-22708
            403295
                         8096528
                                       Plus
                         9438267
                                       Minus
                                                     26009-26178
            403381
            403383
                         9438267
                                                     119837-121197
                                       Minus
                         6862689
                                                     13685-14699
            403398
                                       Minus
 75
            403399
                         6684178
                                       Plus
                                                     61841-62145,62367-62756
            403482
403485
403649
                                                     196964-197135
2888-3001,3198-3532,3655-4117
                         9966050
                                       Plus
                         9966528
                                       Plus
                                                     27141-27247
                         8705159
                                       Minus
                         7710710
            403910
                                       Minus
                                                     5761-6188
 80
                         7710730
                                                      72000-72290,72431-72700,72929-73199
            403912
                                        Minus
            403914
                         7417588
                                       Minus
                                                      7431-8472
                                                      18163-18444
            404182
                         4775644
                                       Plus
                                                      56277-56819
            404502
404567
                         7229863
                                       Minus
                         7249169
                                                      101320-101501
                                       Minus
```

	404678	9797204	Plus	115196-115448
	404743	8894169	Minus	120556-120999
	404780	9887810	Minus	175708-175871
	404790	7230958	Plus	38611-38761
5	404931	7342203	Plus	44226-44382
-	404944	6899705	Plus	4256-4581
	405024	7107727	Plus	88500-88697
	405089	8072523	Plus	103182-103973
	405094	8072579	Plus	135587-135758
10	405108	7107890	Minus	135020-135472
	405145	9438278	Plus	37883-38052,38138-38332
	405192	7230070	Plus	115629-116071
	405224	6731245	Minus	14413-15979
	405295	3818412	Plus	56933-57099
15	405353	2811095	Plus	118525-118692
	405358 -	2341017	Minus	18016-18315
	405421	7243869	Minus	97411-97687
	405426	7243900	Minus	37640-37817
	405452	7656638	Minus	93876-94275
20	405484	5922025	Plus	199214-199579,199672-199920,200262-200495
	405552	1552506	Plus	45199-45647
	405570	2808656	Plus ·	98208-98331
	405626	4508116	Minus	89275-89384,92450-92629,97091-97279,98546-98666
	405699	4165331	Plus	100727-100859
25	405762	5931935	Plus	160502-181110
	405802	5924004	Minus	27743-28264
	405804	7274891	Minus	122557-123551
	406329	6982072	Minus	-607903-608271
••	406429	9256476	Minus	83206-83365,94051-94193
30	406502	7711350	Minus	63430-63602

Table 14A lists about 695 genes up-regulated in ovarian cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03
GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 4.0. The "average" ovarian cancer level was set to the 90th percentile amongst various ovarian cancers. The "average" normal adult tissue level was set to the 90th percentile amongst various non-matignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-matignant tissues was subtracted from both the numerator 35 and the denominator before the ratio was evaluated.

TABLE 14A: ABOUT 695 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES

40

45

Pkey: Primekey
Ex. Acon: Exemplar Accession
UG ID: UniGene ID
Title: UniGene title
ratio: ratio of tumor vs. normal tissues

43				•	
	Pkey	Ex. Acon	UGID	Title	ratio
•	452838	U65011	Hs.30743	Preferentially expressed antigen in melanoma	70.4
	438817	A1023799	Hs.163242	ESTs	62.8
	432938	T27013	Hs.3132	steroidogenic acute regulatory protein .	57.8
50	421478	AI683243	Hs.97258	ESTs	45.7
	415989	Al267700	Hs.111128	ESTs	42.7
	418179	X51630	Hs.1145	Wilms tumor 1	36.0
	449034	A1524049		gb:ts41a09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone	34.0
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	30.5
55	428153	AW513143	Hs.98367	hypothetical protein FLJ22252 similar to SRY-box c	30.1
	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular matrix protei	29.4
	427585	D31152	Hs.179729	collagen; type X; alpha 1 (Schmid metaphyseal chon	27.0
	435094	Al560129	Hs.277523	EST	26.2
	430691	C14187	Hs.103538	ESTs	26.2
60	430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDNA clone EU	26.1
	415511	Al732617	Hs.182352	ESTs	24.8
	448243	AW369771	Hs.77496	ESTs	24.7
	428187	AI687303	Hs.285529	ESTs	23.9
	408081	AW451597	Hs.167409	ESTs	21.9
65	418007	M13509	Hs.83169	Matrix metalloprotease 1 (interstitial collagenase	20.6
	400292	AA250737	Hs.72472	BMPR-lb; bone morphogenetic protein receptor, typ	20.6
	422956	BE545072	Hs.122579	ESTs	20.0
	413335	Al613318	Hs.48442	ESTs	19.9
<b>30</b>	. 423739	AA398155	Hs.97600	ESTs	18.9
70	410929	H47233	Hs.30643	ESTs	18.5
	424086	Al351010	Hs.102267	lysyl oxidase	17.7
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related kinase 2	17.4
	427356	AW023482	Hs.97849	ESTs	17.4
76	407168	R45175		gb:yg40f01.s1 Soares infant brain 1NIB Homo sapien	17.1
75	407638	AJ404672	Hs.288693	EST	17.1
	427469	AA403084	Hs.269347	ESTs	17.0
	438993	AA828995		integrin; beta 8	16.7
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	16.5
00	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDNA clone EU	16.5
80	421155	H87879	Hs.102267	lysyl oxidase	16.1
•	426635	BE395109	Hs.129327	ESTs	15.9
	431989	AW972870	Hs.291069	ESTs	15.9
	422805	AA436989	Hs.121017	H2A histone family; member A	15.9
	444783	AK001468	Hs.62180	. ESTs	15.8

	424581	M62062	Hs.150917	catenin (cadherin-associated protein), alpha 2	15.7
	453197	AI916269	Hs.109057	ESTs, Wealty similar to ALU5_HUMAN ALU SUBFAMIL	15.7
	459325	AW088369	Hs.282184	ESTs	15.6
_	428976	AL037824	Hs.194695	ras homolog gene family, member I	15.1
5	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolog)-li	15.0
	408660	AA525775	Hs.292523	ESTs	15.0
	410247	AF181721	Hs.61345	RU2S	15.0
	418738	AW388633	Hs.6682	solute carrier family 7, member 11	15.0
	459583	AI907673		gb:IL-BT152-080399-004 BT152 Homo sapiens cDNA, mR	14.8
10	413623	AA825721	Hs.246973	ESTs	14.8
	439706	AW872527	Hs.59761	ESTs	14.7
	409041	AB033025	Hs.50081	KIAA1199 protein	14.6
	451110	AI955040	Hs.301584	ESTs	14.5
	436775	AA731111	Hs.291891	ESTs	14.3
15	443211	AI128388	Hs.143655	ESTs	14.3
13	445258	AI635931	Hs.147613	ESTs	14.2
				ESTs; HER4 (c-erb-B4)	14.2
	447350	Al375572	Hs.172634	INTERFERON-GAMMA INDUCED PROTEIN PRECURS	14.1
	428227	AA321649	Hs.2248		13.9
20	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	13.7
20	447033	Al357412	Hs.157601	EST - not in UniGene	
	423811	AW299598	Hs.50895	homeo box C4	13.7
	452461	N78223	Hs.108106	transcription factor	13.7
	451106	BE382701	Hs.25960	N-тус	13.6
25	416208	AW291168	Hs.41295	ESTs	13.5
25	452249	BE394412	Hs.61252	ESTs -,	13.4
	452055	Al377431	Hs.293772	ESTs	13.2
	439243	AA593254	Hs.191349	ESTs	13.1
	420149	AA255920	Hs.88095	ESTs	12.9
••	429125	AA446854	Hs.271004	ESTs	12.9
30	413597	AW302885	Hs.117183	ESTs	12.8
	416566	NM_003914	Hs.79378	cyclin A1	12.8
	442438	AA995998		gb:os26b03.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clon	12.7
	407710	AW022727	Hs.23616	ESTs	12.6
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	12.6
35	428392	H10233	Hs.2265	secretory granule, neuroendocrine protein 1 (7B2 p	12.4
	431725	X65724 .	Hs.2839	Norrie disease (pseudoglioma)	12.3
	447700	Al420183	Hs.171077	ESTs, Weakly similar to similar to serine/threonin	12.2
	458027	L49054	Hs.85195	ESTs, Highly similar to U(3;5)(q25.1;p34) fusion g	12.2
	408460	AA054726	Hs.285574	ESTs	12.2
40	424735	U31875	Hs.152677	short-chain alcohol dehydrogenase family member	12.0
	415263	AA948033	Hs.130853	ESTs	11.9
	400298	AA032279	Hs.61635	STEAP1	11.8
	452096	BE394901	Hs.226785	ESTs	11.7
	421451	AA291377	Hs.50831	ESTs	11.6
45			Hs.265398	ESTs, Weakly similar to transformation-related pro	11.6
73	435496 443715	AW840171 Al583187			11.5
			Hs.9700	cyclin E1	11.5
	402606	#(NOCAT)	Un 120425	CCT.	11.5
	436954	AA740151	Hs.130425	ESTs	11.5
50	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affinity gluta	
JU	410102	AW248508	Hs.279727	ESTs;	11.4
	408562	Al436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein, partial cd	11.4
	452030	AL137578	Hs.27607	Homo sapiens mRNA; cDNA DKFZp564N2464 (from clon	11.4
	442353	BE379594	Hs.49136	ESTs	11.3
55	427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3A	11.2
23	453160	Al263307	Hs.146228	ESTs	11.2
	426427	M86699	Hs.169840	TTK protein kinase	11.1
	449433	A1672096	Hs.9012	ESTs	11.1
	412723	AA648459	Hs.179912	ESTs	11.1
60	400250			0	11.1
ov	419752	AA249573	Hs.152618	ESTs	11.1
	438167	R28363	Hs.24286	ESTs	11.1
	434539	AW74807B	Hs.214410	ESTs	10.9
•	429918	AW873986	Hs.119383	ESTs	10.8
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain 12 (mel	10.8
65	400289	X07820	Hs.2258	Matrix Metatloproteinase 10 (Stromolysin 2)	10.8
	420900	AL045633 .	Hs.44269	ESTs	10.8
	428758	AA433988	Hs.98502	Homo sapiens cDNA FLJ14303 fis, clone PLACE2000132	10.8
	446142	AI754693	Hs.145968	ESTs	10.7
	421285	NM_000102	Hs.1363	cytochrome P450, subfamily XVII (steroid 17-alpha-	10.6
70	433496	AF064254	Hs.49765	VERY-LONG-CHAIN ACYL-COA SYNTHETASE	10.6
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	10.5
	433447	U29195	Hs.3281	neuronal pentraxin II	10.4
	424188	AW954552	Hs.142634	zinc finger protein	10.4
	414245	BE148072	Hs.75850	WAS protein family, member 1	10.3
75	426462	U59111	Hs.169993	dermatan sulphate proteoglycan 3	10.3
-	418601	AA279490	Hs.86368	calmegin	10.3
	444170	AW613879	Hs.102408	ESTs	10.3
	453616		Hs.33846	dynein, axonemal, light intermediate polypeptide	10.3
	407378			gb:EST11752 Uterus Homo sapiens cDNA 5 end simila	10.2
80	440901		Hs.128612	ESTs	10.2
	407366			gb:Homo sapiens cig33 mRNA, partial sequence.	10.2
	415227	AW821113	Hs.72402	ESTs	10.2
	409269		Hs.22972	Homo saptens cDNA FLJ13352 fts, clone OVARC1002165	10.1
	450480		Hs.25040	zinc finger protein 239	10.1
	100400			·	

	440000	AIPOOROS	11	ESTA	40.0
	419088	AJ538323	Hs.77496	ESTS	10.0 9.9
	453922 428253	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1 (yeast hom Homo sapiens mRNA; cDNA DKFZp586C1021 (from clone	9.8
	426471	AL133640 M22440	Hs.183357 Hs.170009	transforming growth factor, alpha	9.8
. 5	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-0-sulfotransferase	9.7
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae, homolo	9.7
	445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	9.7
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequence	9.6
10	423992	AW898292	Hs.137206	Homo sapiens mRNA; cDNA DKFZp564H1663 (from clon	9.6
10	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkinesin6)	9.6
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphorylation regu	9.6
	438209	AL120659 NM_005754	Hs.6111	KIAA0307 gene product Ras-GTP ase-activating protein SH3-domain-binding p	9.5 9.5
	429782 424945	Al221919	Hs.220689 Hs.173438	hypothetical protein FLJ10582	9.5
15	414972	BE263782	Hs.77695	KIAA0008 gene product	9.4
13	439262	AA832333	Hs.124399	ESTs	9.4
	403381	#(NOCAT)	1.2.1.2.1000	0	9.3
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP2003117	9.3
	435509	AI458679	Hs.181915	ESTs	9.3
20	445413	AA151342	Hs.12677	CGI-147 protein	9.2
	414083	AL121282	Hs.257786	ESTs	9.2
	421373	AA808229	Hs.167771	ESTs	9.2
	430510	AW162916	Hs.241576	hypothetical protein PRO2577	9.1
25	446999	AA151520	Hs.279525	hypothetical protein PRO2605	9.1 9.1
25	459587 414569	AA031956	Hs.118258	gb:zk15e04.ş1 Soares_pregnant_uterus_NbHPU Homo sa Prostate cancer associated protein 1	9.1
	406687	AF109298 M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	9.0
	428479	Y00272	Hs.184572	cell division cycle 2. G1 to S and G2 to M	9.0
	408908	BE296227	Hs.48915	serine/ihreonine kinase 15	9.0
30	431548	AJ834273	Hs.9711	Homo sapiens cDNA FLJ13018 fis, clone NT2RP3000685	9.0
	433764	AW753676	Hs.39982	ESTs	9.0
	434636	AA083764	Hs.241334	ESTs	8.9
	451807	W52854	Hs.27099	DKFZP564J0863 protein	8.8
26	437872	AK002015	Hs.5887	RNA binding motif protein 7	8.8
35	443054	Al745185	Hs.8939	yes-associated protein 65 kDa	8.8
	420092	AA814043	Hs.88045	ESTs	8.8
	420159	AI572490	Hs.99785	ESTS	8.8 8.8
	447164 451254	AF026941 AI571016	Hs.17518 Hs.172967	Homo sapiens cig5 mRNA, partial sequence ESTs	8.8
40	432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-a	8.7
40	450434	AA166950	Hs.18645	ESTs, Weakly similar to partial CDS [C.elegans]	8.7
	400301	X03635	Hs.1657	Estrogen receptor 1	8.7
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfotransferase	8.7
	434891	AA814309	Hs.123583	ESTs	8.7
45	436812	AW298067		gb:UI-H-BW0-ajp-g-09-0-UI.s1 NCI_CGAP_Sub6 Homo s	8.7
	438885	AI886558	Hs.184987	EST8	8.7
	449765	N92293	Hs.206832	EST, Moderately similar to ALUS_HUMAN ALU SUBFAM	8.7
	447342	AJ199268	Hs.19322	ESTS; Weakly similar to IIII ALU SUBFAMILY J WARNI	8.6 8.6
50 •	434424 438078	AI811202	Hs.125365	Homo sapiens cDNA: FLJ23523 fis, clone LNG05548	8.6
50	437212	Al016377 Al765021	Hs.131693 Hs.210775	ESTs ESTs	8.5
	417728	AW138437	Hs.24790	KIAA1573 protein	8.5
	438081	H49546	Hs.298964	ESTs	8.5
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	8.4
55	435663	AI023707	Hs.134273	EŜTs	8.4
	424717	H03754	Hs.152213	wingless-type MMTV integration site family, member	8.4
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxygenase COOH	8.4
	450505	NM_004572	Hs.25051	plakophilin 2	8.4
60	436211	AK001581	Hs.80961	polymerase (DNA directed), gamma	8.3
60	436396		Hs.299112	Homo sapiens cDNA FLJ11441 fis, clone HEMBA1001323	8.3 8.3
	425695	NM_005401 AA808189	Hs.159238	protein tyrosine phosphatase, non-receptor type 14 ESTs	8.2
	438180 447268	Al370413	Hs.272151 Hs.36563	Homo sapiens cDNA: FLJ22418 fis, ctone HRC08590	8.2
	433159	AB035898	Hs.150587	kinesin-like protein 2	8.1
65	400195			0	8.1
••	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3' untransla	8.1
	438202	AW169287	Hs.22588	ESTs	8.1
	438915	AA280174	Hs.23282	ESTs	8.1
70	448776	BE302464	Hs.30057	transporter similar to yeast MRS2	8.1
70	453884	AA355925	Hs.36232	KIAA0186 gene product	8.0
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone receptor, t	8.0
	439759		Hs.67709	Homo sapiens mRNA full length insert cDNA ctone EU	8.0
	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	8.0 8.0
75	424001	W67883 RE177404	Hs.137476	KIAA1051 protein gb:RC6-HT0596-270300-011-C05 HT0596 Homo sapiens c	8.0
, 5	434415 417576		Hs.82285	phosphoribosylglycinamide formyltransferase, phosp	7.9
	438956			gb:EST391184 MAGE resequences, MAGP Homo sapiens c	7.9
	415245		Hs.27252	ESTs	7.9
••	422352		Hs.99200	ESTs	7.9
80	425492		Hs.158174	zinc finger protein 184 (Kruppel-like)	7.8
	442655	AW027457	Hs.30323	ESTs	7.8
	445657		Hs.279575	ESTs	7.8
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	7.8
	426320	W47595	Hs.169300	transforming growth factor, beta 2	7.8

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	414142	AW368397	Hs.150042	ESTs	7.7
	412170	D16532	Hs.73729	very low density lipoprotein receptor	7.6
	410011 436476	AB020641 AA326108	Hs.57856 Hs.53631	PFTAIRE protein kinase 1 ESTs	7.6 7.6
5	414132	AI801235	Hs.48480	ESTs	7.6
_	437789	AI581344	Hs.127812	ESTs, Weakly similar to AF141326 1 RNA helicase HD	7.6
	450192	AA263143	Hs.24596	RAD51-interacting protein	7.6
	449328	AI962493	Hs.197647	ESTs	7.5
	440238	AW451970	Hs.155644	paired box gene 2	7.5
10	403657	#(NOCAT)		0	7.5
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	7.5
	418735	N48769	Hs.44609	ESTs	7.5
	413627	BE182082	Hs.246973	ESTs	7.4
15	446293	AI420213	Hs.149722	ESTs	7.4 7.4
13	441627 425465	AA947552	Hs.58086 Hs.1904	ESTs	7.3
	409242	L18954 AL080170	Hs.51692	protein kinase C; iota DKFZP434C091 protein	7.3
	450262	AW409872	Hs.271166	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFA	7.3
	440250	AA876179	Hs.134650	ESTs	7.3
20	451659	BE379761	Hs.14248	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMIL	7.3
	458861	Al630223		gb:ad06g08.r1 Proliferating Erythroid Cells (LCB:a	7.3
•	435032	AA150797	Hs.109276	latexin protein	7.2
	407771	AL138272	Hs.62713	ESTs	7.2
0.5	435039	AW043921	Hs.130526	ESTs	7.2
25	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane glycoprote	7.2
	407829	AA045084	Hs.29725	Homo sapiens cDNA FLJ13197 fis, done NT2RP3004451	7.2
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblastoma cells	7.2
	404253 424120	#(NOCAT)	U= 200270	0 ESTs	7.1 7.1
30	429126	T80579 AW172356	Hs.290270 Hs.99083	ESTs	7.1
50	413573	A1733859	Hs.149089	ESTs	7.1
	421464	AA291553	Hs.190086	ESTs	7.0
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 20kD	7.0
	437938	A1950087		ESTs; Weakly similar to Gag-Pol polyprotein [M.mus	7.0
35	420362	U79734	Hs.97206	huntingtin interacting protein 1	7.0
	444743	AA045648	Hs.11817	nudix (nucleoside diphosphate linked moiety X)-typ	7.0
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 TFPI2	6.9
	410568	AW162948	Hs.64542	pre-mRNA cleavage factor Im (68kD)	6.9
40	429418	Al381028	Hs.99283	ESTs	6.9
40	409178	BE393948	Hs.50915	kallikrein 5	6.9
	446608	N75217	Hs.257846	ESTs	6.9 6.9
	425905 428532	AB032959 AF157326	Hs.161700 Hs.184786	KIAA1133 protein TBP-Interacting protein	6.9
	433426	H69125	Hs.133525	ESTs	6.9
45	431322	AW970622	110.100025	gb:EST382704 MAGE resequences, MAGK Homo sapiens	6.8
	437960	Al669586	Hs.222194	ESTs	6.8
	423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR motif, Y is	6.8
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40kD)	6.8
<b>50</b>	448674	W31178	Hs.154140	ESTs	6.8
50	438122	A1620270	Hs.129837	ESTs	6.B
	440048	AA897461	Hs.158469	ESTs. Weakly similar to envelope protein [H.sapien	6.7
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (melanoma, p1	6.7
	407162	N63855	Hs.142634	zinc finger protein	6.7 6.7
55	410804 424639	U64820 AI917494	Hs.66521 Hs.131329	Machado-Joseph disease (spinocerebellar ataxia 3, ESTs	6.7
55	432415	T16971	Hs.289014	ESTs	6.7
	421470	R27496	Hs.1378	annexin A3	6.7
	445459	AJ478629	Hs.158465	ESTs	6.7
	418203	X54942	Hs.83758	CDC28 protein kinase 2	6.6
60	432809	AA565509	Hs.131703	ESTs	6.6
	409234	AI879419	Hs.27206	ESTs	6.6
	438394	BE379623	Hs.27693	CGI-124 protein	6.6
	452097	AB002364	Hs.27916	ADAM-TS3; a disintegrin-like and metalloproteas	6.6
65	453745	AA952989	Hs.63908	Homo sapiens HSPC316 mRNA, partial cds	6.6
65	414136	AA812434	Hs.178227	ESTs	6.6
	423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	6.6 6.6
	454018	AW016892	Hs.241652	ESTs ESTs	6.5
	452281 424620	T93500 AA101043	Hs.28792 Hs.151254	kaliikrein 7 (chymotryptic; stratum comeum)	6.5
70	452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transporter), me	6.5
	434149	Z43829	Hs.19574	ESTs, Weakly similar to katanin p80 subunit [H.sap	6.5
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	6.4
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	6.4
7.	409517	X90780	Hs.54668	troponin I, cardiac	6.4
75	432666		Hs.129250	ESTs, Wealdy similar to unnamed protein product [H	6.4
	448706		Hs.21814	class II cytokine receptor ZCYTOR7	6.4
	429163		11	gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDN	6.4
	413582		Hs.71331	Homo sapiens cDNA: FLJ21971 fis, clone HEP05790	6.4
80	419917		Hs.93701	Homo saptens mRNA; cDNA DKFZp434E232 (from clone	6.4 6.4
JU	424153 434265		Hs.141496 Hs.130554	MAGE-like 2 Homo sapiens cDNA: FLJ23089 fis, clone LNG07061	6.4
	434203		Hs.186104	Homo sapiens cDNA FLJ13803 fis, clone THYRO1000187	6.4
	441081		Hs.169006	ESTs, Moderately similar to plakophilin 2b (H.sapi	6.4
	443539		Hs.134074	ESTs	6.4

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	443830	Al142095	Hs.143273	ESTs	6.4
	452606	N45202	Hs.90012	Homo sapiens cDNA: FLJ23441 fis, clone HSI00612	6.4
	418384	AW149266	Hs.25130	ESTs	6.3
_	425371	D49441	Hs.155981	mesothelin	6.3
5	429441	AJ224172	Hs.204096	(ipophilin B (uteroglobin family member), prostate	6.3
•	449048	Z45051	Hs.22920	similar to \$68401 (cattle) glucose induced gene	6.3
	. 437117	AL049256	Hs.122593	ESTs	6.3
	449579	AW207260	Hs.134014	prostate cancer associated protein 6	6.3
	453370	A1470523	Hs.182356	ESTs, Moderately similar to translation initiation	6.3
10					6.3
10	426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteogenic protein 1	
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	6.3
	408155	AB014528	Hs.43133	KIAA0628 gene product	6.2
	452904	AL157581	Hs.30957	Homo sapiens mRNA; cDNA DKFZp434E0626 (from clone	6.2
	439138	A1742605	Hs.193696	ESTs	6.2
15	457030	Al301740	Hs.173381	dihydropyrimidinase-like 2	6.2
	436281	AW411194	Hs.120051	ESTs	6.1
	407385	AA610150	Hs.272072	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFA	6.1
	406815	AA833930	Hs.288036	IRNA isopentenylpyrophosphate transferase	6.1
	430437	Al768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PLACE1008369	6.1
20			Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (from clone	6.1
20	428743	AL080060			6.1
	415139	AW975942	Hs.48524	ESTs	6.1
	417404	NM_007350	Hs.82101	.pleckstrin homotogy-like domain, family A, member	
	433527	AW235613	Hs.133020	ESTs	6.1
0.0	449448	D60730	Hs.57471	ESTs ·	6.1
25	457733	AW974812	Hs.291971	ESTs	6.1
	457979	AA776655	Hs.270942	ESTs	6.1
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein	6.0
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transaminase 1	6.0
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phosphate), membe	6.0
30	412733	AA984472	Hs.74554	KIAA0080 protein	6.0
50	422095	AI858872	Hs.288966	ceruloplasmin (ferroxidase)	6.0
			Hs.295901	ESTs	6.0
	449347	AV649748			
	440870	Al687284	Hs.150539	Homo saplens cDNA FLJ13793 fis, clone THYRO1000085	6.0
25	437478	AL390172	Hs.118811	ESTs	6.0
35	411598	BE336654	Hs.70937	H3 histone family, member K	6.0
	418134	AA397769	Hs.86617	ESTs	6.0
	418845	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alpha)	6.0
	452039	A1922988	Hs.172510	ESTs	6.0
	410555	U92649	Hs.64311	a disintegrin and metalloproteinase domain 17 (turn	5.9
40	412719	AW016610	Hs.129911	ESTs	5.9
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PLACE1009150	5.9
	437099	N77793	Hs.48659	ESTs, Highly similar to LMA1_HUMAN LAMININ ALPH	5.9
	453431	AF094754	Hs.32973	glycine receptor, beta	5.9
					5.9
45	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane protein 2	5.9
43	417866	AW067903	Hs.82772	"collagen, type XI, alpha 1"	
	420440	NM_002407	Hs.97644	mammaglobin 2	5.9
	430291	AV660345	Hs.238126	CGI-49 protein	5.9
	405547	#(NOCAT)		0	5.9
~^	427510	Z47542	Hs.179312	small nuclear RNA activating complex, polypeptide	5.9
50	435793	AB037734	Hs.4993	ESTs	5.8
	427975	AI536065	Hs.122460	ESTs	5.8
	428949	AA442153	Hs.104744	ESTs, Wealdy similar to AF208855 1 BM-013 [H.sapie	5.8
	452693	T79153	Hs.48589	zinc finger protein 228	5.8
	440138	AB033023	Hs.6982	hypothetical protein FLJ10201	5.8
55	421246	AW582962	Hs.300961	ESTs, Highly similar to AF151805 1 CGI-47 protein	5.8
55	445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	5.8
		AA262105	Hs.4094	Homo sapiens cDNA FLJ14208 fis, clone NT2RP3003264	5.8
	448186				5.6 5.7
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	
60	419335	AW960146	Hs.284137	Homo sapiens cDNA FLJ12888 fis, clone NT2RP2004081	5.7
60	420637	AW976153		gb:EST388262 MAGE resequences, MAGN Homo sapians	5.7
	431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone ADKA01954	5.7
	446868	AV660737	Hs.135100	ESTs	5.7
	452971	A1873878	Hs.91789	ESTs	5.7
	428927	AA441837	Hs.90250	ESTs .	5.7
65	425282	AW163518	Hs.155485	huntingtin interacting protein 2	5.7
	419247	\$65791	Hs.89764	fragile X mental relardation 1	5.7
		AW969626		ESTs, Weakly similar to KIAA0227 [H.sapiens]	5.7
	445640 422938	NM_001809	Hs.31704 Hs.1594	centromere protein A (17kD)	5.6
70	447078	AW885727	Hs.301570	ESTs	5.6
70	421247	BE391727	Hs.102910	general transcription factor IIH, polypeptide 4 (5	5.6
	407896	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophila homolog	5.6
	436556	Al364997	Hs.7572	ESTs	5.6
	417830	AW504786	Hs.132808	epithelial cell transforming sequence 2 oncogene	5.6
	429826	N93266	Hs.40747	ESTs	5.6
75	432030	A1908400	Hs.143789	ESTs	5.6
	443270		Hs.9192	Homer, neuronal immediate early gene, 18	5.5
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALUB_HUMAN ALU SUBFAMIL	5.5
	411096		Hs.68583	mitochondrial intermediate peptidase	5.5
				ESTs	5.5
QΛ	419558		Hs.278394		
80	427386		Hs.177486	amyloid beta (A4) precursor protein (protease nexi	5.5
	427961		Hs.143134	ESTs	5.5
	404561			0	5.5
	429682		Hs.211602	SMC1 (structural maintenance of chromosomes 1, yea	5.5
	407216	N91773	Hs.102267	, tysyl oxidase	5.5

	410658	AW105231	Hs.192035	ESTs RAB11A, member RAS oncogene family	5.5 5.5
	413930 414315	M86153 Z24878	Hs.75618	gb:HSB65D052 STRATAGENE Human skeletal muscle cD	5.5
_	427878	C05766	Hs.181022	CGI-07 protein	5.5
5	431041	AA490967	Hs.105276	ESTs	5.5
	441645	A1222279	Hs.201555	ESTs	5.5
	428071 436406	AF212848 AW105723	Hs.182339 Hs.125346	transcription factor ESE-3B ESTs	5.4 5.4
	429181	AW979104	Hs.294009	ESTs	5.4
10	410909	AW898161	Hs.53112	ESTs, Weakly similar to ALUB_HUMAN ALU SUBFAMIL	5.4
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, done NT2RP2000814	5.4
	451996	AW514021	Hs.245510	ESTs	5.4 5.4
	449318 441433	AW236021 AA933809	Hs.108788 Hs.42746	ESTs, Weakly similar to zeste [D.melanogaster] ESTs	5.4
15	445495	BE622641	Hs.38489	ESTs	5.4
	410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone NT2RM4002571	5.4
	442611	BE077155	Hs.177537	ESTs	5.4
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced protein 6	5.4 5.4
20	453161 419948	AA628608 AB041035	Hs.61656 Hs.93847	ESTs NADPH oxidase 4	5.3
20	427718	AI798680	Hs.25933	ESTs	5.3
	453867	AI929383	Hs.108196	HSPC037 protein	5.3
	422634	NM_016010	Hs.118821	CGI-62 protein	5.3
25 ·	444478	W07318	Hs.240	M-phase phosphoprotein 1	5.3 5.3
23	428002 443486	AA418703 NM_003428	Hs.9450	gb:zv98c03.ş1 Soares_NhHMPu_S1 Homo sapiens cDNA c zinc finger protein 84 (HPF2)	5.3
	451177	Al969716	Hs.13034	ESTs	5.3
	408298	AI745325	Hs.271923	ESTs; Moderately similar to IIII ALU SUBFAMILY SB2	5.3
20	435867	AA954229	Hs.114052	ESTs	5.3
30	423698 448543	AA329796 AW897741	Hs.1098 Hs.21380	DKFZp434J1813 protein Homo sapiens mRNA; cDNA DKFZp586P1124 (from clone	5.3 5.3
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone CAE06654	5.3
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	5.3
25	433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMAN ALU SUBFA	5.3
35	449532	W74653	Hs.271593	ESTS	5.3 5.3
,	452822 437641	X85689 AA811452	Hs.288617 Hs.291911	Homo saplens cDNA: FLJ22621 fis, clone HSi05658 ESTs	5.2
	418379	AA218940	Hs.137516	fidgetin-like 1	5.2
40	416530	U62801	Hs.79351	kallikrein 6 (neurosin, zyme)	5.2
40	433589	AA886530	Hs.188912	ESTs	5.2
	409143	AW025980	Hs.138965	ESTs Homo sapiens cDNA FLJ12900 fis, clone NT2RP2004321	5.2 5.2
	410303 413384	AA324597 NM_000401	Hs.21851 Hs.75334	exostoses (multiple) 2	5.2
	424698	AA164366	Hs.151973	hypothetical protein FLJ10378	5.2
45	431229	AA496479		gb:zv37h05.r1 Soares ovary tumor NbHOT Homo sapien	5.2
	433377	AJ752713	Hs.43845	ESTs	5.2 5.2
	445236 406367	AK001676 #(NOCAT)	Hs.12457	hypothetical protein FLJ10814 0	5.2
	442500	AJ819068	Hs.209122	ESTs	5.2
50	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	5.2
	419140	A1982647	Hs.215725	ESTs .	5.2 5.2
	411078 423020	Al222020 AA383092	Hs.182364 Hs.1608	ESTs, Wealdy similar to 25 kDa trypsin inhibitor ( replication protein A3 (14kD)	5.2 5.2
	427061	AB032971	Hs.173392	KIAA1145 protein	5.2
55	439042			gb:EST391282 MAGE resequences, MAGP Homo sapiens c	5.2
	452930		Hs.194097	ESTs	5.2
	417791	AW965339	Hs.111471	ESTS	5.1 5.1
	433277 447835	W27266 AW591623	Hs.151010 Hs.164129	ESTs ESTs	5.1
60	434401	AI864131	Hs.71119	Putative prostate cancer tumor suppressor	5.1
	437496		Hs.170144	Homo sapiens mRNA; cDNA DKFZp547J125 (from clone D	5.1
	418849		Hs.53565	ESTs, Weakly similar to 80491.1 [C.elegans]	5.1
	428093 408621		Hs.104830 Hs.46638	ESTs chromosome 11 open reading frame 8; fetal brain (	5.1 5.1
65	453096		Hs.11325	ESTs	5.1
-	418852		Hs.273294	hypothetical protein FLJ20069	5.1
	436787		Hs.192756	ESTs	5.1
	446577		Hs.15420	KIAA1500 protein	5.1 5.0
70	437267 419423		Hs.258110 Hs.90315	ESTs KIAA0007 protein	5.0
, 0	404939		113.50015	0	5.0
	439052		Hs.37921	ESTs	5.0
	447020		Hs.16986	hypothetical protein FLJ11046	5.0
75	453878		Hs.19025	ESTs	5.0 5.0
15	410824 427701		Hs.33264 Hs.221750	ESTs ESTs	5.0
	424602		Hs.301129	Homo sapiens clone 23859 mRNA sequence	5.0
	430044	AA464510	Hs.152812	EST cluster (not in UniGene)	5.0
80	417423		Hs.111164	ESTs	5.0 5.0
OU	421477 433384		Hs.104650 Hs.124244	hypothetical protein FLJ10292 ESTs	5.0
	433364		Hs.114275	ESTs .	5.0
	443555	N71710	Hs.21398	ESTs, Moderately similar to GNPI_HUMAN GLUCOSAM	5.0
	416198	3 H27332	Hs.99598	ESTs	4.9

	424539	L02911	Hs.150402	activin A receptor, type I	4.9
	436645 417251	AW023424 AW015242	Hs.156520 Hs.99488	ESTs ESTs; Weakly similar to ORF YKR074w [S.cerevisiae]	4.9 4.9
	447207	AA442233	Hs.17731	hypothetical protein FLJ12892	4.9
5	416565	AW000960	Hs.44970	ESTs	4.9
-	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	4.9
	435420	AI928513	Hs.59203	ESTs	4.9
	435532	AW291488	Hs.117305	ESTs	4.9
10	443268	AIB00271	Hs.129445	hypothetical protein FLJ12496	4.9
10	446140	AA356170	Hs.26750	Homo sapiens cDNA: FLJ21908 fis, clone HEP03830	4.9
	452891	N75582	Hs.212875	ESTs, Weakly similar to KIAA0357 [H.sapians]	4.9
	431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic protein type; fou ESTs	4.9 4.9
	408938 432842	AA059013 AW674093	Hs.22607 Hs.279525	hypothetical protein PRO2605	4.9
15	436754	A1061288	Hs.133437	ESTs, Moderately similar to gonadotropin inducible	4.9
15	442573	H93366	Hs.7567	Branched chain aminotransferase 1, cytosofic, U215	4.9
	409049	Al423132	Hs.146343	ESTs	4.9
	422475	AL359938	Hs.117313	Meis (mouse) homolog 3	4.9
~~	447112	H17800	Hs.7154	ESTs	4.9
20	458627	AW088642	Hs.97984	ESTs; Wealdy similar to WASP-family protein [H.sap	4.8
	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc bela 1,3-galactosyltransferase,	4.8
	410530	M25809	Hs.64173	ESTs, Highly similar to VAB1_HUMAN VACUOLAR AT	4.8
	429414	AI783656	Hs.202095	empty spiracles (Drosophila) homolog 2	4.8 4.8
25	418882 422505	NM_004996 AL120862	Hs.89433 Hs.124165	ATP-binding cassette, sub-family C (CFTR/MRP), mem ESTs; (HSA)PAP protein (programmed cell death 9;	4.8
23	425977	R15138	Hs.165570	Homo sapiens clone 25052 mRNA sequence	4.8
	428555	NM_002214	Hs.184908	Integrin, beta 8	4.8
	452909	NM_015368	Hs.30985	pannexin 1	4.8
	449535	W15267	Hs.23672	low density lipoprotein receptor-related protein 6	4.8
30	452232	AW020603	Hs.271698	ESTs	4.8
	409732	NM_016122	Hs.56148	NY-REN-58 antigen	4.8
	415115	AA214228	Hs.127751	hypothetical protein	4.7
	423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (from clon	4.7
25	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT2RM4000200	4.7
35	423575	C18863	Hs.163443	ESTS	4.7
	415211 418804	R64730.comp	Hs.155986	ESTs; Highly similar to SPERM SURFACE PROTEIN SP1	4.7 4.7
	428405	AA809632 Y00762	Hs.2266	gb:nz17h04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA do cholinergic receptor, nicolinic, alpha polypeptide	4.7
	432865	AI753709	Hs.152484	ESTs	4.7
40	433330	AW207084	Hs.132816	ESTs	4.7
••	453047	AW023798	Hs.286025	ESTs	4.7
	421308	AA687322	Hs.192843	ESTs	4.7
	456273	AF154846	Hs.1148	zinc finger protein	4.7
4.5	443933	Al091631	Hs.135501	Homo sapiens two pore potassium channel KT3.3	4.7
45	434551	BE387162	Hs.280858	ESTs, Highly similar to XPB_HUMAN DNA-REPAIR PRO	4.7
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	4.7
	426300	U15979	Hs.169228	delta-like homolog (Orosophila)	4.7
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37kD)	4.7
50	446102 420547	AW168067 AF155140	Hs.252956 Hs.98738	ESTs	4.7 4.7
50	429486	AF155140 AF155827	Hs.203963	gonadotropin-regulated testicular RNA helicase hypothetical protein FLJ10339	4.7
	429944	R13949	Hs.226440	Homo sapiens clone 24881 mRNA sequence	4.7
	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HEMBA1004610	4.7
	434988	Al418055	Hs.161160	ESTs	4.6
55	452571	W31518	Hs.34665	ESTs	4.6
	434361	AF129755	Hs.117772	ESTs	4.6
	406400	#(NOCAT)		0	4.6
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	4.6
60	419945	AW290975	Hs.118923	ESTs	4.6
60	428301	AW628666	Hs.98440	ESTS	4.6
	430153	AW968128	LI- 450040	gb:EST380338 MAGE resequences, MAGJ Homo sapiens c	4.6
	431349	AA503653	Hs.156942	ESTs, Moderately similar to ALU2_HUMAN ALU SUBFA	4.6 4.6
	446254 447505	BE179829 AL049266	Hs.179852 Hs.18724	Homo sapiens cDNA FLJ12832 fis, clone NT2RP2003137 Homo sapiens mRNA; cDNA DKFZp564F093 (from clone	4.6
65	448027	A1458437	Hs.177224	ESTs	4.6
05	449611	Al970394	Hs.197075	ESTs	4.6
	459574	Al741122	Hs.101810	Homo sagiens cDNA FLJ14232 fis, clone NT2RP4000035	4.6
	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	4.6
	409387	AW384900	Hs.123526	ESTs	4.6
70	424078	AB006625	Hs.139033	paternally expressed gene 3	4.6
	435244	N77221	Hs.187824	ESTs	4.6
	404996	#(NOCAT)		0	4.6
	407905	AW103655	Hs.252905	ESTs	4.6
75	411560	AW851186		gb:IL3-CT0220-150200-071-H05 CT0220 Homo sapiens c	4.6
75	424341	AA385074	Un E/C4	gb:EST98673 Thyroid Homo sapiens cDNA 5' end simil	4.6
	441675	AI914329	Hs.5461	ESTS Home springs mPNA for KIAA1230 ambain, cartial of	4.6
	452172	H00797 AA290938	Hs.133207	Homo sapiens mRNA for KIAA1230 protein, partial cd ESTs, Highly similar to mosaic protein LR11 [H.sap	4.6 4.5
	420276 402820	#(NOCAT)	Hs.190561	0	4.5
80	419699	AA248998	Hs.31246	ESTs	4.5
	422529	AW015128	Hs.256703	ESTs	4.5
	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	4.5
	441826	AW503603	Hs.129915	phosphotriesterase related	4.5
	453931	AL121278	Hs.25144	ESTS	4.5

	435538	AB011540	Hs.4930	low density lipoprotein receptor-related protein 4	4.5
	457465	AW301344	Hs.195969	ESTs	4.5
	418848	AIB20961	Hs.193465	ESTs	4.5
_	408321	AW405882	Hs.44205	corfistatin	4.5
5	447499	AW262580	Hs.147674	KIAA1621 protein	4.5
	424513	BE385864	Hs.149894	mitochondrial translational initiation factor 2 fibronectin 1	4.5 4.5
	432731 448275	R31178 BE514434	Hs.287820 Hs.20830	synaptic Res GTPase activating protein 1 (homolog	4.5
	430371	D87466	Hs.240112	KIAA0276 protein	4.5
10	448593	AW004854	Hs.228320	Homo sapiens cDNA: FLJ23537 fis, clone LNG07690	4.5
	407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MAMMA100042	4.4
	448141	AJ471598	Hs.197531	ESTs	4.4
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HEMBB1001304	4.4
15	417718	T86540	Hs.193981 Hs.269783	ESTS ESTS Weathy similar to ALLIA HUMAN ALLI SUBEAMI	4.4 4.4
13	436464 427528	AI016176 AU077143	Hs.179565	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMIL minichromosome maintenance deficient (S. cerevisia	4.4
	409092	AI735283	Hs.172608	ESTs	4.4
	416241	N52639	Hs.32683	ESTs	4.4
	432005	AA524190	Hs.120777	ESTs, Weakly similar to ELL2_HUMAN RNA POLYMER	4.4
20	440234	AW117264	Hs.126252	ESTs	4.4
	448743	AB032962	Hs.21896	KIAA1136 protein	4.4
	451389	N73222	Hs.21738	KIAA1008 protein	4.4 4.4
	453331 454036	Al240665 AA374756	Hs.8895 Hs.93560	ESTs ESTs, Wealdy similar to unnamed protein product [H	4.4
25	448133	AA723157	Hs.73769	folate receptor 1 (adult)	4.4
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain 9 (melt	4.4
	453279	AW893940	Hs.59698	ESTs	4.4
	409459	D86407	Hs.54481	tow density lipoprotein receptor-related protein 8	4.4
20	431708	AI698136	Hs.108873	ESTs	4.4
30	433906	Al167816	Hs.43355	ESTs	4.4 4.4
	437958 441423	8E139550 Al793299	Hs.121668 Hs.126877	ESTs ESTs	4.4
	429876	AB028977	Hs.225974	KIAA1054 protein	4.3
	446770	AV660309	Hs.154986	ESTs, Weakly similar to AF137386 1 plasmotipin [H.	4.3
35	412078	X69699	Hs.73149	paired box gene 8	4.3
	422093	AF151852	Hs.111449	CGI-94 protein	4.3
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE; Human selenium	4.3
	448390	AL035414	Hs.21068	hypothetical protein	4.3 4.3
40	453628 449722	AW243307 BE280074	Hs.170187 Hs.23960	ESTs cyclin B1	4.3
70	436679	Al127483	Hs.120451	ESTs, Weakly similar to unnamed protein product [H	4.3
	431592	R69016	Hs.293871	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMIL	4.3
	432383	AK000144	Hs.274449	Homo sapiens cDNA FLJ20137 fis, clone COL07137	4.3
15	419926	AW900992	Hs.93798	DKFZP586D2223 protein	4.3
45	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	4.3
	401644 410044	#(NOCAT) BE566742	Hs.58169	0 highly expressed in cancer, rich in leucine heptad	4.3 4.3
	413775	AW409934	Hs.75528	nucleolar GTPase	4.3
	424296	AI631874	Hs.169391	ESTs	4.3
50	431118	BE264901	Hs.250502	carbonic anhydrase VIII	4.3
	432201	AI538613	Hs.135657	TMPRSS3a mRNA for serine protease (ECHOS1) (TADG-1	4.3
	451073	A1758905	Hs.206063	ESTs	4.3
	451592	A1805416	Hs.213897	ESTs ab:QV-BT009-101198-051 BT009 Homo sapiens cDNA, m	4.3 4.3
55	452453 441020	Al902519 W79283	Hs.35962	ESTs	4.3
J J	439024	R96696	Hs.35598	ESTs	4.2
	453619	H87648	Hs.33922	H.sapiens novel gene from PAC 117P20, chromosome 1	4.2
	453459	BE047032	Hs.257789	ESTS	4.2
60	408427	AW194270	Hs.177236	ESTs	4.2
60	419311	AA689591	Un 402700	gb:nv66a12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA do	4.2
	426460 444540	D79721 Al693927	Hs.183702 Hs.265165	Homo sapiens cDNA FLJ11752 fis, clone HEMBA1005582 ESTs	4.2 4.2
	452943	BE247449	Hs.31082	typothetical protein FLJ 10525	4.2
	453913	AW004683	Hs.233502	ESTs	4.2
65	417847	AI521558	Hs.288312	Homo sapiens cDNA: FLJ22316 fis, clone HRC05262	4.2
	428856	AA436735	Hs.183171	Homo sapiens cDNA: FLJ22002 fis, clone HEP05638	4.2
	428679	AA431765		gb:zw80c03.s1 Soares_testis_NHT Homo sapiens cDNA	4.2
	441006	AW605267	Hs.7627	CGI-60 protein ESTs, Moderately similar to unnamed protein produc	4.2 4.2
70	436209 446936	AW850417 H10207	Hs.254020 Hs.47314	ESTs woderately similar to unhance protein produc	4.2
	405076	AL390179	Hs.137011	Homo saplens mRNA; cDNA DKFZp547P134 (from clone	4.2
	428819	AL135623	Hs.193914	KIAA0575 gene product	4.2
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth factor recep	4.2
75	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedia C)	4.2
75	417048	AI088775	Hs.55498	geranylgeranyl diphosphate synthase 1	4.2
	431750	AA514986	Hs.283705	ESTs EST-	4.2 4.2
	439314 448582	AA382413 AI538880	Hs.178144 Hs.94812	ESTs ESTs	4.2
	449554	AA682382	Hs.59982	EST\$	4.2
80	455700			gb:CM1-BT0368-061299-060-g07 BT0368 Homo sapiens c	4.2
	409073	AA063458		gb:zf71a07.s1 Soares_pineal_gland_N3HPG Homo sapie	4.1
	433929	Al375499	Hs.27379	ESTS	4.1
	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMIL	4.1
	444381	BE387335	Hs.283713	, ESTs	4.1

	451024	AA442176		gbzw63b08.r1 Soares_total_fetus_Nb2HF8_9w Homo sa	4.1
	415539	AI733881	Hs.72472	BMPR-lb; bone morphogenetic protein receptor; typ	4.1 4.1
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialytransferase I, long form	4.1
5	420736	AI263022	Hs.82204	ESTs	4.1
J	453293	AA382267	Hs. 10653	ESTs fracture callus 1 (rat) homolog	4.1
	409564 418378	AA045857 AW962081	Hs.54943	gb:EST374154 MAGE resequences, MAGG Homo saplens	4.1
	429628	H09604	Hs.13268	ESTs	4.1
	439635	AA477288	Hs.94891	Homo sapiens cDNA: FLJ22729 fis, clone HSI15685	4.1
10	440452	Al925136	Hs.55150	ESTs, Wealty similar to CAYP_HUMAN CALCYPHOSIN	4.1
10	443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780 1 retinal short-c	4.1
	448816	AB033052	Hs.22151	KIAA1226 protein	4.1
	452795	AW392555	Hs.18878	hypothetical protein FLJ21620	4.1
	443171	BE281128	Hs.9030	TONDU	4.1
15	425322	U63630	Hs.155637	protein kinase; DNA-activated; catalytic polypepti	4.1
	442717	R88362	Hs.180591	ESTs, Weakly similar to R06F6.5b [C.elegans]	4.1
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosin)	4.1
	417300	Al765227	Hs.55610	solute carrier family 30 (zinc transporter), membe	4.1
20	417389	BE260964	Hs.82045	Midkine (neurite growth-promoting factor 2)	4.1
20	448105	AW591433	Hs.170675	ESTs, Weakly similar to TMS2_HUMAN TRANSMEMBR	4.1
	419131	AA406293	Hs.301622	ESTs	4.1
	406348	#(NOCAT)	11- 400444	0	4.1 4.1
	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT2RP4000515	4.1
25	419790	U79250	Hs.93201 Hs.100261	glycerol-3-phosphate dehydrogenase 2 (mitochondria Homo sapiens mRNA; cDNA DKFZp564B222 (from clone	4.1
23	420908 421039	AL049974 NM_003478	Hs.101299	culin 5	4.1
	426890	AA393167	Hs.41294	ESTs	4.1
	428571	NM_006531	Hs.2291	Probe hTg737 (polycystic kidney disease, autosomal	4.1
	452834	A1638627	Hs.105685	ESTs	4.1
30	428771	AB028992	Hs.193143	KIAA1069 protein	4.0
	437949	U78519	Hs.41654	ESTs	4.0
	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT2RP4000448	4.0
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	4.0
25	418375	NM_003081	Hs.84389	synaptosomal-associated protein, 25kD	4.0
35	447204	Al366881	Hs.157897	ESTs, Moderately similar to ALUC_HUMAN !!!! ALU CL	4.0 4.0
	407910	AA650274	Hs.41296	fibraneclin leucine rich transmembrane protein 3	4.0
	412314 436291	AA825247 BE568452	Hs.250899 Hs.5101	heat shock factor binding protein 1 ESTs; Highly similar to protein regulating cytokin	4.0
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	4.0
40	426991	AK001536	Hs.285803	Homo sapiens cDNA FLI12852 fis, clone NT2RP2003445	4.0
	409365	AA702376	Hs.226440	Homo sapiens clone 24881 mRNA sequence	4.0
	410784	AW803201		gb:IL2-UM0077-070500-080-E06 UM0077 Homo sapiens c	4.0
	413374	NM_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	4.0
4.0	413425	F20956		gb:HSPD05390 HM3 Homo sapiens cDNA clone 032-X4-1	4.0
45	417655	AA780791	Hs.14014	ESTs, Weakly similar to KIAA0973 protein [H.sapien	4.0
	424783	AA913909	Hs.153088	TATA box binding protein (TBP)-associated factor,	4.0
	425024	R39235	Hs.12407	ESTs	4.0 4.0
	445941 448595	Al267371 AB014544	Hs.172636 Hs.21572	ESTs KIAA0544 gene product	4.0
50	453448	AL036710	Hs.209527	ESTs	4.0
50	458944	N93227	Hs.98403	ESTs	4.0
	400284		***************************************	Estrogen receptor 1	4.0
	441134	W29092	Hs.7678	cellular retinoic acid-binding protein 1	4.0
	408796	AA688292	Hs.118553	ESTs:	4.0
55 ·	408296	AL117452	Hs.44155	DKFZP586G1517 protein	4.0
	438913	AI380429	Hs.172445	ESTs	4.0
	402408			0	4.0
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppressor	4.0
60	450701	H39960	Hs.288467	Homo sapiens cDNA FL112280 fis, clone MAMMA100174	4.0 4.0
UU	439780	AL109688	Un 107C10	gb:Homo saplens mRNA full length insert cDNA clone	4.0
•	418301	AW976201 AW512260	Hs.187618 Hs.87767	ESTs ESTs	4.0
	420077 426572		Hs.170623	hypothetical protein FLJ11183	4.0
	403721	AD001100	113.170000	0	4.0
65	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncogene homoto	4.0
	408684		Hs.12727	hypothetical protein FLJ21610	4.0
	414869		Hs.72163	ESTs	4.0
	437980		Hs.278436	KIAA1474 prolein	4.0
70	451050	AW937420	Hs.69662	ESTs	4.0
70					
	TABLE		_1 1 d 1 C _ a	<b>.</b>	
		Inique Eos probes		iber	
		mber: Gene cluste on: Genbank acc			
75	MUUDO	nit Gennank ave	COOKUI IIMITUCIO		
, ,	Pkey	CAT Number	Accession		
	409073			8 AA063018 Al444822	
	410784			1 BE079700 BE062940	
	411560			6 AW996967 BE143456	
80	413425		F20956 A	A129374 AA133740 AW819878	
	414315	143512_1		A494098 F13654 AA494040 AA143127	
	418378			31 AA218925 AA354237	•
	418804		AA80963	2 AI917245 AI701732 AA228405	
	419311	183793_1	AA58959	1 AW974261 AA236240 AI077451 AA631399 AW974262	
				202	

```
AW976153 AA278945 AA747691
AA385074 AA339054 AA339115 AW956359
AA418703 AA418711 BE071915 BE071920 BE071912
           420637
                       195241_1
           424341
                       238294_1
           428002
                       285602_1
                                           AA431765 AA432015
           428679
                       294049_1
  5
                                          AA884766 AW974271 AA592975 AA447312
           429163
                       300543_1
                                           AW968128 AA468102 AA468165
           430153
                       313709 1
                                           AA496479 T89859 AW020056 AW135251 AI221100 AA628705 AI263148 T79074
           431229
                       330060_1
                                           AW970622 AA503009 AA502998 AA502989 AA502805 T92188
           431322
                       331543_1
                                           BE177494 AW276909 AA632849
           434415
                       385931_1
10
                                          AW298057 AA731645 AA810101 AW194180 Al690673 AW978773
           436812
                       427323 1
                                          AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598
AA251875 AI820501 N820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578
F13493 AA927794 AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346
                       44573_2
           437938
                                          AI689052 AA282915 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813
15
                                          AL539642 AA642789 AA856975 AW505512 AL961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538
                                          AA180009 AA337499 AW961101 AA251669 AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741
AW072629 AW513996 AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456
                                          AJ373032 AJ564269 F00531 H83488 W37181 W78802 R66056 AJ002839 R67840 AA300207 AW959581 T63226 F04005
                                          AW979074 AA834841 AA828650
AA828995 AA834879 Al926361
           438966
                       467435_1
20
           438993
                       467651_1
                       468079_1
                                          AW979172 AA829595 R96050
           439042
                                          AL109688 R23665 R26578
                       47673_1
           439780
                       542469_1
                                          AA995998 AI916584 R61781 T77332 F07756 F08149 F07647
           442438
                                           Al624049 AW117770 Al858360
           449034
                       794817_1
25
                       85565_1
918300_1
                                           AA442176 AA259181
           451024
                                           Al902519 Al902518 Al902516
           452453
                                           BE068115 BE068104 BE068102 BE068096 BE068103 BE068154 BE068198
           455700
                       1351264_1
                       798085_1
                                           AI630223 AI630470
           458861
30
           TABLE 14C:
           Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of
                  human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
           Strand: Indicates DNA strand from which exons were predicted
35
           Nt_position: Indicates nucleotide positions of predicted exons
           Pkey
401644
                                       Strand
                                                     Nt position
                         8576138
                                                     82655-83959
                                       Plus
           402408
                                       Minus
                                                     110326-110491
                         9796239
40
           402606
                         9909429
                                       Minus
                                                     81747-82094
                                                     82274-82443
                         6456853
           402820
                                       Minus
           403381
                         9438267
                                                     26009-26178
                                       Minus
           403657
                         8843996
                                        Minus .
                                                      156223-156370
           403721
                          7528046
                                                      156647-157366
                                       Minus
45
           404253
404561
                         9367202
                                       Minus
                                                     55675-56055
                                                     69039-70100
                         9795980
                                       Minus
           404939
                         6862697
                                       Plus
                                                     175318-175476
                                                     37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
           404996
                          6007890
                                       Plus
           405547
                          1054740
                                       Plus
                                                     124361-124520,124914-125050
50
           406348
                         9255985
                                       Minus
                                                     71754-71944
           406367
                         9256126
                                       Minus
                                                     58313,58489
                                                     1553-1712,1878-2140,4252-4385,5922-6077
           406400
                         9256298
                                       Plus
55
           Table 15A lists about 499 genes up-regulated in ovarian cancer compared to normal adult lissues that are likely to be extracellular or cell-surface proteins. These were selected
            as for Table 14A, except that the ratio was greater than or equal to 3.0, and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g.,
           ig, fn3, egf, 7tm domains). Predicted protein domains are noted.
            TABLE 15A: ABOUT 499 UP-REGULATED GENES ENCODING EXTRACELLULAR/CELL SURFACE PROTEINS, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES
60
            Pkey: Primekey
            UG ID: UniGene ID
            Title: UniGene title
            Prot. Dom.: Predicted protein structural domains
            ratio: ration tumor vs normal tissues
 65
                                                                                                              Prot Dom
                                                                                                                                             ratio
                                                                                                                                              42.7
            415989
                        A1267700
                                          Hs.111128
                                                          ESTs
                                                                                                              TM
                                                          G protein-coupled receptor 64
                                                                                                              TM
                                                                                                                                              30.5
                        NM 005756
            428579
                                          Hs.184942
                                          Hs.98367
                                                          similar to SRY-box containing gene 17
                        AW513143
                                                                                                              TM
            428153
 70
                                                          spondin 1, (f-spondin) extracellular matrix
                                                                                                                                              29.4
            436982
                        AB018305
                                          Hs.5378
                                                                                                              C1q,Collagen
                         D31152
                                          Hs.179729
                                                          collagen; type X; atpha 1 (Schmid metaphy
                                                                                                                                              27.0
            427585
                                          Hs.103538
Hs.83169
Hs.72472
                        C14187
M13509
                                                                                                                                              26.2
            430691
                                                          ESTs
                                                                                                              TM
                                                          Matrix metalloprotease 1 (interstitial collag
BMPR-lbr; bone morphogenetic protein rec
                                                                                                               SS.,Peptidase_M10
                                                                                                                                              20.6
            418007
                         AA250737
                                                                                                                                              20.6
             400292
 75
                                                                                                               Lysyl_oxidase
                         Al351010
                                          Hs.102267
                                                                                                                                              17.7
             424086
                                                          lysyl oxidase
                                                                                                              pkise,pkinase
TM
             424905
                         NM_002497
                                          Hs.153704
                                                          NIMA (never in mitosis gene a)-related kin
                                                                                                                                              17.4
                                                                                                                                              17.4
             427356
                         AW023482
                                          Hs.97849
                                                          ESTs
                         AJ404672
                                                                                                               TM
                                                                                                                                              17.1
            407638
427469
                                          Hs.288693
                                                          EST
                         AA403084
                                          Hs.269347
                                                          ESTs
 80
                                                                                                               SS,integrin_B
                                                                                                                                              16.7
             438993
                         AA828995
                                                          integrin; beta 8
                                                          lysyl oxidase
                                                                                                                                              16.1
                         H87879
                                          Hs.102267
                                                                                                               SS
             421155
                                                                                                               SS
             431989
                         AW972870
                                          Hs.291069
                                                          ESTs
                                                                                                                                              15.9
                                                          ras homolog gene family, member l
                                                                                                                                              15.1
             428976
                         ALD37824
                                          Hs.194695
                                          Hs.79078
                                                          MAD2 (mitotic arrest deficient, yeast, hom
             416209
                         AA236776
```

	442622	A A 02C224	Hs.246973	ESTs	TM	14.8
	413623 447350	AA825721 AI375572	Hs.172634	ESTs; HER4 (c-erb-B4)	SS.TM.Furin-like,pkinase	14.2
	428227	AA321649	Hs.2248	INTERFERON-GAMMA INDUCED PRO	IL8	14.1
	452461	N78223	Hs.108106	transcription factor	G9a,PHD	13.7
5	451106	BE382701	Hs.25960	N-myc	Myc_N_term	13.6
,	416208	AW291168	Hs.41295	ESTs	TM	13.5
	452249	BE394412	Hs.61252	ESTs	homeobox	13.4
•	416566	NM_003914	Hs.79378	cyclin A1	cyclin	12.8
		AA634543	Hs.79440	IGF-II mRNA-binding protein 3	TM	12.6
10	416661	X65724	Hs.2839	Norrie disease (pseudoglioma)	SS,Cys_knot	123
10	431725		Hs.85195	ESTs, Highly similar to 1(3;5)(q25.1;p34) f	TM	12.2
	458027	L49054 AA054726	Hs.285574	ESTs	TM	12.2
	408450	AA948033	Hs.130853	ESTs	histone	11.9
•	415263 400298	AA032279	Hs.61635	STEAP1	TM	11.8
15		AA291377	Hs.50831	ESTs	TM	11.6
13	421451 443715	AI583187	Hs.9700	cyclin E1	cyclin	11.5
		BE242870	Hs.75379	solute carrier family 1 (glial high affinity gl	TM,SDF	11.5
	413472 410102	AW248508	Hs.279727	ESTs:	SS	11.4
	408562	AJ436323	Hs.31141	Homo sapiens mRNA for KIAA1568 prote	TM	11.4
20	442353	BE379594	Hs.49136	ESTs .	TM	11.3
20	427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3	TM,neur_chan	11.2
	453160	AI263307	Hs.146228	ESTs	histone	11.2
		AA648459	Hs.179912	ESTs	TM	11.1
	412723 400250	707070733	115.17 55 12	0 '	Hist_deacetyl+F105	11.1
25	438167	R28363	Hs.24285	ESTs	7tm_1	11.1
23	434539	AW748078	Hs.214410	ESTs	TM	10.9
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain	TM	10.8
	400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin 2	SS,hemopexin	10.8
		A1754693	Hs.145968	ESTs	Cadherin_C_term	10.7
30	446142			cytochrome P450, subfamily XVII (steroid	TM,p450	10.6
50	421285	NM_000102	Hs.1363	VERY-LONG-CHAIN ACYL-COA SYNT	SS,TM	10.6
	433496	AF064254	Hs.49765		TM	10.5
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	SS	10.4
	433447	U29195	Hs.3281	neuronal pentraxin II	TM	10.4
35	414245	BE148072	Hs.75850	WAS protein family, member 1	SS,LRRNT	10.3
22	426462	U59111	Hs.169993	dermatan sulphate proteoglycan 3		10.3
	418601	AA279490	Hs.86368	calmegin	SS TM	10.3
	415227	AW821113	Hs.72402	ESTs	TM	10.1
	409269	AA576953	Hs.22972	Homo sapiens cDNA FLJ13352 fis, clone O	SS.EGF	9.8
40	426471	M22440	Hs.170009	transforming growth factor, alpha	SS	9.7
40	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfotran		9.7
	445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	SS,EGF	
	414972	BE263782	Hs.77695	KIAA0008 gene product	TM	9.4
	435509	AJ458679	Hs.181915	ESTs	TM	9.3
AF	445413	AA151342	Hs.12677	CGI-147 protein	UPF0099	9.2
45	446999	AA151520	Hs.279525	hypothetical protein PRO2605	TM	9.1
	414569	AF109298	Hs.118258	Prostate cancer associated protein 1	TM	9.1
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	hemopexin	9.0
	408908	BE296227	Hs.48915	serine/threonine kinase 15	pkise,TM	9.0
50	451807	W52854	Hs.27099	DKFZP564J0863 protein	TM	8.8 8.8
30	420159	AI572490	Hs.99785	ESTs	TM Dieie D teefie	8.7
	432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:poly	TM.Ricin_B_lectin	8.7
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfotran	TM ·	8.7
	438885	AI886558	Hs.184987	ESTS	TM	8.6
55	447342	Al199268	Hs.19322	ESTs; Weakly similar to !!!! ALU SUBFAM	TM UDPGT	8.5
55	437212	AI765021	Hs.210775	ESTs		8.4
	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	wnt	8.4
	450505	NM_004572	Hs.25051	plakophilin 2	TM	8.3
	436396	A1683487	Hs.299112	Homo sapiens cDNA FLJ11441 fis, done H	wnt	
60	425695	NM_005401	Hs.159238	protein tyrosine phosphatase, non-receptor	Y_phosphalase	8.3 8.2
UU	447268	Al370413	Hs.36563	Homo sapiens cDNA: FLJ22418 fis, clone	Ribosomal_S8	8.1
	400195	ALCCCORC	116 450740	O Home agricus DNA for Homeb 23 gratain	TM	8.1
	424906	A1566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein,	TM · TM	8.1
	438202	AW169287	Hs.22588	ESTS		8.0
65	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	TM TM,Fz,Frizzled	8.0
05	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10		8.0
	424001	W67883	Hs.137476	KIAA1051 protein	TM TM	7.8
	442655	AW027457	Hs.30323	ESTs	7tm_1	7.8
	445657	AW612141	Hs.279575	ESTs	SS.TGF-beta	7.8
70	426320	W47595	Hs.169300	transforming growth factor, beta 2		7.6
70	412170	D16532	Hs.73729	very low density lipoprotein receptor	TM,ldl_recept_b,EGF TM	7.6
	436476	AA326108	Hs.53631	ESTs	TM	7.6
	414132	AI801235	. Hs.48480	ESTs		
	437789	Al581344	Hs.127812	ESTs, Wealdy similar to AF141326 1 RNA	TM	7.6
75	450192	AA263143	Hs.24596	RAD51-interacting protein	TM	7.6 7.5
75	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	TM	
	413627	BE182082	Hs.246973	ESTs	TM	7.4
	446293	AI420213	Hs.149722	ESTs	LIM,homeobox	7.4
	409242	AL080170	Hs.51692	DKFZP434C091 protein	TM,7tm_1	7.3
00	450262	AW409872	Hs.271166	ESTs, Moderately similar to ALU7_HUMA	TM	7.3
80	451659	BE379761	Hs.14248	ESTs, Weakly similar to ALU8_HUMAN A	TM	7.3
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane g	TM	7.2
	429126	AW172356	Hs.99083	ESTs	7tm_1	7.1
	421464	AA291553	Hs.190086	ESTs	TM	7.0
	420362	U79734	Hs.97206 .	huntinglin interacting protein 1	TM	7.0
				205		

	444743	AA045648	Hs.11817	nudix (nucleoside diphosphate linked molet	TM	7.0
	415138	C18356	Hs.78045	fissue factor pathway inhibitor 2 TFP12	Kunitz_BPTI,G-gamma	6.9
	429418	AJ381028	Hs.99283	ESTs	AAA	6.9
_	409178	BE393948	Hs.50915	kallikrein 5	SS,trypsin	6.9
5	425905	AB032959	Hs.161700	KIAA1133 protein	TM	6.9
	428532	AF157326	Hs.184786	TBP-interacting protein	TM	6.9
	433426	H69125	Hs.133525	ESTs	TM	6.9 6.8
	448674	W31178 T16971	Hs.154140	ESTs ESTs	TM TM	6.7
10	432415 418203	X54942	Hs.289014 Hs.83758	CDC28 protein kinase 2	TM	6.6
10	438394	BE379623	Hs.27693	CGI-124 protein	pro_isomerase	6.6
	452097	AB002364	Hs.27916	ADAM-TS3; a disintegrin-like and metal	Reprolysin	6.6
	453745	AA952989	Hs.63908	Homo sapiens HSPC316 mRNA, partial cd	TGFb_propeptide	6.6
	423248	AA380177	Hs.125845	ributose-5-phosphate-3-epimerase	filament	6.6
15	452281	T93500	Hs.28792	ESTs	TGF-beta	6.5
	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic; stratum comeum	SS,trypsin	6.5
	452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transporter)	TM,Sulfate_transp	6.5
	434149	Z43829	Hs.19574	ESTs, Weakly similar to katanin p80 subun	pkinase,fn3	6.5 6.4
20	425776 409517	U25128 X90780	Hs.159499 Hs.54668	parathyroid hormone receptor 2 troponin I, cardiac	TM,7tm_2 Y_phosphatase	6.4
20	432666	AW204069	Hs.129250	ESTs, Weakly similar to unnamed protein p	ТМ	6.4
	448706	AW291095	Hs.21814	class II cytokine receptor ZCYTOR7	SS	6.4
	413582	AW295647	Hs.71331	Homo sapiens cDNA: FLJ21971 fis, clone	TM	6.4
0.5	424153	AA451737	Hs.141496	MAGE-like 2	TM	6.4
25	441081	Al584019	Hs.169006	ESTs, Moderately similar to plakophilin 2b	PAX	6.4
	443539	AI076182	Hs.134074	ESTs	TM	6.4
	418384	AW149266	Hs.25130	ESTs	TM	6.3
	425371	D49441	Hs.155981	mesothelin	SS	6.3
30	449048 437117	Z45051 AL049256	Hs.22920 Hs.122593	similar to \$68401 (cattle) glucose induced g	SS TM	6.3 6.3
50	457117	AL049236 Al470523	Hs.182356	ESTs ESTs, Moderately similar to translation init	ABC_tran	6.3
	426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteogenic p	SS,TGF-beta	6.3
	452904	AL157581	Hs.30957	Homo sapiens mRNA; cDNA DKFZp434E	TM	6.2
	457030	Al301740	Hs.173381	dihydropyrimidinase-like 2	TM	6.2
35	436281	AW411194	Hs.120051	ESTs	TM	6.1
	415139	AW975942	Hs.48524	ESTs	TM	6.1
	449448	D60730	Hs.57471	ESTs	TM	6.1
	457979	AA776655	Hs.270942	ESTs	TM CO FOEtha 2	6.1
40	422867 421502	L32137	Hs.1584 Hs.105039	cartilage oligomeric matrix protein solute carrier family 34 (sodium phosphate)	SS,EGF,tsp_3 TM	6.0 6.0
+0	421302	AF111856 AA984472	Hs.74554	KIAA0080 protein	C2	6.0
	422095	AI868872	Hs.288966	ceruloplasmin (ferroxidase)	SS .	6.0
	418845	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alp	Chromo_shadow	6.0
	410555	U92649	Hs.64311	a disintegrin and metalloproteinase domain	TM, disintegrin, Reprotysin	5.9
45	437099	N77793	Hs.48659	ESTs, Highly similar to LMA1_HUMAN L	laminin_EGF	5.9
	453431	AF094754	Hs.32973	glycine receptor, beta	TM,neur_chan	5.9
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1"	TSPN,Collagen,COLFI	5.9
	430291	AV660345	Hs.238126	CGI-49 protein	TM ADC	5.9
50	405547 435793	#(NOCAT) AB037734	Hs.4993	0 ESTs	TM,ABC_membrane TM	5.9 5.8
50	440138	AB033023	Hs.6982	hypothetical protein FLJ10201	TM	5.8
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	SS,Collagen,TSPN	5.7
	419335	AW960146	Hs.284137	Homo sapiens cDNA FLJ12888 fis, clone N	TM	5.7
	452971	AI873878	Hs.91789	ESTs	TM	5.7
55	428927	AA441837	Hs.90250	ESTs ·	TM	5.7
	419247	S65791	Hs.89764	fragile X mental retardation 1	TM	5.7
	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sap	TM .	5.7
	447078	AW885727	Hs.301570	ESTs	kazal	5.6
60	421247 432030	BE391727 AI908400	Hs.102910 Hs.143789	general transcription factor IIH, polypeptid ESTs	TM SS	5.6 5.6
00	443270	NM_004272	Hs.9192	Homer, neuronal immediate early gene, 18	TM	5.5
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	Peptidase_M3	5.5
	419558	AW953679	Hs.278394	ESTs	ss <sup>i</sup>	5.5
	427386	AW836261	Hs.177486	amyloid beta (A4) precursor protein (protea	TM	5.5
65	427961	AW293165	Hs.143134	ESTs	TM	5.5
	407216	N91773	Hs.102267	lysyl oxidase	TM	5.5
	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	ras,TM	5.5
	414315	Z24878	U- 204000	gb:HSB65D052 STRATAGENE Human sk	TM SS	5.5
70	441645 449318	AJ222279 AW236021	Hs.201555 Hs.108788	ESTs ESTs, Weakly similar to zeste [D.melanoga	SS TM	5.5 5.4
70	441433	AA933809	Hs.42746	ESTs Weakly surmar to zeste (D.meranoga	TM	5.4
	445495	BE622641	Hs.38489	ESTs	I_LWEQ.ENTH	5.4
	410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone N	Glycos_transf_2	5.4
7.	442611	BE077155	Hs.177537	ESTs	TM	5.4
75	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced protein	XIink,CUB	5.4
	419948	AB041035	Hs.93847	NADPH oxidase 4	TM	5.3
	427718	AI798680	Hs.25933	ESTs HCDC037 contain	histone	5.3
	453867 408298	AI929383 AI745325	Hs.108196 · Hs.271923	HSPC037 protein ESTs; Moderately similar to IIII ALU SUB	TM Glycos_transf_2,DSPc	5.3 5.3
80	448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P	TM	5.3
	433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMA	TM	5.3
	449532	W74653	Hs.271593	ESTs	TM	5.3
	452822	X85689	Hs.288617	Homo sapiens cDNA: FLJ22621 fis, clone .	TM,EGF,fn3	5.3
	418379	AA218940	Hs.137516 .	fidgetin-like 1	AAA	5.2
				200		

	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	TM,trypsin	5.2
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	TM	5.2
	445236	AK001676	Hs.12457	hypothetical protein FLJ10814	TM .	5.2
~	406367	#(NOCAT)		0	proteasome,trypsin	5.2
5	442500	AI819068	Hs.209122	ESTs	SS	5.2
	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	TM	5.2
	419140	Al982647	Hs.215725	ESTs	TM	5.2
	417791	AW965339	Hs.111471	ESTs	Ald_Xan_dh_C	5.1
10	437496	AA452378	Hs.170144	Homo sapiens mRNA; cDNA DKFZp547J1	TSPN.Folate_carrier	5.1
10	418849	AW474547	Hs.53565	ESTs, Weakly similar to B0491.1 [C.elegan	TM	5.1
	428093	AW594506	Hs.104830	ESTs	TM .	5.1
	408621	AI970672	Hs.46638	chromosome 11 open reading frame 8; feta	TM	5.1
	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	TM	5.1
	404939			0	TM	5.0
15	447020	T27308	Hs.16986	hypothetical protein FLJ11046	TM	5.0
	410824	AW994813	Hs.33264	ESTs	TM	5.0
	417423	AA197341	Hs.111164	ESTs	TM	5.0
	421477	A1904743	Hs.104650	hypothetical protein FLJ10292	TM	5.0
	443555	N71710	Hs.21398	ESTs, Moderately similar to GNPI_HUMA	Glucosamine_iso	5.0
20⋅	424539	L02911	Hs.150402	activin A receptor, type I	SS,Activin_recp,pkinase	4.9
	416565	AW000960	Hs.44970	ESTs	TM	4.9
	431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic protein ty	SS	4.9
	408938	AA059013	Hs.22607	ESTs	TM	4.9
	435754	AI061288	Hs.133437	ESTs, Moderately similar to gonadotropin i	TM .	4.9
25	409049	Al423132	Hs.146343	ESTs	TM	4.9
	458627	AW088642	Hs.97984	ESTs; Weakly similar to WASP-family pro	TM	4.8
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	TM_ABC_membrane	4.8
	422505	AL120862	Hs.124165	ESTs; (HSA)PAP protein (programmed ce	TM	4.8
	428555	NM_002214	Hs.184908	integrin, beta 8	SS,Integrin_B	4.8
30	452909	NM_015368	Hs.30985	pannexin 1	TM	4.8
50	449535	W15267	Hs.23572	low density lipoprotein receptor-related pro	SS,ldl_recept_a,EGF	4.8
	452232	AW020603	Hs.271698	ESTs	TM	4.8
				Homo sapiens mRNA; cDNA DKFZp564N	Cadherin_C_term	4.7
	423161	AL049227 Y00762	Hs.124776		TM.neur chan	4.7
35	428405		Hs.2266	cholinergic receptor, nicotinic, alpha polype		4.7
22	433330	AW207084	Hs.132816	ESTs	TM	
	443933	Al091631	Hs.135501	Homo sapiens two pore potassium channel	TM	4.7
	440351	AF030933	Hs.7179	RAD1 (S. pambe) hamolog	TM	4.7
	426300	U15979	Hs.169228	delta-like hornolog (Drosophila)	TM,EGF	4.7
40	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37kD)	AAA,DEAD,helicase_C	4.7
40	429944	R13949	Hs.226440	Homo sapiens clone 24881 mRNA sequenc	TM	4.7
	434988	Al418055	Hs.161160	ESTs	TM	4.6
	406400	#(NOCAT)		0	trypsin,TM	4.6
	428301	AW628666	Hs.98440	ESTs	TM	4.6
4.5	446254	BE179829	Hs.179852	Homo sapiens cDNA FLJ12832 fis, clone N	TM	4.6
45	459574	Al741122	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone N	TM	4.6
	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	TM	4.6
	435244	N77221	Hs.187824	ESTs	pkinase,fn3	4.6
	404996	#(NOCAT)		0	Peptidase_C1	4.6
c0	407905	AW103655	Hs.252905	ESTs	SS,Ephrin	4.6
50	441675	Al914329	Hs.5461	ESTs	TM	4.6
	420276	AA290938	Hs.190561	ESTs, Highly similar to mosaic protein LR1	TM,fn3,ldl_recept_a	4.5
	422529	AW015128	Hs.256703	ESTs	TM	4.5
	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	TM	4.5
	457465	AW301344	Hs.195969	ESTs	Pribosyltran	4.5
55	418848	AI820961	Hs.193465	ESTs ·	TM,pkise	4.5
	447499	AW262580	Hs.147674	KIAA1621 protein	TM	4.5
	432731	R31178	Hs.287820	fibronectin 1	SS	4.5
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone H	Nucleoside_tra2	4.4
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	TM	4.4
60	409092	AI735283	Hs.172608	ESTs	TM	4.4
	451389	N73222	Hs.21738	KIAA1008 protein	TM	4.4
	453331	A1240665	Hs.8895	ESTs	, TM	4.4
	448133	AA723157	Hs.73769	folate receptor 1 (adult)	TM	4.4
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain	TM	4.4
65 ·	453279	AW893940	Hs.59698	ESTs	TM	4.4
	409459	D86407	Hs.54481	low density lipoprotein receptor-related pro	TM,EGF,kll_recept_a	4.4
	431708	AI698136	Hs.108873	ESTs	TM	4.4
	433906	AI167816	Hs.43355	ESTs	TM	4.4
	441423	Al793299	Hs.126877	ESTs	TM	4.4
70	446770	AV660309	Hs.154986	ESTs, Weakly similar to AF137386 1 plasm	TM	4.3
	412078	X69699	Hs.73149	paired box gene 8	TM	4.3
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE; H	AIRS	4.3
	448390	AL035414	Hs.21068	hypothetical protein	TM	4.3
	453628	AW243307	Hs.170187	ESTs	TM	4.3
75	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	TM	4.3
. •	413775	AW409934	Hs.75528	nucleolar GTPase	MMR_HSR1	4.3
	451592	AI805416	Hs.213897	ESTs	TM	4.3
	419311	AA689591		gbmv66a12.s1 NCL_CGAP_GC81 Homo s	TM	4.2
	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	TM	4.2
80	428679	AA431765		gb:zw80c03.s1 Soares_testis_NHT Homo s	TM	4.2
_ •	436209	AW850417	Hs.254020	ESTs, Moderately similar to unnamed prote	TM	4.2
	406076	AL390179	Hs.137011	Homo sapiens mRNA; cDNA DKFZp547P	TM	4.2
	428819	AL135623	Hs.193914	KIAA0575 gene product	TM	4.2
	406671	AA129547	Hs.285754 .		F-actin_cap_A	4.2

					L	
	431750	AA514986	Hs.283705	ESTs	TM	4.2
	449554	AA682382	Hs.59982	ESTs	TM	4.2
	409073	AA063458		gb:zf71a07.s1 Soares_pineal_gland_N3HP	SEA	4.1
_	433929	A1375499	Hs.27379	ESTs	TM	4.1
5	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN A	TM	4.1
	444381	BE387335	Hs.283713	ESTs	TM	4.1
	415539	AI733881	Hs.72472	BMPR-lb; bone morphogenetic protein rec	TM	4.1
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-siatyltransferase I, long	TM	4.1
10	453293	AA382267	Hs.10653	ESTs	TM	4.1
10	409564	AA045857	Hs.54943	fracture callus 1 (rat) homolog	TM	4.1
	429628	H09604	Hs.13268	ESTs	TM	4.1
	440452	AI925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN	TM	4.1
	443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780 1 retina	TM	4.1
1.5	425322	U63630	Hs.155637	protein kinase; DNA-activated; catalytic po	TM	4.1
15	417300	AI765227	Hs.55610	solute carrier family 30 (zinc transporter), m	TM	4.1
	417389	BE260964	Hs.82045	Midkine (neurite growth-promoting factor 2	SS,TM	4.1
	452834	AI638627	Hs.105685	ESTs	kinesin	4.1
	428771	AB028992	Hs.193143	KIAA1069 protein	PIPLC-XPI-PLC-Y	4.0
20	412314	AAB25247	Hs.250899	heat shock factor binding protein 1	TM	4.0 -
20	436291	BE568452	Hs.5101	ESTs; Highly similar to protein regulating c	TM	4.0
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	KRAB	4.0
	409365	AA702376	Hs.226440	Homo sapiens clone 24881 mRNA sequenc	TM	4.0
	413374	NM_001034	Hs.75319	ribonucleolide reductase M2 polypeptide	nbonuc_red	4.0
25	417655	AA780791	Hs.14014	ESTs, Weakly similar to KIAA0973 protein	TM .	4.0
23	445941	AI267371	Hs.172636	ESTs	TM.lactin_c	4.0
	441134	W29092	Hs.7678	cellular retinoic acid-binding protein 1	lipocalin TM	4.0 4.0
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppressor		4.0
	418301	AW976201	Hs.187618	ESTS	TM TCE hata khoa Ni tarm	4.0
30	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncog	TGF-beta,Myc_N_term TM	4.0
20	408684	R61377	Hs.12727	hypothetical protein FLJ21610	TM	4.0
	414869	AA157291	Hs.72163	ESTs	Cation_efflux	3.9
	420281	AI623693	Hs.191533	ESTs Shellin 2 (consential contractural arreshed	EGF,TB	3.9
	416658	·U03272	Hs.79432	fibrillin 2 (congenital contractural arachnod kalikrein 10		3.9
35	411274	NM_002776	Hs.69423		trypsin,TM TM	3.9
22	437222	AL117588	Hs.299963	ESTs		3.9
	431958	X63629	Hs.2877	Cadherin 3, P-cadherin (placental)	TM,cadherin, TM	3.9
	430634 415716	AI860651	Hs.26685	ESTS	NAP_family	3.9
		N59294	Hs.301141	Homo sapiens cDNA FLJ11689 fis, clone H	TM	3.8
40	420179	N74530	Hs.21168	ESTS	TM	3.8
40	451250	AA491275	Hs.236940	Homo sapiens cDNA FLJ12542 fis, clone N	TM	3.8
	429496	AA453800	Hs.192793	ESTS	TM	3.8
	421764	AI681535	Hs.99342	ESTs, Weakly similar to KCC1_HUMAN C	TM,SDF	3.8
	447197 422939	R36075	No 00427	gb:yh88b01.s1 Soares placenta Nb2HP Hom ESTs	TM	3.8
45	414737	AW394055 Al160386	Hs.98427 Hs.125087	ESTs	TM	3.8
73	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	SS,trypsin	3.8
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin 3)	SS,Peptidase_M10	3.7
	424433	H04607	Hs.9218	ESTs	TM	3.7
	431846	8E019924	Hs.271580	Uroplakin 1B	TM,transmembrane4	3.7
50	407792	Al077715	Hs.39384	putative secreted ligand homologous to fix1	SS	3.7
50	417531	NM_003157	Hs.1087	serine/threonine kinase 2	pkise,pkinase	3.7
	434836	AA651629	Hs.118088	ESTs	TM	3.7
	439810	AL109710	Hs.85568	EST	TM	3.7
	418693	A1750878	Hs.87409	thrombospondin 1	SS,EGF,TSPN	3.7
55	407864	AF069291	Hs.40539	chromosome 8 open reading frame 1	TM	3.7
55	436304	AA339622	Hs.108887	ESTs	TM	3.7
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (transloco	TM	3.7
	453468	W00712	Hs.32990	DKFZP566F084 protein	TM	3.6
	428943	AW086180	Hs.37636	ESTs, Weakly similar to KIAA1392 protein	TM	3.6
60··	411402	BF297855	Hs.69855	NRAS-related gene	CSD.ras.CSD	3.6
	425176	AW015644	Hs.301430	ESTs, Moderately similar to TEF1_HUMA	TM	3.6
	400296	AA305627	Hs.139336	ATP-binding cassette; sub-family C (CFTR	ABC_tran	3.6
	407340	AA810168	Hs.232119	ESTs	TM	3.6
	418524	AA300576	Hs.85769	acidic 82 kDa protein mRNA	TM	3.6
65	438279	AA805166	Hs.165165	ESTs, Moderately similar to ALU8_HUMA	TM	3.6
••	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	AAA,AAA	3.6
	441111	AI806867	Hs.126594	ESTs	· TM	3.6
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	TM	3.6
	409542	AA503020	Hs.36563	ESTs	Ribosomal_S8	3.6
70	425441	AA449644	Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone N	Aa_trans	3.6
. •	428137	AA421792	Hs.170999	ESTs	AAA	3.6
	433692	AI805860	Hs.208675	ESTs, Weakly similar to neuronal thread pr	TM	3.6
	438689	AW129261	Hs.250565	ESTs	TM	3.6
	443341	AW531480	Hs.8688	ESTs	TM	3.6
75	446261	AA313893	Hs.13399	hypothetical protein FLJ12615 similar to m	ATP-synt_D,PH	3.6
	414343	AL036166	Hs.75914	coated vesicle membrane protein	TM	3.5
	414812	X72755	Hs.77367	monokine induced by gamma Interferon	SS,IL8	3.5
	410361	BE391804	Hs.62661	quanylate binding protein 1, interferon-indu	· TM	3.5
	415786	AW419196	Hs.257924	ESTs	TM	3.5
80	427177	AB006537	Hs.173880	Interleukin 1 receptor accessory protein	TM,ig	3.5
-	427687	AW003867	Hs.112403	ESTs	7tm_1	3.5
	444619	BE538082	Hs.8172	ESTs	TM	3.5
	447336	AW139383	Hs.245437	ESTs	AhpC-TSA	3.5
	412519	AA196241	Hs.73980 .	troponin T1, skeletal, slow	TM	3.5
			•	200		

	418792	AB037805	Hs.88442	KIAA1384 protein	TM	3.5
	408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone N	TM	3.5
	416892	L24498	Hs.80409	growth arrest and DNA-damage-inducible,	TM	3.5
_	418793	AW382987	Hs.88474	prostagiandin-endoperoxide synthase 1 (pro	EGF	3.5
5	448089	A1467945	Hs.173696	ESTs	SS	3.5
	422278	AF072873	Hs.114218	ESTs	TM,Fz,Frizzled	3.5
	442133	AW874138	Hs.129017	ESTs	TM	3.5
	410908	AA121686	Hs.10592	ESTs	GTP_EFTU	3.5
10	452198	AI097560	Hs.61210	ESTs DKFZP586N0819 protein	TM	3.5 3.4
10	408730 436488	AV660717 BE620909	Hs.47144 Hs.261023	hypothetical protein FLJ20958	pkinase TM	3.4
	409745	AA077391	FIS.201025	gb:7B14E12 Chromosome 7 Fetal Brain cD	TM	3.4
	445870	AW410053	Hs.13406	syntaxin 18	TM	3.4
	451743	AW074266	Hs.23071	ESTs	TM	3.4
15	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, with G	TM	3.4
	432350	NM_005865	Hs.274407	protease, serine, 16 (thymus)	SS	3.4
	412848	AA121514	Hs.70832	ESTs	TM	3.4
	413625	AW451103	Hs.71371	ESTs	filament	3.4
20	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like repeat d	SS	3.4
20	422972	N59319	Hs.145404	ESIS	TM	3.4
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4; MAP kinas	DSPc,Rhodanese	3.4
	450377	AB033091	Hs.24936	ESTs . ESTs	TM TM	3.4 3.4
	443475 419452	A1066470 U33635	Hs.134482 Hs.90572	PTK7 protein tyrosine kinase 7	TM,pkise,ig,SRF-TF	3.4 3.4
25	409744	AW675258	Hs.56265	Homo sapiens mRNA; cDNA DKFZp586P	TM	3.4
23	422789	AK001113	Hs.120842	hypothetical protein FLJ10251	TM	3.4
	404440	#(NOCAT)		0	TM_neur_chan	3.4
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	SS,TIR,Ig	3.4
	411828	AW161449	Hs.72290	wingless-type MMTV integration site fami	wnt	3.4
30	417177	NM_004458	Hs.81452	fatty-acid-Coenzyme A ligase, long-chain 4	SS	3.4
	421013	M62397	Hs.1345	mutated in colorectal cancers	TM .	3.4
	427072	H38046		gb:yp58c10.r1 Soares fetal liver splean 1NF	Ribosomal_L22e	3.4
	433703	AA210863	Hs.3532	nemo-like kinase	pkinase	3.4
35	434294	AJ271379	Hs.21175	ESTs ESTs	TM TM	3.4
33	444188 446109	Al393165 N67953	Hs.19175 Hs.145920	ESTs	TM TM	3.4 3.4
	400881	1401.333	115.143320	0	Asparaginase_2	3.3
	450236	AW162998	Hs.24684	KIAA1376 protein	TM	3.3
	418836	AI655499	Hs.161712	ESTs	TM	3.3
40	437951	T34530	Hs.4210	Homo sapiens cDNA FLJ13059 fis, clone N	TM	3.3
	446896	T15767	Hs.22452	Homo sapiens cDNA: FLJ21084 fis, clone	TM	3.3
	430687	BE274217	Hs.249247	heterogeneous nuclear protein similar to rat	rm	3.3
	410060	NM_001448	Hs.58367	glypican-4	SS	3.3
15	419546	AA244199		gb:nc06c05.s1 NCI_CGAP_Pr1 Homo sapi	TM	3.3
45	429609	AF002246	Hs.210863	cell adhesion molecule with homology to L	TM,fn3,ig	3.3
	413289	AA128061	Hs.114992	ESTs	TM TM	3.3 3.3
	440006 401435	AK000517 #(NOCAT)-	Hs.6844	hypothetical protein FLJ20510 0	TM	3.3
	420072	AW961196	Hs.207725	ESTs	TM	3.3
50	421426	AA291101	Hs.33020	Homo saplens cDNA FLJ20434 fis, clone K	TM	3.3
	425851	NM_001490	Hs.159642	glucosaminyl (N-acelyl) transferase 1, core	SS	3.3
	443295	AI049783	Hs.241284	ESTs	TM	3.2
	453116	AJ276680	Hs.146086	ESTs	Ribosomat_L5_C	3.2
	456546	A1690321	Hs.203845	ESTs, Weakly similar to TWIK-related acid	TM	3.2
55	430016	NM_004736	Hs.227656	xenotropic and polytropic retrovirus recepto	TM	3.2
	418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9,	asp,Glyco_hydro_18	3.2
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated glyco	TM	3.2
	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspartat	TM	3.2
60	428882	AA436915	Hs.131748	ESTs, Moderately similar to ALU7_HUMA	carb_anhydrase TM	3.2 3.2
00	409533 411248	AW969543 AA551538	Hs.21291 Hs.69321	mitogen-activated protein kinasé kinase kin KIAA1359 protein	TM	3.2
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cys-	SS,IL8	3.2
	430259	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog	TM	3.2
	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	SS	3.2
65	444471	AB020684	Hs.11217	KIAA0877 protein	TM	3.2
	421674	T10707	Hs.296355	neuronal PAS domain protein 2	Ribosomal_L31e	3.2
	434163	AW974720	Hs.25206	ESTs	TM	· 3.2
	421991	NM_014918	Hs.110488	KIAA0990 protein	SS	3.2
70	409589	AW439900	Hs.256914	ESTs	TM	3.2 3.2
70	414147	BE091634	U- 24030	gb:IL2-BT0731-240400-069-C03 BT0731	TM	3.2
	414661 437537	T97401 AA758974	Hs.21929 Hs.121417	ESTs ESTs, Wealtly similar to unnamed protein p	TM TM	3.2 3.2
	439702	AW085525	Hs.134182	ESTs	A2M	3.1
	420552	AK000492	Hs.98806	hypothetical protein	TM	3.1
75	441028	AI333660	Hs.17558	ESTs	ICE_p20,CARD	3.1
	425264	AA353953	Hs.20369	ESTs, Weakly similar to gonadotropin indu	TM	3.1
	422109	S73265	Hs.1473	gastrin-releasing peptide	SS,Bombesin	3.1
	441859	AW194364	Hs.128022	ESTs, Wealdy similar to FIG1 MOUSE FIG	TM	3.1
0.0	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMA	SS,Ephrin	3.1
80	447866	AW444754	Hs.211517	ESTs	homeobox	3.1
	419978	NM_001454	Hs.93974	forkhead box J1	Fork_head	3.1
	446219	A1287344	Hs.149827	ESTs	MIP	3.1
	448428	AF282874	Hs.21201	nectin 3; DKFZP566B0846 protein	TM,ig	3.1
	407615	AW753085	•	gb:PM1-CT0247-151299-005-a03 CT0247	TM	3.1
				200		

	440540	AMERICA 40		ECT.	PARCEE BY BARGEE	3.1	
	410518	AW976443	Hs.285655	ESTs	RasGEF,PH,RhoGEF	3.1	
	418396	A1765805	Hs.26691	ESTs	TM	3.1	
	427855	R61253	Hs.98265	ESTs	TM		
-	429272	W25140	Hs.110667	ESTs	TM	3.1	
5	450171	AL133661	Hs.24583	hypothetical protein DKFZp434C0328	TM	3.1	
	414774	X02419	Hs.77274	plasminogen activator, urokinase	SS, kringle, trypsin	3.1	
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38kD)	TM	3.1	
	420062	AW411096	Hs.94785	hypothetical protein LOC57163	TM	3.1	
	428698	AA852773	Hs.297939	ESTs; Wealty similar to neogenin (H.sapie	TM	3.1	
10	427051	BE178110	Hs.173374	ESTs	TM	3.1	
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic diffe	SS	3.1	
	452906	BE207039	Hs.75621	serine (or cysteine) proteinase inhibitor, cla	TM	3.1	
	429419	AB023226	Hs.202276	KIAA1009 protein	TM	3.1	
	417517	AF001176	Hs.82238	POP4 (processing of precursor, S. cerevisia	TM	3.1	
15	406137	#(NOCAT)		n	TM	3.1	
IJ	424800	AL035588	Hs.153203	MyoD family inhibitor	TM	3.1	
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	TM	3.1	
				KIAA0328 protein	SS	3.1	
	420392	Al242930	Hs.97393		voltage_CLC,CBS	3.1	
20	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone		3.1	
20	429334	D63078	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone	Glyco_hydro_2		
	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	TM	3.1	
	450506	NM_004460	Hs.418	fibroblast activation protein; alpha	SS,Peptidase_S9	3.0	
	433849	BE465884	Hs.280728	ESTs	TM	3.0	
	411984	NM_005419	Hs.72988	signal transducer and activator of transcript	SH2,STAT	3.0	
25	422530	AW972300	Hs.118110	bone marrgw stromal ceil antigen 2	TM	3.0	
	422128	AW881145		gb:QV0-OT0033-010400-182-a07 OT0033	TM	3.0	
	409757	NM_001898	Hs.123114	cystatin SN	SS,cystatin	3.0	
	418727	AA227609	Hs.94834	ESTs	TM	3.0	
	422244	Y08890	Hs.113503	karyopherin (importin) beta 3	TM	3.0	
30	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatidat	TM	3.0	
50	432358	Al093491	Hs.72830	ESTs	SS	3.0	
	416896		Hs.5638	KIAA1572 protein	BTB	3.0	
		AI752862			TM	3.0	
	447312	AI434345	Hs.36908	activating transcription factor 1	TM	3.0	
25	445021	AK002025	Hs.12251	Homo sapiens cDNA FLJ11163 fis, clone P			
35	422611	AA158177	Hs.118722	fucosyltransferase 8 (alpha (1,6) fucosyltran	SS	3.0	
	453597	BE281130	Hs.33713	myo-inositol 1-phosphate synthase A1	TM	3.0	
	401197	#(NOCAT)		0	arf,Ets	3.0	
	403000	BE247275	Hs.151787	U5 snRNP-specific protein, 116 kD	TM	3.0	
	410008	AA079552		gb:zm20h12.s1 Stratagene pancreas (93720	TM,FG-GAP	3.0	
40	413268	AL039079	Hs.75256	regulator of G-protein signalling 1	RGS	3.0	
	414080	AA135257	Hs.47783	ESTs, Weakly similar to T12540 hypotheti	TM	3.0	
	426882	AA393108	Hs.97365	ESTs	TM	3.0	
	427651	AW405731	Hs.18498	Homo sapiens cDNA FLJ12277 fis, clone M	TM	3.0	
	439444	Al277652	Hs.54578	ESTs	TM	3.0	
45	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	TM	3.0	
	444895	AI674383	Hs.301192	EST cluster (not in UniGene)	TMASC	3.0	
	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone	TM	3.0	
	414725	AA769791	Hs.120355	Homo sapiens cDNA FLJ13148 fis, clone N	TM,7tm_1	3.0	
					SS	3.0	
50	434241	AF119913	Hs.283607	hypothetical protein PRO3077	TM	3.0	
30	424962	NM_012288	Hs.153954	TRAM-like protein		3.0	
•	411987	AA375975	Hs.183380	ESTs, Moderately similar to ALU7_HUMA	TM		
	421977	W94197	Hs.110165	ribosomal protein L26 homolog	TM	3.0	
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-conju	TM	3.0	
	407872	AB039723	Hs.40735	frizzled (Drosophila) homolog 3	TM,7tm_2,Fz,Frizzled	3.0	
55	442577	AA292998	Hs.163900	ESTs	TM	3.0	
	416120	H46739		gb:yo14h02.s1 Soares adult brain N2b5HB5	TM	3.0	
	443775	AF291664	Hs.204732	matrix metalloproteinase 26	TM,Peptidase_M10,7tm_1	3.0	
	414664	AA587775	Hs.66295	Homo sapiens HSPC311 mRNA, partial cd	TM	3.0	
	457590	Al612809	Hs.5378	spondin 1, (f-spondin) extracellular matrix	SS	3.0	
60	418946	Al798841	Hs.132103	ESTs	TM	3.0	
00	457940	AL360159	Hs.30445	Homo sapiens mRNA full length insert cDN	TM,SPRY,7tm_1	3.0	
	701070	. 2000103	. 60.00770	Tomo copiono tina es ten renger mont cost			
	TADIE 4	ED.					
	TABLE 1		l Identifica a				
65		ique Eos probese					
65		ber: Gene cluster					
	ACCESSIO	n: Genbank acce	ssion numbers				
	-	04741					
	Pkev	CAT Number	Accession				

	Pkey	CAT Number	Accession
70	407615	1005404_1	AW753085 AW753082 AW054744 AW753107 AW753087
	409073	109851_1	AA063458 AA063018 Al444822
	409745	115237_1	AA077391 Al347618 Al361453 Al088754 AW207491 AW960912 AA921874 AA286833 AA150722 BE152353 AW188822 BE152450
	410008	116812_1	AA079552 BE142525 BE142527
	414147	1421271	BE091634
	414315	143512_1	Z24878 AA494098 F13654 AA494040 AA143127 ·
75	416120	1571266_1	H46739 H51513 H19779
	419311	183793_1	AA689591 AW974261 AA236240 Al077451 AA631399 AW974262
	419546	185766_1	AA244199 AA244272 H57440
	422128	211994_1	AW881145 AA490718 M85637 AA304575 T05067 AA331991
	427072	274884_1	H38046 W69645 AA397968 H38047
80	428679	294049_1	AA431765 AA432015
	438993	467651_1	AA828995 AA834879 A1926361
	447197	711623_1	R36075 Al366546 R36167

5

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TABLE 15C:
Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
Strand: Indicates DNA strand from which exons were predicted
Nt. position: Indicates nucleotide positions of predicted exons

	Pkey	Ref	Strand	Nt_position
	400881	2842777	Minus	91446-91603,92123-92265
10	401197	9719705	Pius	176341-176452
	401435	8217934	Minus '	54508-55233
	404440	7528051	Plus	80430-81581
	404939	6862697	Plus	175318-175476
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
15	405547	1054740	Plus	124361-124520,124914-125050
	406137	9166422	Minus	30487-31058
	406357	9256126	Minus	58313-58489
	406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

Table 16A lists about 92 genes up-regulated in mucinous-type ovarian cancer compared to normal adult tissues. These were selected as for Table 14A, except that the "average" ovarian cancer level was set to the 75th percentile amongst various mucinous-type ovarian cancers, and the tumor/normal tissue ratio was greater than or equal to 2.5.

TABLE 16A: ABOUT 92 UP-REGULATED GENES, MUCINOUS OVARIAN CANCER VERSUS NORMAL ADULT TISSUES Pkey: Primekey Ex. Accn: Exemplar Accession
UG ID: UniGene ID
Title: UniGene title
Prot. Dom: Predicted protein domain structure **25** .

30 ratio: ratio tumor vs. normal tissues

	Pkey	Ex. Acon	UGID	Title	Prot. Dom.	ratio .
	430691	C14187	Hs.103538	ESTs		34.9
25	432938	T27013	Hs.3132	steroidogenic acute regulatory protein	START	28.0
35	418007	M13509	Hs.83169	Matrix metalloprotease 1 (interstitial collag	SS,Peptidase_M10	22.3
	451181	Al796330	Hs.207461	ESTs		10.8
	452838	U65011	Hs.30743	Preferentially expressed antigen in melanom		10.0
	407638	AJ404672	Hs.288693	EST		9.3
40	450159	AI702416	Hs.200771	ESTs, Weakly similar to CAN2_HUMAN		9.2
40	426890	AA393167	Hs.41294	ESTs		9.1
	421155	H87879	Hs.102267-	lysyl oxidase	SS,Lysyi_oxidase	8.9
	437099	N77793	Hs.48659	ESTs, Highly similar to LMA1_HUMAN L	laminin_EGF	7.6
	453866	AW291498	Hs.250557	ESTs		7.6
	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-rel		7.4
45	418738	AW388633	Hs.6682	solute carrier family 7, member 11		7.2
	431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone P	RA .	7.0
	449579	AW207260	Hs.134014	prostate cancer associated protein 6		6.7
	424586	NM_003401	Hs.150930	X-ray repair complementing defective repa		6.7
	445891	AW391342	Hs.199460	ESTs		6.2
50	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	wnt .	6.1
	452705	H49805	Hs.246005	ESTs		6.1
	421285	NM_000102	Hs.1353	cytochrome P450, subfamily XVII (steroid	TM,p450	5.5
	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 prote	•	5.3
	420159	AI572490	Hs.99785	ESTs		5.3
55	451105	AI761324		gb:wi60b11.x1 NCI_CGAP_Co16 Homo s		5.2
	409049	A1423132	Hs.146343	ESTs		5.0
	448674	W31178	Hs.154140	ESTs	TM	5.0
	423811	AW299598	Hs.50895	homeo box C4		4.9
	427469	AA403084	Hs.269347	ESTs		4.9
60	447033	AI357412	Hs.157601	EST - not in UniGene	PH	4.9
	424433	H04607	Hs.9218	ESTs		4.9
	448811	AI590371	Hs.174759	ESTs	TM .	4.8
	444330	Al597655	Hs.49265	ESTs		4.8
	409041	AB033025	Hs.50081	KIAA1199 protein		4.7
65	418735	N48769	Hs.44609	ESTs		4.5
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	KH-domain	4.5
	430073	U86136	Hs.232070	telomerase-associated protein 1	WD40	4.4
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfotran	SS	4.4
	422260	AA315993	Hs.105484	ESTs; Weakly similar to LITHOSTATHIN		4.4
70	421110	AJ250717	Hs.1355	cathepsin E	SS,asp	4.3
	445676	Al247763	Hs.16928	ESTs		4.2
	430704	AW813091		qb:RC3-ST0186-240400-111-d07 ST0186	Epimerase	3.8
	414569	AF109298	Hs.118258	Prostate cancer associated protein 1	TM	3.8
	438078	AI016377	Hs.131693	ESTs		3.7
75	434032	AW009951	Hs.206892	ESTs		3.7
	445657	AW612141	Hs.279575	ESTs	7tm_1	3.6
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN		3.5
	455666	BE055813		gb:RC2-BT0318-110100-012-a08 BT0318		3.5
	448844	AJ581519	Hs.177164	ESTs .		3.5
80	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induced g	SS	3.5
	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	TM -	3.4
	458123	AW892676		gb:CM3-NN0004-280300-131-c12 NN0004		3.4
	407385	AA610150	Hs.272072	ESTs, Moderately similar to ALU7_HUMA		3.4
	424894	H83520	Hs.153678	reproduction 8	SS,UBX	3.3
				•		

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	424639	Al917494	Hs.131329	ESTs		3.3 3.2
	414083	AL121282	Hs.257786	ESTs transforming growth factor, alpha	SS,EGF	3.2
	426471 428927	M22440 AA441837	Hs.170009 Hs.90250	ESTs	00,20	3.1
5	406129	#(NOCAT)		0	TM,cNMP_binding	3.1
	452699	AW295390	Hs.213062	ESTs	homeobax	3.1 3.1
	425842 428976	AI587490 AL037824	Hs.159623 Hs.194695	NK-2 (Drosophila) homolog B ras homolog gene family, member I	ras	3.1
	436396	AI683487	Hs.299112	Homo sapiens cDNA FLJ11441 fis, clone H	wni	3.0
10	454077	AC005952	Hs.37052	insulin-like 3 (Leydig cell)	SS,Insulin,pkinase	3.0
	404253	#(NOCAT)	11- 400400	0 Ironomining factor	histone G9a,PHD	2.9 2.9
	452461 429597	N78223 NM_003816	Hs.108106	transcription factor a disintegrin and metalloproteinase domain	TM	2.9
	413289	AA128061	Hs.114992	ESTs		2.9
15	429703	T93154	Hs.28705	ESTs .		2.9 2.8
	407829	AA045084 AW298244	Hs.29725 Hs.293507	Homo sapiens cDNA FLJ13197 fis, clone N ESTs		2.8
•	424796 424086	A1351010	Hs.102267	lysyl oxidase ·	Lysyl_oxidase	2.8
	408427	AW194270	Hs.177236	ESTs		2.7
20	450375	AA009547	Hs.8850	a disintegrin and metalloproteinase domain		2.7 2.7
	446999 428819	AA151520 AL135623	Hs.279525 Hs.193914	hypothetical protein PRO2605 KIAA0575 gene product		2.7
	422956	BE545072	Hs.122579	ESTs		2.7
	428949	AA442153	Hs.104744	ESTs, Wealdy similar to AF208855 1 BM-0		2.7
25	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	TM,EGF	2.6 2.6
	420380 428651	AA640891 AF196478	Hs.102406 Hs.188401	ESTs annexin A10	TM,annexin	2.6
	417849	AW291587	Hs.82733	Nidogen 2	EGF,ldl_recept_b	2.6
20	453700	AB009426	Hs.560	apolipoprotein B mRNA editing enzyme, ca	TM .	2.6
30	417975	AA641836	Hs.30085	Homo sapiens cDNA: FLJ23186 fis, clone		2.6 2.6
	448756 425087	A1739241 R62424	Hs.171480 Hs.126059	ESTs ESTs		2.5
	444153	AK001610	Hs.10414	hypothetical protein FLJ10748	Kelch	2.5
2.5	443211	AJ128388	Hs.143655	ESTs	tion	2.5
35	415263	AA948033	Hs.130853 Hs.233364	ESTs ESTs	histone GSHPx	2.5 2.5
	432867 438639	AVV016936 Al278360	Hs.31409	ESTs	30.11 N	2.5
	455386	AW935875		gb:QV3-DT0019-120100-055-d06 DT0019		2.5
40	419092	J05581	Hs.89603	mucin 1, transmembrane	TM,SEA	2.5 2.5
40	452055	Al377431	Hs.293772	ESTs		23
45	CAT number	i: ue Eos probese er: Gene cluste Genbank acce	er number			
50	Pkey 430704 451105 455386 455666 458123	CAT Numbe 322217_1 859083_1 1287756_1 1349545_1 479942_1	AW813091 A AI761324 AV AW935875 BE065813 B	AW206655 AA484440 W880941 AW880937 BE069116 BE160251 BE065788 BE065889 BE065832 AA853877 D44747		•
	TABLE 160	:		•		
55	Pkeyr Unic	ue number con	responding to	an Eos probesel	have the second and the section in the se	-utilization political The DNA coguence of
				bers in this column are Genbank Identifier (GI) num n, et al. (1999) <u>Nature</u> 402:489-495	ders. Dumlam I. et al. Teleis to the	publication entitled. The DNA sequence of
	Strand: Inc	licates DNA str	rand from which	h exons were predicted		
60	Nt_position	: Indicates nuc	cleotide positio	ns of predicted exons		
oo	Pkey	Ref	Strand	Nt_position		
	404253	9367202	Minus	55675-56055		
	406129	9160131	Plus	2567-3056		
65						
03	Table 17A	lists about 183	genes up-reg	ulated in endometricid-type ovarian cancer compare	d to normal adult tissues. These wer	e selected as for Table 14A, except that the
	"average"	ovarian cancer	level was set	to the 75th percentile amongst various endometrioid	-type ovarian cancers, and the tumori	normal tissue ratio was greater than or equal to
	25.					
70	TARIF 17	A- AROUT 183	HP-REGULA	TED GENES, ENDOMETRIOID OVARIAN CANCER	VERSUS NORMAL ADULT TISSUE	S
, ,	Pkey: Prin	nekey				
	Ex. Acon:	Exemplar Acce	ession			
	UG ID: Ur Title: UniO					
75		.: Predicted pro	otein domains			
		tumor vs. nom				
	Dhen	Ex. Acon	UGID	Title	Prot. Dom.	ratio
	Pkey 452838	U65011	Hs.30743			38.9
80	435094	AI560129	Hs.277523	EST		28.8
	428153 428187	AW513143 AI687303	Hs.98367 Hs.285529	hypothetical protein FLJ22252 similar to 3 ESTs	or .	24.1 23.9
	449034	A1624049	. 2.200023	gb:ts41a09.x1 NCI_CGAP_Ut1 Homo sa		19.9
	453102	NM_00719	7 Hs.31664	frizzled (Drosophila) homolog 10	TM,Fz,Frizzled	15.7
				21:	2	

				-0		
	412925	AI089319	Hs.179243	ESTs		15.7 13.6
	438817 447033	Al023799 Al357412	Hs.163242 Hs.157601	ESTs EST - not in UniGene	PH	13.5
	433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMA	rn	13.1
5	422956	BE545072	Hs.122579	ESTs		12.9
	450451	AW591528	Hs.202072	ESTs		11.9
	453964	AI961486	Hs.12744	ESTs gb:os26b03.s1 NCI_CGAP_Kid5 Homo sa	homeobox	11.5 11.4
	442438 431989	AA995998 AW972870	Hs.291069	ESTs	SS	10.3
10	413623	AA825721	Hs.246973	ESTs	•	9.7
	440901	AA909358	Hs.128612	ESTs		9.6
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	KH-domain	9.6 9.3
	421478 448706	Al683243 AW291095	Hs.97258 Hs.21814	ESTs . class II cytokine receptor ZCYTOR7	SS,Tissue_fac	9.2
15	410566	AA373210	Hs.43047	Homo saplens cDNA FLJ13585 fis, clone P	00(1.0000000	8.7
	438993	AA828995		integrin; beta 8	SS.integrin_B	8.7
	427121	AI272815	Hs.173656	KIAA0941 protein	C2, homeobox	8.4 8.1
	420610 427356	AI683183 AW023482	Hs.99348 Hs.97849	distal-less homeo box 5 ESTs	IROITEODOX	8.0
20	446577	AB040933	Hs.15420	KIAA1500 protein		8.0
	431118	BE264901	Hs.250502	carbonic anhydrase VIII	carb_anhydrase	7.5
	448112		Hs.301018	ESTs, Weakly similar to ALUB_HUMAN	18 11 Mars Al James	6.9
	451106 449433	BE382701 AI672096	Hs.25960 Hs.9012	N-myc ESTs	HLH,Myc_N_term	6.6 6.3
25	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1 (y		6.3
	434536	AA083764	Hs.241334	ESTs		6.1
	453688	AW381270	Hs.194110	Homo sapiens mRNA; cDNA DKFZp434C	Materia	5.9 5.8
	422805 400292	AA436989 AA250737	Hs.121017 Hs.72472	H2A histone family; member A BMPR-lb; bone morphogenetic protein rec	histone	5.0 5.7
30	443179	AI928402	Hs.6933	Homo sapiens cDNA FLJ12684 fis, clone N		5.6
-	418134	AA397769	Hs.86617	ESTs		5.5
	452249	BE394412	Hs.61252	ESTs	homeobox	5.5
	409269 413335	AA576953 Al613318	Hs.22972 Hs.48442	Homo sapiens cDNA FLJ13352 fis, clone O ESTs	TM,UPF0016	5.5 5.4
35	441081	AL584019	Hs.169006	ESTs, Moderately similar to plakophilin 2b	PAX	5.4
	428029	H05840	Hs.293071	ESTs		5.3
	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitami	p450	5.3 5.2
	409094 432938	AW337237 T27013	Hs.3132	gb:xw82f01.x1 NCI_CGAP_Pan1 Homo sa steroidogenic acute regulatory protein	START	5.2 5.1
40	410102	AW248508	Hs.279727	ESTs;	SS	5.1
	447835	AW591623	Hs.164129	ESTs		5.1
	438202	AW169287	Hs.22588	ESTS		5.0 5.0
	423992 425905	AW898292 AB032959	Hs.137206 Hs.161700	Homo sapiens mRNA; cDNA DKFZp564H KIAA1133 protein	TM	5.0
45	452461	N78223	Hs.108106	transcription factor	G9a,PHD	4.9
	430691	C14187	Hs.103538	ESTs		4.8
	441675 425695	Al914329 NM_005401	Hs.5461	ESTs protein tyrosine phosphatase, non-receptor	Band_41,Y_phosphatase	4.7 4.6
	440340	AW895503	Hs.125276	ESTs	omo_iiii Thiashama	4.5
50	428579	NM_005756		G protein-coupled receptor 64	TM	4.5
	444783	AK001468 Al797515	Hs.62180	ESTs ESTs Madarataly similar to ALLIT VIIMA	PH	4.4 4.4
	451459 413395	AI266507	Hs.270560 Hs.145689	ESTs, Moderately similar to ALU7_HUMA ESTs		4.3
	415263	AA948033	Hs.130853	ESTs	histone	4.2
55	413988	M81883	Hs.75668	glutamate decarboxylase 1 (brain, 67kD)	pyridoxal_deC	4.2
	452030	AL137578	Hs.27607	Homo sapiens mRNA; cDNA DKFZp564N hypothetical protein FLJ20069		4.1 4.1
	418852 446431	BE537037 R45652	Hs.273294 Hs.153486	ESTs		4.1
	434891	AA814309	Hs.123583	ESTs		4.0
- 60	415139	AW975942	Hs,48524	ESTs	G-patch	4.0
	453197	Al916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN A ESTs		4.0 3.9
	447112 420633	H17800 NM_014581	Hs.7154 Hs.99526	odorant-binding protein 2B	TM,lipocalin	3.9
	459574	Al741122	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone N		3.9
65	415138	C18356	Hs.78045	tissue factor pathway Inhibitor 2 TFPI2	Kunitz_BPTI,G-gamma	3.9
	414083 442006	AL121282 AW975183	Hs.257786 Hs.292663	ESTs ESTs		3.7 3.7
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblastoma	Thymosin	3.7
	424906	Al566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein.		3.7
70	456662	NM_002448		msh (Drosophila) homeo box homolog 1 (fo	homeobox	3.7
	429125 435538	AA446854 AB011540	Hs.271004 Hs.4930	ESTs low density lipoprotein receptor-related pro		3.6 3.6
	458861	A1630223	18.4500	gb:ad06g08r1 Proliferating Erythroid Cells	PHD	3.5
~-	418506	AA084248	Hs.85339	G protein-coupled receptor 39		3.5
75	423123		Hs.124027	SELENOPHOSPHATE SYNTHETASE; H	AIRS,AIRS	3.4
	437960	A1669586 AA032279	Hs.222194	ESTS STEAP1	TM	3.4 3.4
	400298 407162	N63855	Hs.61635 Hs.142634	zinc finger protein	***	3.4
00	408621	Al970672	Hs.46638	chromosome 11 open reading frame 8; feta	•	3.3
80	445829	A1452457	Hs.145526	ESTs		3.3 3.3
	450262 457979	AW409872 AA776655	Hs.271166 Hs.270942	ESTs, Moderately similar to ALU7_HUMA ESTs	TM	3.3
	402606	#(NOCAT)	. 10.21 1374	20.0		3.2
	426471	M22440	Hs.170009 .	transforming growth factor, alpha	SS,EGF	3.2

	430294	AI538226	Hs.135184	ESTs	potyprenyt_synt	3.2
	448027	AJ458437	Hs.177224	ESTs		3.2
	432619	AW291722	Hs.278526	related to the N terminus of tre	TBC	3.2
_	413627	BE182082	Hs.246973	ESTs		3.2
5	441377	BE218239	Hs.202656	ESTs		3.2
	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone N		3.2
	433527	AW235613	Hs.133020	ESTs		3.2
	450171	AL133661	Hs.24583	hypothetical protein DKFZp434C0328	TM	3.2
	419807	R77402		gb:yi75f11.s1 Soares placenta Nb2HP Hom		3.1
10	418867	D31771	Hs.89404	msh (Orosophila) homeo box homolog 2	homeobox	3.1
	419335	AW960145	Hs.284137	Homo sapiens cDNA FLJ12888 fis, clone N		3.1
	450480	X82125	Hs.25040	zinc finger protein 239	zf-C2H2	3.1
	420149	AA255920	Hs.88095	ESTs		3.1
	413415	AA829282	Hs.34969	ESTs	•	3.1
15	438966	AW979074		gb:EST391184 MAGE resequences, MAGP		3.1
	431041	AA490967	Hs.105276	ESTs	Oxysterol_BP	3.1
	415245	N59650 ·	Hs.27252	ESTs		3.0
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkinesin6	kinesin	3.0
•	431707	R21326	Hs.267905	hypothetical protein FLJ10422		3.0
20	448816	AB033052	Hs.22151	KIAA1226 protein		3.0
	447866	AW444754	Hs.211517	ESTs	homeobox	3.0
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	•	3.0
	406997	U07807	Hs.194762	Human metallothionein IV (MTIV) gene, c		3.0
~ ~	433426	H69125	Hs.133525	ESTs '	TM	3.0
25	420440	NM_002407	Hs.97644	mammaglobin 2	Uteroglobin	3.0
	420181	Al380089	Hs.158951	ESTs		3.0
	458627	AW088642	Hs.97984	ESTs; Weakly similar to WASP-family pro		2.9
	452055	Al377431	Hs.293772	ESTs		2.9
••	429663	M68874	Hs.211587	Human phosphatidylcholine 2-acylhydrolas	C2,PLA2_B	2.9
30	415125	AF061198	Hs.301941	Homo sapiens mRNA for norepinephrine tr	TM,SNF	2.9
	412708	R26830	Hs.106137	ESTs	TM,7tm_2,Rho_GDI	2.9
	451389	N73222	Hs.21738	KIAA1008 protein		2.9
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	DIX,RGS	29
25	435185	AA669490	Hs.289109	dimethylarginine dimethylaminohydrolase		2.9
35	428054	A1948688	Hs.266619	ESTs		2.9
	448243	AW369771	Hs.77496	ESTs	_0	2.9
	425723	NM_014420		dickkopf (Xenopus taevis) homolog 4	SS	29
	432415	T16971	Hs.289014	ESTs		2.9
40	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosin)		2.9
40	400195			0		2.9
	449874	AA135688	Hs.10083	ESTs		2.8
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	Hydrolase	2.8
	428093	AW594506	Hs.104830	ESTs		2.8
45	409640	U78722	Hs.55481	zinc finger protein 165	TM,zf-C2H2,SCAN	2.8
45	424169	AA336399	Hs.153797	ESTs	mito_can	2.8
	409638	AW450420	Hs.21335	ESTs		2.8
	440048	AA897461	Hs.158469	ESTs, Wealthy similar to envelope protein [		2.8
	426890	AA393167	Hs.41294	ESTs		2.8
5Λ	452771	T05477		gb:EST03366 Fetal brain, Stratagene (cat93		2.8
50	422505	AL120862	Hs.124165	ESTs; (HSA)PAP protein (programmed ce	4.00110.4	2.8
	416624	H69044		gb:yr77h05.s1 Soares fetal liver spleen 1NF	zf-C3HC4	2.8
	445870	AW410053	Hs.13406	syntaxin 18	TM	2.7
	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone		2.7
<i>5 5</i>	447342	AI199268	Hs.19322	ESTs; Weakly similar to !!!! ALU SUBFAM		2.7
55	421247	BE391727	Hs.102910	general transcription factor IIH, polypeptid		2.7
	419752	AA249573	Hs.152618	ESTs		2.7
	410658	AW105231	Hs.192035	ESTs		2.7
	437698	R61837	Hs.7990	ESTs .		2.7
60	458027	L49054	Hs.85195	ESTs, Highly similar to t(3;5)(q25.1;p34) f		2.7
60	438689	AW129261	Hs.250565	ESTS	CCAN	2.7
	439876	AJ376278	Hs.100921	ESTs, Weakly similar to ALU7_HUMAN A	SCAN	2.7
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to M	pkinase	2.7
	436406	AW105723	Hs.125346	ESTs		2.7
65	437938	AI950087	11.00704	ESTs; Weakly similar to Gag-Pol polyprote		2.7
65	419917	AA320068	Hs.93701 .	Homo sapiens mRNA; cDNA DKFZp434E		2.7
	434836	AA651629	Hs.118088	ESTs		2.7 2.7
	448404	BE089973	11- 40000	gb:RC6-BT0709-310300-021-G07 BT0709	WD40	
	444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-	WD40	2.7
70	409757		Hs.123114	cystatin SN	SS,cystatin	2.6
70	443775	AF291664	Hs.204732	matrix metalloproteinase 26	TM,Peptidase_M10,7tm_1	2.6
	427961	AW293165	Hs.143134	ESTs		2.6 2.6
	426668	AW136934	Hs.97162	ESTs '		
	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	wni historia A1 no DHE27	26 26
75	434669	AF151534	Hs.92023	core histone macroH2A2.2	histone,A1pp,DUF27	
13	417389	BE260964	Hs.82045	Midkine (neurite growth-promoting factor 2	ss,tm,ptn_mk	2.6 2.6
•	451009	AA013140	Hs.115707	ESTs	nkinosa	
	429774	AI522215	Hs.50883	ESTs	pkinase	2.6
	439951	AI347067	Hs.124636	ESTs	TM AIDS formul transf	2.6
δU	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfera	AIRS,formyl_transf	2.5
80	416806		3 Hs.79993	peroxisomal biogenesis factor 7	WD40	2.5
	420900	AL045633	Hs.44269	ESTs	Ald_Xan_dh_C	2.5
	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	Dihydroorotase	2.5
	459583	A1907673	11- 450500	gb:IL-BT152-080399-004 BT152 Homo sa	DAV	2.5
	440870	A1687284	Hs.150539 .	Homo sapiens cDNA FLJ13793 fis, clone T	PAX,	2.5
				014		

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	446693 407289	AW750373 AA135159	Hs.42315 Hs.203349	Homo sapiens cDNA FLJ13036 fis, clone N Homo sapiens cDNA FLJ12149 fis, clone M	тм	2.5 2.5 2.5	
5	400882 431322 424081 451995 403381	AW970622 NM_006413 AW514021 #(NOCAT)	Hs.245510	0 gb:EST382704 MAGE resequences, MAGK ribonuclease P (30kD) ESTs 0		25 25 25 25 25	
10	419488 418882	AA316241 NM_004996	Hs.90691 Hs.89433	nucleophosmin/nucleoplasmin 3 ATP-binding cassette, sub-family C (CFTR	SS TM_ABC_membrane	2.5 2.5	
	TABLE 17B: Pkey: Unique Eos probeset identifier number CACHESTON: Gene cluster number Accession: Genbank accession numbers						
15	Pkey CAT Number Accession 409094 1099611_1 AW337237 AW861642 AW861655 AW858008 AW857990 AW858007 416624 1604694_1 H69044 T47567 H75691 T50292						
20	419807 431322 437938	188252_1 331543_1 44573_2	R77402 AA262462 AA25098B R06794 AW970622 AA503009 AA502998 AA502989 AA502805 T92188 AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493 AA927794 AI560251 AW874068 AL 134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI689062				
25	AA282915 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539642 AA642789 AA856975 AW505512 AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW855538 AA180009 AA337499 AW961101 AA251669 AA251874 AI81925 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513995 AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531 H83488 W37181 W78802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005						
30	438966 438993 442438 448404 449034	467436_1 467651_1 542469_1 761515_1 794817_1	AW979074 AA834841 AA828650 AA828995 AA834879 A1926361 AA995998 A1916584 R61781 T77332 F07756 F08149 F07647 BEDR9973 Al498612 AW805032 AI624049 AW117770 Al858360				
35	452771 458861	930983_1 798085_1	T05477 T07855 AI917711 AI630223 AI630470				
40	TABLE 17C: Pkey: Unique number corresponding to an Eos probeset Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled 'The DNA sequence of human chromosome 22' Dunham, et al. (1999) Nature 402:489-495 Strand: Indicates DNA strand from which exons were predicted NL_position: Indicates nucleotide positions of predicted exons						
45	Pkey 400882 402606 403381	Ref 2842777 9909429 9438267	Minus I	NL_position 110431-110708 31747-82094 26009-26178			
50	Table 18 lists lists 178 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode proteins that are secreted into blood, lymph, or other bodily fluids. These genes, and/or their protein products, in combination or alone, are ideal candidates for the early diagnosis of ovarian cancer. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the railo of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 24, and that are likely to encode secreted or extracellularly-shed proteins. The "average" ovarian cancer level was set to the 90th percentile amongst various ovarian cancer						
55	samples. The "average" normal adult tissue level was set to the 90th percentile amongst various non-matignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various 149 non-matignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.						
60	TABLE 18: ABOUT 178 UP-REGULATED GENES ENCODING SECRETED PROTEINS, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES Pkey: Primekey Ex. Aca:: Exemplar Accession UG ID: UniGene ID Title: UniGene title ratio: ratio tumor vs. normal tissues						
65	Pkey 428579 436982 427585	Ex. Acon NM_005756 AB018305 D31152	Hs.184942 Hs.5378	Title G protein-coupled receptor 64 spondin 1, (f-spondin) extracellular mat collagen; type X; atpha 1 (Schmid metaph	ratio 30.5 29.4 27.0		
70	423739 418007 438993 428664 439820	AA398155 M13509 M73780 AK001666 AL360204	Hs.97600 Hs.83169 Hs.52620 Hs.189095	ESTs Matrix metalloprotease 1 (interstilial c Integrin; beta 8 similar to SALL1 (sal (Drosophila)-like Homo sapiens mRNA full length insert cDN	22.7 20.6 16.7 16.5 16.5		
75	400289 421155 431989 426635 424581	X07820 H87879 AW972870 BE395109 M62062	Hs.2258 Hs.102267 Hs.291069 Hs.129327	Matrix Metalloproteinase 10 (Stromolysin lysyl oxidase ESTs ESTs catenin (cadherin-associated protein), a	16.2 16.1 15.9 15.7		
80	424561 428976 416209 439706 452055 410102 428392	AL037824 AA236776 AW872527 AI377431 AW248508 H10233	Hs.194695 Hs.79078 Hs.59761 Hs.293772	Catalan (Catalana-Sociate) protein, a ras homolog gene family, member I MAD2 (mitotic arrest deficient, yeast, h ESTs ESTs; secretory granule, neuroendocrine protei	15.1 15.0 14.7 13.2 12.5 12.4		

	402606	AA434329	Hs.36563	hypothetical protein FLJ22418	11.5
	443715	AL583187	Hs.9700	cyclin E1	10.7
	433496	AF064254	Hs.49765	VLCS-H1 protein	10.6
5	418601	AA279490	Hs.86368	calmegin	10.3
3	409269	AA576953	Hs.22972	Homo sapiens cDNA FLJ13352 fis,	10.1
	445537 427344	AJ245571 NM_000869	Hs.12844 Hs 2142	EGF-like-domain; multiple 6 5-hydroxytryptamine (serotonin) receptor	9.9 9.7
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	9.7
10	429782	NM_005754		Ras-GTPase-activating protein SH3-domain	9.5
10	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	9.4
	407881 435509	AW072003 AI458679	Hs.40968 Hs.181915	heparan sulfate (glucosamine) 3-0-sulfot ESTs	9.4 9.3
	408908	BE296227	Hs.48915	serine/threonine kinase 15	9.0
	433764	AW753676	Hs.39982	ESTs	9.0
15	445413	AA151342	Hs.12677	CGI-147 protein	8.7
	438078	A1016377	Hs.131693	ESTs	8.6
	447342 415138	Al199268 C18356	Hs.19322 Hs.78045	ESTs; Weakly similar to !!!! ALU SUBFA tissue factor pathway inhibitor 2 TFP12	8.1 7.7
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	7.5
20	426320	W47595	Hs.169300	transforming growth factor, beta 2	7.5
	424001	W67883	Hs.137476	KIAA1051 protein	7.4
	458861 425465	NM_007358 L18964	Hs.31016 Hs.1904	DNA-BINDING PROTEIN M96 protein kinase C; iota	7.3 7.2
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	7.1
25	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic; stratum com	7.0
	409178	BE393948	Hs.50915	kallikrein 5	6.8
	433159	AB035898	Hs.150587	kinesin-like protein 2	6.6
	410530 449048	M25809 Z45051	Hs.64173 Hs.22920	ESTs, Highly similar to VAB1 similar to S68401 (cattle) glucose induc	6.5 6.5
30	422095	A1868872	Hs.288966	ceruloplasmin (ferroxidase)	6.4
	425371	D49441	Hs.155981	mesothelin	6.4
	448706	AW291095	Hs.21814	class II cytokine receptor ZCYTOR7	6.4
	441081	AI584019	Hs.169006 Hs.17731	ESTs, Moderately similar to plakophilin	6.4 6.3
35	447207 420440	AA442233 NM_002407	Hs.97644	hypothetical protein FLJ12892 mammaqlobin 2	6.2
	457030	Al301740	Hs.173381	dihydropyrimidinase-like 2	6.2
	415139	AW975942	Hs.48524	ESTs	6.1
	440870	AI687284	Hs.150539	Homo sapiens cDNA FLJ13793 fis, clone TH	6.0
40	417866 437960	AW067903 AI669586	Hs.82772 Hs.222194	*collagen, type XI, alpha 1* ESTs	6.0 6.0
	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	5.9
	433447	U29195	Hs.3281	neuronal pentraxin II	5.9
	437099	N77793	Hs.48659	ESTs, Highly similar to LMA1	5.9
45	427510 422867	Z47542 L32137	Hs.179312 Hs.1584	small nuclear RNA activating complex, po	5.9 5.8
72	444478	W07318	Hs.240	cartilage oligomeric matrix protein M-phase phosphoprotein 1	5.7
	445640	AW969626	Hs.31704	ESTs, Wealthy similar to KIAA0227 [H.sapi	5.7
	453775	NM_002916		replication factor C (activator 1) 4 (37	5.6
50	419917	AA320068	Hs.93701	Homo sapiens mRNA; cDNA DKFZp434E232	5.6 5.5
50	424539 441645	L02911 A1222279	Hs.150402 Hs 201555	activin A receptor, type I ESTs	5.5
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT	5.4
	426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteogenic	5.4
55	425154	NM_001851		collagen, type IX, alpha 1	5.4
55	416530 445236	U62801 AK001676	Hs.79361 Hs.12457	kalikrein 6 (neurosin, zyme) hypothetical protein FLJ10814	5.3 5.2
	452930	AW195285	Hs.194097	ESTs	5.2
	431130	NM_006103		epididymts-specific; whey-acidic protein	5.1
60	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	5.1
60	432158 447020	W33165 T27308	Hs.55548 Hs.16986	ESTs, Wealdy similar to unknown protein hypothetical protein FLJ11046	5.0 5.0
	443268	AI800271	Hs.129445	hypothetical protein FLJ12496	4.9
	448133	AA723157	Hs.73769	folate receptor 1 (adult)	4.9
65	418882	NM_004996		ATP-binding cassette, sub-family C (CFTR	4.8
65	428555 427528	NM_002214 AU077143		integrin, beta 8	4.8 4.7
	406400	AA343629	Hs.179565 Hs.104570	minichromosome maintenance deficient (S. kallkrein 8 (neuropsin/ovasin)	4.7
	439024	R96696	Hs.35598	ESTs	4.6
70	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	4.6
70	448027	AJ458437	Hs.177224	ESTs Cethoodin I 0	4.6
	404996 443933	NM_001333 AI091631	Hs.87417 Hs.135501	Cathepsin L2 ESTs	4.6 4.5
	409459	D86407	Hs.54481	low density lipoprotein receptor-related	4.4
76	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosin	4.3
75	423123	NM_012247		SELENOPHOSPHATE SYNTHETASE	4.3
	448275 419926	BE514434 AW900992	Hs.20830 Hs.93796	synaptic Ras GTPase activating protein 1 DKFZP586D2223 protein	4.2 4.1
	420736	A1263022	Hs.82204	ESTs	4.1
0.0	419790	U79250	Hs.93201	glycerol-3-phosphate dehydrogenase 2 (mi	4.1
80	414343	AL036166	Hs.75914	coated vesicle membrane protein	4.0
	450654 445808	AJ245587 AV655234	Hs.25275 Hs.298083	Kruppel-type zinc finger protein ESTs	4.0 3.9
	445606	BE260964	Hs.82045	Midkine (neurite growth-promoting factor	3.9
	425247		Hs.155324	matrix metalloproteinase 11 (stromelysin	3.8

	420024	A)rienera	H- occor	ECT.	20
	430634 431846	A1860651 BE019924	Hs.26685 Hs.271580	ESTs Uropiakin 1B	3.8 3.7
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	3.7
_	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	3.7
5	420585	AW505139	Hs.279844	hypothetical protein FLJ10033	3.7
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	3.6 3.6
	411773 421928	NM_006799 AF013758	Hs.72026 Hs.109643	protease, serine, 21 (testisin) polyadenylate binding protein-interactin	3.5
	431958	X63629	Hs.2877	Cadherin 3, P-cadherin (placental)	3.5
10	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	3.5
	418793	AW382987	Hs.88474	prostaglandin-endoperoxide synthase 1 (p	3.5
	422278	AF072873	Hs.114218	ESTS	3.5
	431840 408730	AA534908 AV660717	Hs.2860 Hs.47144	POU domain, class 5, transcription facto DKFZP586N0819 protein	3.4 3.4
15	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	3.3
	421841	AA908197	Hs.108850	KIAA0936 protein	3.3
	439864	AI720078	Hs.291997	ESTs	3.3
	456546	AI690321	Hs.203845	ESTs, Wealthy similar to TWIK-related aci lysyl oxidase-like 1	3.2 3.2
20	410687 414774	U24389 X02419	Hs.65436 Hs.77274	plasminogen activator, urokinase	3.2
20	420552	AK000492	Hs.98806	hypothetical protein	3.1
·	421991	NM_014918		KIAA0990 protein	3.1
	418140	BE613836	Hs.83551	microfibrillar-associated protein 2	3.1
25	458924	BE242158	Hs.24427	DKFZP56601646 protein	3.1 3.1
23	411789 434241	AF245505 AF119913	Hs.72157 Hs.283607	Homo sapiens-mRNA; cDNA DKFZp564I19 hypothetical protein PRO3077	3.1
	422611	AA158177	Hs.118722	fucosyltransferase 8 (alpha (1,6) fucosy	3.1
	409533	AW969543	Hs.21291	mitogen-activated protein kinase kinase	3.1
20	416391	AI878927	Hs.79284	mesoderm specific transcript (mouse) hom	3.1
30	412604 425851	AW978324 NM_001490	Hs.47144	DKFZP586N0819 protein glucosaminyl (N-acetyl) transferase 1, c	3.1 3.0
	431259	NM_006580		claudin 16	3.0
	418557	BE140602	Hs.246645	ESTs	3.0
25	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	3.0
35	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	3.0
	457590 419741	AI612809 NM_007019	Hs.5378	spondin 1, (f-spondin) extracellular mat ubiquitin carrier protein E2-C	2.9 2.9
	428330	1.22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	2.9
	417315	AI080042	Hs.180450	ribosomal protein S24	2.9
40	438777	AA825487	Hs.142179	ESTs, Weakly similar to ORF2 (M.musculus	2.9
	442295	A!827248	Hs.224398	ESTs	2.9
	428248 403019	A1126772 AA834626	Hs.40479 Hs.66718	ESTs RAD54 (S.cerevisiae)-like	2.9 2.8
	436252	AI539519	Hs.120969	Homo sapiens cDNA FLJ11562 fis	2.8
45	419488	AA316241	Hs.90691	nucleophosmin/nucleoplasmin 3	2.8
	434288	AW189075	Hs.116265	ESTs	2.7
	407872	AB039723	Hs.40735	frizzled (Drosophila) homolog 3	2.7 2.7
	431611 443881	U58766 R64512	Hs.264428 Hs.237146	tissue specific transplantation antigen Homo sapiens cDNA FLJ14234 fis, clone NT	2.7
50	453779	N35187	Hs.43388	ESTs	2.7
	433068	NM_006456		sialyltransferase	2.7
	426841	AI052358	Hs.193726	ESTs	2.7
	428778	AK000530	Hs.193326	fibroblast growth factor receptor-like 1	2.7 2.6
55	451346 443883	NM_006338 AA114212	Hs.9930	glioma amplified on chromosome 1 protein serine (or cysteine) proteinase inhibito	26
55	420162	BE378432	Hs.95577	cyclin-dependent kinase 4	2.6
	447149	BE299857	Hs.326	TAR (HIV) RNA-binding protein 2	2.6
	433656	AW974941	Hs.292385	ESTs	2.6
60	408210	N81189	Hs.43104	ESTs	26 25
00	430651 422599	AA961694 BE387202	Hs.105187 Hs.118638	kinesin protein 9 gene non-metastatic cells 1, protein (NM23A)	25
	421802	BE261458	Hs.108408	CGI-78 protein	2.5
	446211	AI021993	Hs.14331	S100 calcium-binding protein A13	2.5
65	404029	W72881	Hs.266470	protocadherin beta 2	2.5
65	453012 419981	T95804 AA897581	Hs.31334 Hs.128773	putative mitochondrial outer membrane pr ESTs	2.5 2.5
	448153	Y10805	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	2.5
	419220	AA811938	Hs.291759	ESTs	2.5
70	432180	Y18418	Hs.272822	RuvB (E coli homolog)-like 1	2.4
70	406850	A1624300	Hs.172928	collagen, type I, alpha 1	24
	409893 421654	AW247090 AW163267	Hs.57101 Hs.106469	minichromosome maintenance deficient (S. suppressor of var1 (S.cerevislae) 3-like	2.4 2.4
	409956	AW103267	Hs.727	H.sapiens activin beta-A subunit (exon 2	2.4
	407584	W25945	Hs.18745	ESTs	2.4
75	448798	AA147829	Hs.33193	ESTs, Highly similar to AC007228 3 BC372	2.4

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Table 19 lists about 17 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode proteins that are secreted into blood, lymph, or other bodily fluids. These genes, and/or their protein products, in combination or alone, are ideal candidates for the early diagnosis of ovarian cancer. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 2.4, and that are likely to encode secreted or extracellularly-shed proteins. The "average" ovarian cancer level was set to the 90th percentile amongst various ovarian cancer samples. The "average" normal adult tissue level was set to the 90th percentile amongst various non-malignant tissues. In order to remove genes-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 19: ABOUT 17 GENES, AND COMBINATIONS THEREOF, USEFUL FOR DIAGNOSIS OF OVARIAN CANCER UG ID: UniGene ID
Title: UniGene Title

% tumors: percent of tumors detected expressing gene

	Single gener		
	UGID	Title	% tumors
	Hs.5378	spondin 1, (f-spondin) extracellular matrix protein	77
10	Hs.12844	EGF-like-domain 6	86
	Hs.151254	kallikrein 7 (chymotryptic; stratum comeum)	66
	Hs.97644	mammaglobin 2	73
	Hs.155981	mesothelin (cytokine)	57
	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin 2)	21
15	Hs.50915	kallikrein 5	27
	Hs.301122	bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)	54
	Hs.79361	kallikrein 6 (neurosin, zyme)	38
	Hs.83169	MMP 1 (interstitial collagenase)	23
	Hs.72026	protease, serine, 21 (testisin)	16
20	Hs.39384	putative secreted ligand homologous to fix1	46
	Hs.2719	epididymis-specific; whey-acidic protein type; four-disulfide core	91
	Hs.155324	matrix metalloproteinase 11 (stromelysin 3)	11
	Hs.1584	cartilage oligomeric matrix protein	25
	Hs.169300	TGF beta 2	21
25	Hs.2250	leukemia inhibitory factor (cholinergic differentiation factor)	23
	Exemplary C	Combinations:	
		EGF-like-domain 6 + mammaglobin 2	93
		kallikrein 7 + mesothelin	71
30		mammaglobin 2 + bone morphogenic protein 7	88
		EGF-fike-domain 6 + bone morphogenic protein 7	91
		kallikrein 7 + bone morphogenic protein 7 + testisin	75
		kallikrein 7 + mammaglobin 2 + mesothelin	84
		mammaglobin 2 + bone morphogenic protein 7 + TGF beta 2	91
35		EGF-like-domain 6 + bone morphogenic protein 7 + MMP 1	95

Table 20A lists about 1025 genes up-regulated in ovarian cancer compared to normal adult tissues. Genes associated with ovarian cancer were selected from the 53462 range 20x1sts about 1025 genes up-regulated in ovarian cancer to "average" normal adult tissues was greater than or equal to 5.0. The "average" ovarian cancer love average" normal adult tissues was greater than or equal to 5.0. The "average" ovarian cancer sevel was set to the 93rd percentile value amongst various ovarian cancer speciments; the "average" normal adult tissue level was set to the 95th percentile value amongst various on-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated. 40

Tables 208-24B list accession numbers for Pkey's lacking UnigenelD's for tables 20A-24A. For each probeset is listed a gene cluster number from which dilgonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oaktand California). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column. 45

Tables 20C-24C list genomic positioning for Pkey's lacking Unigene ID's and accession numbers in tables 20A-24A. For each predicted exon is listed genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

TABLE 20A:

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Pkey: Unique Eos probeset identifier number ExAccn: Exemplar Accession number, Genbank accession number UnigenelD: Unigene number Unigene Title: UniGene title Pred. Protein Dom.: Predicted protein domain R1: Ratio of turnor to normal body tissue

60.	Pkey 421296 453028 422310	ExAccn NM_002666 AB006532 AA316622	UniGene ID Hs.103253 Hs.31442 Hs.98370	Unigene Title perilipin RecQ protein-like 4 cytochrome P450, subtamily IIS	Pred. Protein Dom. peritipin,SS DEAD,helicase_C,Fork_head SS,TM,pkinase,fn3.ig	R1 32.5 27.6 26.5
65	437897 446374 441021 409518	AA770561 AA329256 AW578716 BE384836	Hs.146170 Hs.24756 Hs.7644 Hs.3454	hypothetical protein FLJ22969 ESTs, Moderately similar to al H1 histone family, member 2 KIAA1821 protein	SS,TM,zf-DHHC  SS DAGKc	26.3 22.6 22.3 21.3 21.2
70	413436 424420 422645 422098 429556	AF238083 BE614743 L40027 H03117 AW139399	Hs.68061 Hs.146688 Hs.118890 Hs.111497 Hs.98988	sphingosine kinase 1 prostagtandin E synthase glycogen synthase kinase 3 alp similar to mouse neuronal prot ESTs	MAPEG,SS,TM,MAPEG pkinase,SS,Ets TM SS,pkinase,PMP22_Claudin	20.7 20.7 20.2 20.1
75	436485 423652 431773 422179 420839	X59135 AF052122 BE409442 AF091619 AJ792682	Hs.156110 Hs.130712 Hs.268557 Hs.112667 Hs.282960	immunoglobulin kappa constant Homo sapiens chone 23929 mRNA pleckstrin homology-like domai dynein, axonemal, intermediate hypothetical protein MGC10870	SS.ig.SS ABC1,SS.PID,PID PH,SS,LIM,Troponin WD40,SS SS,DS,UPF0139,Glyco_hydro	19.9 19.8 19.4 19.3 18.5
80	441356 424659 439924 458814 451643 439108	BE384361 AW891298 AI985897 AI498957 M64437 AW163034	Hs.182885 Hs.331601 Hs.125293 Hs.170861 Hs.234799 Hs.6467	ESTs, Weakly similar to JC5024 Homo sapiens, Similar to cyste ESTs ESTs, Weakly similar to Z195_H breakpoint cluster region synaptogynin 3	SS,TM,ank SS,Fork_head SS SS SS,TM,ld1_recept_a_kd1_re RhoGEF,RhoGAP,PH,C2 Synaptogyrtn,SS,TM,PDZ,WD	18.5 18.4 18.1 17.5 17.2 16.9
	432945	AL043683	115.0407	hypothetical protein FLJ10803	SS	16.8

	410418	D31382	Hs.63325	transmembrane protease, serine	SS,TM,ldl_recept_a,trypsi	16.8
	438424	AI912498	Hs.25895	hypothetical protein FLJ14996	SS,TM	16.7
	409435	AI810721	Hs.95424	ESTs	SS ·	16.4
	418969	W33191	Hs.28907	hypothetical protein FLJ20258	SH3,SH3	16.2
5	421612	AF161254	Hs.106196	8D6 antigen	ldi_recept_a,SS,TM	16.0
9	456177	NM_012391		prostate epithelium-specific E	Ets,SAM_PNT	15.7
	414837	U24266	Hs.77448	aldehyde dehydrogenase 4 famil	aldedh	15.6
		H08379		hypothetical prolein DKFZp434N	TM,DnaJ,UBA,ArfGap,homeob	15.5
	432631		Hs.165563		SS,TM,myosin_head,RA,DAG_	15.5
10	454017	AW023617	Hs.347130	hypothetical protein FLJ22709		15.4
10	401278	41004450	11- 00450	Target Exon	Band_41	15.4
	444804	AI084452	Hs.22158	hypothetical protein FLJ21988	SS COURT MANA CEO IDU MANA	15.4
	410259	AK000337	Hs.61485	hypothetical protein	GFO_IDH_MocA_GFO_IDH_MocA	
	406620	M81105	Hs.146550	myosin, heavy polypeptide 9, n	myosin_head,Myosin_tail,I	15.1
1.5	423081	AF262992	Hs.123159	sperm associated antigen 4	TM	14.9
15	421495	AI583067	Hs.149152	ESTs, Weakly similar to RHOP M		14.7
	416893	AA455588	Hs.62406	hypothetical protein FLJ22573	SS,rm,SS	14.7
	413244	AW955951	Hs.159265	kruppel-related zinc finger pr	SS,TM,BTB,Pep_M12B_propep	14.6
	406901	M14624		gb:Human 4-beta-galactosyltran		14.6
~ ~	416006	AA324251	Hs.78950	branched chain keto acid dehyd	E1_dehydrog	14.6
20	436186	BE390717	Hs.5074	similar to S. pombe dim1	DIM1,SS	. 14.5
	455557	AW995839		gb:QV4-BN0044-110200-108-h07 B	Metallophos	14.4
	434518	H56995	Hs.37372	Homo sapiens DNA binding pepti	SS	14.2
	421489	Al922821	Hs.32433	ESTs	SS,PI-PLC-X,PI-PLC-Y,C2	14.1
	444441	AW613841	Hs.301394	hypothetical protein MGC3101		14.0
25	435017	AA336522	Hs.12854	angiotensin II, type I recepto		14.0
	446572	AV659151	Hs.282961	ESTs		13.9
	434068	AA977935	Hs.127274	ESTs	SS	13.7
	432481	AW451645	Hs.151504	Homo sapiens cDNA FLJ11973 fis	SS, Collagen, COLFI, TSPN	13.7
	447304	Z98883	Hs.18079	phosphatidylinositol glycan, c	SS,Peptidase_C2	13.6
30	421182	AA284855	Hs.104480	ESTs	SS,Topoisomerase_I,Topois	13.3
50	407767	W15398	Hs.38628	hypothetical protein	SS,zi-CCCH	13.3
			Hs.109752		00,2-0001	13.3
	456642	AW451623		putative c-Myc-responsive	SQS_PSY	13.2
	437457	AA757900	Hs.270823	ESTs, Weakly similar to \$65657	SS	13.1
35	430178	AW449612	Hs.152475	ESTs		12.9
33	430399	AI916284	Hs.199671	ESTs	Sec7,PH	
	436725	BE045223	Hs.136912	hypothetical protein MGC10796	00 TH 0 1 F- DID	12.9
	410219	T98226 .	Hs.171952	occludin -	SS,TM,Occludin,BIR	12.7
	442620	C00138	Hs.8535	Homo sapiens mRNA for KIAA1668	SS,RNA_pol_K	12.7
40	439233	AA831893	Hs.292767	hypothetical protein FLJ23109	zf-C3HC4,TM,Sulfate_trans	12.7
40	425018	BE245277	Hs.154196	E4F transcription factor 1	zf-C2H2,LIM,SS,Exo_endo_p	12.6
	423801	NM_015071		GTPase regulator associated wi	RhoGAP,SH3,PH	12.6
	417826	TB5105	Hs.15471	ESTs	SS,cadherin,Cadherin_C_te	12.6
	409261	BE315042	Hs.19210	hypothetical protein MGC11308		12.6
	420568	F09247	Hs.247735	protocadherin alpha 10	cadherin,SS,TM,cadherin	12.6
45	411570	BE144584	Hs.314341	ESTs		12.5
	430397	AI924533	Hs.105607	bicarbonate transporter relate	HCO3_cotransp,SS,TM	12.5
	423767	H18283	Hs.132753	F-box only protein 2	F-box, SS, F-box, HORMA	12.4
	441805	AA285136	Hs.301914	neuronal specific transcriptio	LIM,SS,LIM	12.3
	402365			Target Exon	SS,SS,TM,ig	12.2
50	414371	Al905865		thymosin, beta 4, X chromosome	Thymosin	12.2
	446780	R31107		gb:yh61g01.s1 Soares placenta		12.1
	428782	X12830	Hs.193400	interleukin 6 receptor	SS,TM,fn3,ig,SS,TM	12.1
	427695	R88483	Hs.172862	intron of Bicaudal D homolog 1	oo;,	12.1
	400460	100100	,	C11002253*:gi[129091]sp]P23267	SS,TM,SCAN,zf-C2H2,KRAB	12.0
55	407341	AA918886	Hs.204918	ESTs, Weakly similar to ALU8_H	SS,TM	12.0
55	424049	AB014524	Hs.138380	KIAA0624 protein	SS	11.9
	422872	BE326786	Hs.187646	ESTs	TM	11.9
			Hs.1390		SS	11.8
	450800	BE395161	Hs.188021	proteasome (prosome, macropain potassium voltage-gated channe	cNMP_binding	11.7
60	428648	AF052728		C100 seleium binding aretain A	S_100,efhand,SS,efhand,S_	11.7
UU	432329	NM_002962		S100 calcium-binding protein A		11.6
	417061	AI675944	Hs.188691	Horrio sapiens cDNA FLJ12033 fis	CTF_NFI	
	451195	U10492	Hs.438	mesenchyme homeo box 1	homeobox,SS	11.5 11.5
	417595	AA424317	Hs.6259	KIAA1698 protein	SS,TM,Glyco_hydro_31,Glyc	
65	426500	NM_014638		KIAA0450 gene product	SS	11.4
03	433124	U51712	Hs.13775	hypothetical protein SMAP31		11,4
	444001	AI095087	Hs.152299	ESTs, Moderately similar to S6		11.4
	419298	AA853479	Hs.89890	pyruvate carboxylase	CPSase_L_chain,PYC_OADA,H	11.4
	428593	AW207440	Hs.185973	degenerative spermatocyte (hom	SS	11.3
~~	411408	U76666	Hs.69949	calcium channel, voltage-depen	ion_trans,SS,TM	11.2
70	404438			Target Exon		11.2
	427448	BE246449	Hs.2157	Wiskott-Aldrich syndrome (ecze	WH1,PBD,WH2,SS	11.2
	406230			Target Exon		11.2
	432125	AW972667	Hs.183006	Homo sapiens cDNA FLJ12300 fis	Band_41,ERM	11.2
	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_H		11.1
75	400206			Eas Control	SS,SS,Glyco_tranf_43,COLF	11.1
-	450503	R35917	Hs.301338	hypothetical protein FLJ 12587	SS	11.0
	407605	W03512	Hs.6479	hypothetical protein MGC13272	SS,Sema,pkinase,TIG,PSI,e	11.0
	432143	AL040183	Hs.123484	Homo sapiens, clone IMAGE:4178	SS,TM,cys_rich_FGFR	10.9
	446839	BE091926	Hs.16244	mitalic spindle coiled-coil re	Troponin,SS,glycolytic_en	10.8
80	443559	Al076765	Hs.269899	ESTs, Moderately similar to AL	SS,TM,BIR,UQ_con	10.8
23	411298	AW835858		gb:PM0-LT0017-031299-001-h07 L		10.8
	409557	BE182896	Hs.211193	ESTs		10.8
	435158	AW563317	Hs.65588	DAZ associated protein 1	rm,SS,rm	10.8
	444410	BE387360	Hs.33719	ESTs, Moderately similar to S6	SS	10.6
	***************************************	220.000		Co.o, mooning on the ov		13.0
					210	

	428948	BE514362		FK506-binding protein 3 (25kD)	FKBP,PIP5K	10.6 10.6
	424707	BE061914	Hs.10844	Homo sapiens cDNA FLJ14476 fis	SS,SS,TM,Sema pkinase,SS,TM,OTU,K_tetra	10.5
	416819 419341	U77735	Hs.80205	pim-2 oncogene ESTs, Weakly similar to ALU1_H	SS,TM,UPF0016	10.5
5	444359	N71463 Al697160	Hs.118888 Hs.143594	ESTs, Weakly similar to HS4L_H	og mor rom	10.5
9	404333	74057 100	16.170057	C7001735*:gij7768636 dbj BAA95	vwd	10.5
	401210			C12000519:gi 7710046 ref NP_05		10.5
	457941	A1004525	Hs.14587	ESTs, Weakly similar to AF1518	SS,TM,SS,TM	10.4
10	401594	*******	11. 400000	NM_024817:Homo sapiens hypothe		10.3 10.3
10	441790	AW294909	Hs.132208	ESTs. Weakly similar to SFR4_H	SS,SS,SAC3_GANP	10.3
	444008 438185	BE544855 Y19188	Hs.236572 Hs.320461	ESTs	SS	10.2
	432031	AF039196	Hs.272357	hairless protein (putative sin	jmjC	10.2
	410471	T88872		gb:yd31a12.s1 Soares fetal liv	••	10.1
15	433573	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G	SS,TM,7tm_2,EGF,cadherin,	10.1
	417371	N74613	Hs.269149	ESTs		10.0
	428167	AA770021	Hs.16332	ESTs .	SS,ig,fn3	10.0 10.0
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis	efhand,SS,CAP_GLY	10.0
20	412674 425863	X04105 U43604	Hs.74451 Hs.159901	calpain 4, small subunit (30K) Human unidentified mRNA, parti	endiatoolog _oci	9.9
20	442739	NM_007274		cytosolic acyl coenzyme A thio	Acyl-CoA_hydro,SS,TM	9.9
	429469	M64590	Hs.27	glycine dehydrogenase (decarbo ·	GDC-P,GDC-P	9.9
	420029	BE258876	Hs.94446	polyamine-modulated factor 1	aldo_ket_red,SS,TM,gla	9.8
25	445625	BE246743		hypothetical protein FLJ22635	SS,TM .	9.8 9.8
25	435339	AI358300	Un 400407	ESTS ~	SS,ras SS,TM,Ribosomal_S13,Galac	9.8
	407235 428758	D20569 AA433988	Hs.169407 Hs.98502	SAC2 (suppressor of actin muta CA125 antigen; mucin 16	SS SS	9.8
	401349	7770000	15.50002	inositol polyphosphate-1-phosp	33	9.7
	437915	A1637993	Hs.202312	Homo sapiens clone N11 NTera2D		9.7
30	424511	BE300512	Hs.193557	ESTs, Moderately similar to AL		9.7
	423366	Z80345	Hs.127610	acyl-Coenzyme A dehydrogenase,	Acyl-CoA_dh,Acyl-CoA_dh_M	9.7
	405143			NM_013432*:Homo sapiens nuclea	ank,SS,TM,CPSF_A	9.6 9.6
	427497	AW139476	Hs.31240	ESTs	SS	9.6
35	420423 431512	AA827718 BE270734	Hs.88218 Hs.2795	ESTs lactate dehydrogenase A	ldh,ldh_C,SS,ldh	9.6
55	450052	Al681298	Hs.236524	ESTs	zf-C3HC4.zf-B_box	9.5
	412738	N34731	Hs.74562	siah binding protein 1; FBP in	homeobox	9.5
	444202	AL031685	Hs.12785	KIAA0939 protein	SS,TM,Na_H_Exchanger,ABC2	9.5
40	451165	AI340575	Hs.286084	MRIP-1 protein	90 -li	9.5 9.5
40	411450	H49619	Hs.127301	ESTS	SS.pkinase pkinase,UM,PDZ	9.5
	405371 435782	N49433	Hs.285737	NM_005569":Homo sapiens LIM do Homo sapiens cDNA: FLJ20895 fi	SS,G6PD,Glucosamine_iso,G	9.5
	416866	AA297356	Hs.80324	serine/threonine protein phosp	Metallophos, Metallophos	9.4
	405474	70 20.000		NM_001093*:Homo sapiens acetyl	CPSase_L_chain,biotin_lip	9.4
45	412837	A1922293	Hs.58389	hypothetical protein MGC4090		9.3
	448133	AA723157	Hs.73769	folate receptor 1 (adult)	Folate_rec,SS	9.3
	431081	AA491594	Hs.75813	polycystic kidney disease 1 (a	SS,TM	9.3 9.2
	427640	AF058293	Hs.180015	D-dopachrome tautomerase	MIF, late_protein_L2, SS, GS SS	9.2 9.2
50	427435 407688	AW938739 W25317	Hs.115412 Hs.37616	hypothetical protein FLJ13881 Human D9 splice variant B mRNA	33	9.2
50	407507	U73799	113.01010	gb:Human dynactin mRNA, partia	SS,TM,HCO3_cotransp,CAP_G	9.2
	400833	•		C11000890:gi[3746443[gb]AAC639	SS,TM,7tm_1	9.2
	422064	AW452589	Hs.335742	ESTs	TM	9.2
55	452434	D30934	Hs.29549	C-type tectin-like receptor-1	lectin_c,SS,TM	9.2 9.2
22	451752	AB032997	U= 202752	KIAA1171 protein	TBC,SS,TM,pkinase,laminin	9.1
	432931 407893	AF174487 BE408359	Hs.293753 Hs.43621	Bcl-2-related ovarian killer p Homo sapiens, Similar to hypot	SS,SS,arf,ras,fn3,ras	9.1
	427397	AI929685	Hs.177656	calmodulin 1 (phosphorylase ki	efhand,RmaAD,SS,efhand	9.1
٠.	405159			ENSP00000243337*:CDNA FLJ13984		9.1
60	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45,	CDC45	9.1
	407058	X94563	11.00400	gb:H.sapiens dbi/acbp gene exo	SS CC THE HIDAD LIVE towin CC T	9.0 9.0
	448045 400772	AJ297436	Hs.20166	prostate stem cell antigen NM_003105":Homo sapiens sortil	SS,TM,UPAR_LY6,toxin,SS,T ldl_recept_a,fn3,ldl_rece	9.0
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp5	spectrin,SH3,PH,CH	9.0
65	414391	BE409872	110.110000	gb:601299655F1 NIH_MGC_21 Homo	Special desired	9.0
	447867	AI525268	· Hs.164303	ESTs	TM	9.0
	422639	AI929377	Hs.173724	creatine kinase, brain	ATP-gua_Ptrans,ATP-gua_Pt	9.0
	454319	AW247736	Hs.101617	ESTs, Weakly similar to T32527	SS	8.9 8.9
70	428781	AF164799	Hs.193384	putatative 28 kDa protein	SS,TM	8.9
70	408645 429527	AW245738 AA454184	Hs.109274 Hs.289014	hypothetical protein MGC4365 ESTs	33,1 M	8.9
	406651	A1559224	113.203014	gb:tq32c02.x1 NCI_CGAP_Ut1 Hom		8.9
	430893	BE502068	Hs.282067	ESTs		8.8
7.	414413	BE294877		gb:601174162F1 NIH_MGC_17 Homo	SS	8.8
75	413726	AJ278465	Hs.75510	annexin A11	annexin,SS,annexin	8.8
	432211	BE274530	Hs.273333	hypothetical protein FLJ10986		. 8.8 8.8
	421694 453683	BE387430	Hs.106880		SS	8.8
•	453683 456741	AL079854 W37608	Hs.118598 Hs.184492		SS,pkinase	8.7
80	442995	AA532511	Hs.288455		,	8.7
	415898	Z43379	Hs.177193	gb:HSC1AE111 normalized infant		8.7
	456977	AK000252	Hs.169758		00 TM bearing - 1 4	8.7
	439632	AW410714			SS,TM,transmembrane4	8.7 8.7
	431462	AW583672	Hs.256311	granin-like neuroendocrine pep	SS	a.r
					220	

	400128			Eos Control	TM,E1-E2_ATPase,HMA,Hydro	8.7
	438582	A!521310	Hs.283365	ESTs, Wealdy similar to ALU5_H	SS	8.7
	450958	AL137669	Hs.348012	Homo sapiens mRNA; cDNA DKFZp4		8.7
_	410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	SNF2_N,helicase_C,SS	8.7
5	415126	D60945		gb:HUM141D04B Clontech human f	SS.TM	8.7
-	418736	T18979	Hs.87908	Snf2-related CBP activator pro	SS,helicase_C,AT_hook,SS,	8.6
	431157	AI823969	Hs.132678	ESTs .	SS,MAPEG,SS,MAPEG	8.6
	418843	AJ251016	Hs.89230	potassium intermediate/small c	TM,CaMBD,SK_channel,TM	8.6
	419167	AI589535	Hs.94875	ESTs, Weakly similar to A35363	SS	8.6
10	432343	NM_002960		S100 calcium-binding protein A	S_100,SS,efhand,S_100,efh	8.6
	458440	AI095468	Hs.135254	Homo sapiens clone 1 thrombosp		8.6
	407065	Y10141		gb:H.sapiens DAT1 gene, partia	SNF,SS,TM	8.6
	452851	AW173191	Hs.213117	ESTs	SS,Sema	8.6
	422418	AK001383	Hs.116385	hypothetical protein FLJ10521	RhoGEF	8.6
15	420836	AW958453	Hs.204959	hypothetical protein FLJ14886	SS,ras	8.6
13	455588	Al129903	Hs.74669	vesicle-associated membrane pr	synaptobrevin,SS,TM	8.5
	431974	AW972689	Hs.200934	ESTs	bZIP	8.5
	410720	AF035154	Hs.65756	regulator of G-protein signall	RGS,G-gamma,DEP,SS,RGS,DI	8.5
	449751	AW207115	Hs.25555	ESTs	Mode Samuel Columbia	8.5
20	434030	AW162336	Hs.3709	low molecular mass ubiquinone-	SS	8.5
20	405557	711102000	113.0700	Target Exon	Els,SAM_PNT	8.5
	443780	NM_012068	He 075A	activating transcription facto	bZIP,NTP_transf_2,SS,TBC	8.5
	428860	U38291	Hs.194301	microtubule-associated protein	M	8.5
	421901	AB014554	Hs.109299	protein tyrosine phosphatase,	SAM,SS,TM,mm,PDZ	8.4
25	421901	MDU 14004	N5.105255	Target Exon ->	kinesin,SS,TM	8.4
23	449382	AI650407	Hs.197875	ESTs	SS,rm,zf-RanBP	8.4
	432862		Hs.236720		SS,MATH,zt-TRAF,zt-C3HC4	8.4
		AW004958	Hs.126825	amnionless protein ESTs, Weakly similar to A46302	SS,TM,HSP20,7tm_1	8.4
	441363	AW450211 AF035032	Hs.181125			8.4
30	407363	AA356389		gb:Homo sapiens clone MCA1L my	SS.ig.SS.G_glu_transpept	8.4
50	425380		Hs.32148	AD-015 protein	SS,TM,LRR,P,Peptidase_S8 SS,SAM,SS,TM,7tm_1	8.4
•	424893	AW295112	Hs.153648	Homo sapiens cDNA FLJ13303 fis	22'2WN'22'1 W'1R1-1	8.3
	424080	AW189983	Hs.139119	Homo sapiens cDNA FLJ10967 fis		8.3
	439772	AL365405	Hs.10268	Homo sapiens mRNA full length	CU2 CC TM	8.3
35	431765	AF124249	Hs.268541	novel SH2-containing protein 1	SH2,SS,TM	
22	404365	4 4 0000 40	11. 50004	Target Exon	SS	8.3
	424310	AA338648	Hs.50334	testes development-related NYD	SS,TM	8.3
	401935			Target Exon	PH	8.3
	434796	AA812046		ESTs	SS,myb_DNA-binding,myb_DN	8.3
40	423098	AA321980	Hs.204682	ESTs	••	8.3
40	434552	AA639618	Hs.325116	Homo sapiens, clone MGC:2962,	SS	8.2
	457082	AA470687	Hs.104772	ESTs	SS	8.2
	432603	AA554920	Hs.105794	UDP-glucose:glycoprotein gluco	SS,TM	8.2
	402445			Target Exon	m3,SS,TM,BNR	8.2
15	422078	AW872378	Hs.120170	hypothetical protein FLJ21415	SS	8.2
45	418361	AW505368	Hs.12460	gb:UI-HF-BN0-alu-d-03-0-UI.r1		8.2
	431354	BE046956	Hs.251673	DNA (cytosine-5-)-methyltransf	SS,PWWP,PHD	8.2
	403885			Target Exon	TM,Sulfate_transp,STAS,HM	8.2
	450029	AW073380	Hs.267963	hypothetical protein FLJ10535	SS,Pyridox_oxidase,zf-C2H	8.2
50	452512	AW363486	Hs.337635	ESTs	SS	8.2
50	420138	BE268854	Hs.177729	ESTs	SS	8.2
	439788	N71241	Hs.119275	ESTs	UQ_con	8.2
	423662	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc	SS	8.2
	449656	AA002008	Hs.188633	ESTs	PIP5K	8.1
	452295	BE379936	Hs.28866	programmed cell death 10	SS,serpin	. 8.1
55	448650	AW769385	Hs.204891	ESTs	SS,ILB	8,1
	446035	NM_006558	Hs.13565	Sam68-like phosphotyrosine pro .	KH-domain	8.1
	444406	AI147237		immunoglobulin heavy constant	SS	8.1
	437215	AL117488		Human clone 23564 mRNA sequenc	SS	8.1
<b>C</b> 0	408891	NM_006577	Hs.284284	ESTs, Highly similar to beta-1	SS,TM,DIX,POZ,DEP,Disheve	8.1
60	400409	AF153341		Homo sapiens winged helix/fork	SS	8.0
	443801	AW206942	Hs.253594	intron of: trichorhinophalang	GATA	8.0
	425281	AA444390	Hs.155482	hydroxyacyl glutathione hydrol	lactamase_B,SS	8.0
	458216	AW024282	Hs.104938	hypothetical protein MGC15906		8.0
65	401507			C15000810*:gij11131272[spjP793		8.0
65	401180			eukaryotic translation elongat	SS,TM,ion_trans,IQ	8.0
	454291	AW384847	Hs.213534	ESTs, Weakly similar to MUC2_H	SS,XRCC1_N,BRCT,lactamase	8.0
	444014	AI095718	Hs.135015	ESTs		8.0
	412128	AW894709		gb:CM1-NN0032-020500-212-d05 N	SCAN, z-C2H2, KRAB	7.9
70	408363	NM_003389		coronin, actin-binding protein	WD40	7.9
70	425694	U51333	Hs.159237	hexokinase 3 (white cell)	hexokinase,hexokinase2,he	7.9
	425263		Hs.155419	BCL2-interacting killer (apopt	SS,TM,TspO_MBR	7.9
	447045	AW392394		sorting nexin 17	SS,IF-2B,PP2C	7.9
	457613	AA598869	Hs.173770	ESTs		7.9
75	410338	W03445	Hs.38205	gb:za05g11.r1 Soares melanocyt	pkinase	7.9
75	402545			Target Exon		7.9
	454246	AW245185	Hs.6996	ESTs		7.9
	410079	U94362	Hs.58589	glycogenin 2	Glyco_transf_8	7.9 .
	443678	AW009605	Hs.231923	ESTs	SS	7.9
oΛ	404676			Target Exon		7.9
80	406649	Al569392		gb:tn86a02.x1 NCI_CGAP_Ut2 Hom		7.9
	420230	AL034344	Hs.284186	forkhead box C1	Fork_head,SS,Fork_head	7.9
	413534	BE146961	11. 4:4	gb:QV4-HT0222-011199-019-b12 H	SS,TM	7.8
	444628	U01120	Hs.242	glucose-6-phosphalase, catalyt	PAP2,SS,TM	7.8
	410839	NM_006849	Hs.66581	protein disuffide isomerase	thiored,Rho_GDI,gntR,SS,T	7.8
					221	

	444046	AI360834	Hs.135094	ESTs	SS,GTP_EFTU,EFG_C,GTP_EFT	7.8
	439501	AF086321	Hs.287452	Homo sapiens cDNA FLJ11760 fis	TM	7.8
					144	7.8
	415441	R13977	Hs.9634	ESTS		
-	450461	BE408081	Hs.45736	hypothetical protein FLJ23476	SS	7.8
5	448993	A1471630		KIAA0144 gene product		7.8
	400923			Target Exon	SS,TM,DUF289	7.8
	440546	AJ491994		gb:to07g09.x1 NCI_CGAP_Ut2 Hom	SS,HATPase_c	7.8
	419757	AA773820	Hs.63970	ESTs	SS,TM	7.8
		NM_006946				7.8
10	451721			spectrin, beta, non-erythrocyt	spectrin,PH,CH,SS,Peptida	
10	458834	A1566883	Hs.196448	ESTs		7.8
	422633	X56832	Hs.118804	enolase 3, (beta, muscle)	enolase, SS, TM, kinesin, FHA	7.7
	438452	Al220911	Hs.288959	hypothetical protein FLJ20920	SS	7.7
	421445	AA913059	Hs.104433	Homo sapiens, done IMAGE:4054	asp,SS,TM,ion_trans,K_tet	7.7
	434743	AI363410		ribosomal protein S18	SS,TM	7.7
15	450635		Hs.25237	mesenchymal stem cell protein	4HBT	7.7
13		AW403954			ומחו	
	442394	R62926	Hs.285193	ESTs		7.7
	434333	AA186733	Hs.292154	stromal cell protein		7.7
	427221	L15409	Hs.174007	von Hippel-Lindau syndrome	VHLTM	7.7
	429099	BE439952	Hs.196177	phosphorylase kinase, gamma 2	pkinase,SS,SNF2_N,helicas	7.7
20	444670	H58373	Hs.332938	hypothetical protein MGC5370	SS,zf-RanBP,MDM2	7.7
	449495	AI652833		gb:wb22c11.x1 NCl_CGAP_GC6 Hom	SS	7.7
	444607	AW405635	Hs.293687	ESTs	SS,PI-PLC-X,PH,PI-PLC-Y,C	. 7.7
						7.7
	449125	AJ671439	Hs.196029	Homo sapiens mRNA for KIAA1657	TIMP	
0.5	447151	AI022813	Hs.92679	Homo sapiens clone CDABP0014 m	SS,TM,LRR,aminotran_1_2	. 7.6
25	448626	W27670	Hs.55613	hypothetical protein FLJ22531		7.6
	430432	AB037758	Hs.241419	KIAA1337 protein	TM,Patched,TM	7.6
	401822			C17001422:gi 2695866 emb CAA75		7.6
	428909	Al190714	Hs.98945	ESTs		7.6
					CC harmon and of C4	
20	414534	BE257293	Hs.76366	BCL2-antagonist of cell death	SS,hormone_rec,zf-C4	7.6
30	421620	AA446183	Hs.91885	ESTs, Wealtly similar to 155214		7.6
	441650	Al261960	Hs.132545	ESTs	SS,TM,KOW	7.6
	442232	AI357B13	Hs.337460	ESTs, Weakly similar to A47582	SS,TM,TGFb_propeptide,TGF	7.6
	439539	BE348395	Hs.121589	ESTs	SS,Fork_head	7.5
		00000	113.12.1000			7.5
35	400286	05550004		C16000922:gi[7499103[pid]T209	TM,ABC_tran,ABC_membrane	
22	452833	BE559681	Hs.30736	KIAA0124 protein	WD40	7.5
	417390	AA196552	Hs.85852	hypothetical protein MGC3169		7.5
	427721	AI582843	Hs.180455	RAD23 (S. cerevisiae) homolog	ubiquitin,UBA,integrin_B,	7.5
	450716	T57758	Hs.10255	ESTs		7.5
	407435	AF211976		gb:Homo sapiens LENG9 mRNA, pa		7.5
40	413956	AI821351	Hs.193133	ESTs, Weakly similar to ALU7_H		7.5
-10					- AAO 20 aniatana AAO 20	
	427899	AA829286	Hs.332053	serum amyloid A1	SS,SAA_proteins,SS,SAA_pr	7.5
	406495			Target Exon	SRCR,TM,Acetyltransf	7.5
	430387	AW372884	Hs.240770	nuclear cap binding protein su	mm,SS,TM,rrm	7.5
	408601	U47928	Hs.86122	protein A	SS,7tm_1,SS,ig,WD40,zf-UB	7.5
45	424364	AW383226	Hs.163834	ESTs, Weakly similar to G01763	SS,ras	7.4
	409832	AW963293	1.0.100001	gb:EST375366 MAGE resequences,	SS	7.4
			U- 201001			7.4
	448043	A1458653	Hs.201881	ESTs	PHD	
	421148	AF008936	Hs.102178	syntaxin 16	Syntaxin,SS,Peptidase_M17	7.4
~~	420970	AA305079	Hs.1342	cytochrome c oxidase subunit V	COX58	7.4
50	419295	BE397712	Hs.144027	ESTs	myb_DNA-binding,myb_DNA-b	7.4
	448330	AL036449		ESTs		7.4
	419639	AK001502	Hs.91753	hypothetical protein		7.4
	431488	AB037785	Hs.257594	KIAA1364 protein	SS,CH,LIM,SS	7.4
			FIS.231354		33,01,1101,03	
55	456487	AF064804		suppressor of Ty (S.cerevisiae		7.4
22	448615	Al910868	Hs.212957	ESTs	SS	7.4
	427433	D82070	Hs.177972	chromosome 4 open reading fram	SS,pkinase	7.4
	441076	N49809	Hs.11197	Homo sapiens, clone IMAGE:3343		7.4
	452554	AW452434	Hs.58006	ESTs, Weakly similar to ALU5_H	SS,PAS,HLH	7.4
	411448	AA178955	Hs.271439	ESTs, Weakly similar to I38022	rm,PDZ	7.4
60	442318	Al792199	113.27 1703		SS.zI-C2H2	7.4
00			11-00040	ESTs	المراجات الد	
	425055	AW961959	Hs.96940	ESTs	00 TH.	7.4
	412935	BE267045	Hs.75064	tubulin-specific chaperone c	SS,TM,transmembrane4	7.4
	403748			Target Exon	TM	7.4
	447282	A1989963	Hs.197505	ESTs	TM	7.3
65	422305	A1928242	Hs.293438	ESTs, Highly similar to AF1984	SS	7.3
	416472	AA180756	Hs.340316	ESTs, Moderately similar to AL	zf-C2H2	7.3
	427273	AW139032	Hs.107376	hypothetical protein DKFZp434N	SS,SS,TM	7.3
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	UPP_synthetase,HMG14_17	7.3
70	447859	AK002194	Hs.19851	peroxisornal biogenesis factor		7.3
70	432747		Hs.278907	calcium channel, voltage-depen	PMP22_Claudin,SS,TM,PMP22	7.3
	405727	AJ219282	Hs.2186	eukaryotic translation elongat	SS,G-gamma	7.3
	404199			ENSP00000211797*:Helicase SKI2	SS,RasGAP,PH,SS,PHD	7.3
	445434	BE391690	Hs.9265	hypothetical protein FLJ20917	SS,PWWP,Exonuclease,lipoc	7.2
	428550	AW297880	Hs.98661	ESTs	SS,homeobox,homeobox	7.2
75		AW815144	, w		SS,ATP-synt_ab,ATP-synt_a	7.2
15	454718		Lin doon to	gb:QV4-ST0212-120100-075-d10 S		
	407686	AW901268	Hs.126043	chromosome 21 open reading fra	SS,TM,ISK_Channel	7.2
	418304	AA215702		gb:zr97g10.r1 NCI_CGAP_GC81 Ho	serpin	7.2
	424263	M77640	Hs.1757	L1 cell adhesion molecule (hyd	fn3,ig,IRK,SS,TM,fn3,ig,R	7.2
	407581	R48402	Hs.173508	P3ECSL	SS,TM,7tm_1	7.2
80	430746	AW977370	Hs.222012	ESTs	SS	7.2
50			• 10.222012	NM_000721*:Homo sapiens calciu	ion_trans	7.2
	402651	A A 404400	11- 44000			
	407323	AA181183	Hs.143504	gb:zp57c02.s1 Stratagene endot	SS,Ribosomal_S4e,ubiquiti	7.2
	407619	AL050341	Hs.37165	collagen, type IX, alpha 2	SS,Collagen,SS,Collagen	7.2
	434035	AJ762074	Hs.204769	ESTs, Weakly similar to T28770	SS,TM	7.2
					222	
					111	

	400419	AF084545		Target	EGF,ig,lectin_c,sushi,Xli	7.2
	424241	AW995948	Hs.182339	Homo sapiens pyruvate dehydrog	SAM_PNT	7.2
	445837	Al261700	11 400=22	ESTs	aldana	7.2 7.1
5	427725	U56839	Hs.180533	mitogen-activated protein kina	pkinase	7.1
,	421879 418285	AW959607 H68616	Hs.293756	gb:EST371677 MAGE resequences, ESTs	SS,EMP24_GP25L	7.1
	442893	H78133	113.233130	gb:yu86c11.s1 Soares fetal liv	00,277 24_01 202	7.1
	437829	A1358522	Hs.103834	ESTs		7.1
	450873	BE464016	Hs.238956	ESTs	SS,zf-C2H2,rm	7.1
10	433396	AJ742071	Hs.133205	ESTs	SS,TM	7.1
	415595	R54144	Hs.278707	chromosome 21 open reading fra	SS	7.1
	436629	AA851011	Hs.249795	ESTs gb:601273249F1 NIH_MGC_20 Homo	TM	7.1 7.1
	414593 422765	BE386764 AW409701	Hs.1578	baculoviral IAP repeat-contain	BIR,TK,SS,TM	7.1
15	419823	AW271708	Hs.118918	ESTs, Weakly similar to M2OM_H	SS.TM	7.1
	405247	,		Target Exon	SS	7.1
	455778	BE088746		gb:CM2-BT0693-210300-123-d09 B		7.1
	431005	AA490544	Hs.127269	ESTs, Weakly similar to T02345	WD40	7.1
20	435717	AF227905	Hs.105794	UDP-glucose:glycoprotein gluco	Glyco_transf_8	7.1
20	405113	Teonto	Hs.182313	Target Exon	SS lipocalin, lipocalin, WD40	7.1 7.1
	428070 429029	T63918 AA443443	Hs.85524	retinol-binding protein 2, cel for muscle specific ring finge	SS	7.1
	430354	AA954810	Hs.239784	human homolog of Drosophila Sc	SS,TM,ig	7.0
	412970	AB026436	Hs.177534	dual specificity phosphatase 1	Rhodanese, DSPc, SS, DSPc	7.0
25	438701	AA937112	Hs.207788	ESTs	TM,sushi	7.0
	454756	AW819273		gb:CM2-ST0284-061299-046-a12 S		7.0
	401264			C18000090*:gi 6678656 ref NP_0	SS,laminin_Nterm,laminin_	7.0
	408080	AW149754	Hs.248652	ESTs, Weakly similar to T00273	SS disintaggia Pangakasia Pa	7.0 7.0
30	418641 431402	BE243136 AA743534	Hs.86947 Hs.250861	a disintegrin and metalloprote ESTs	disintegrin,Reprolysin,Pe	7.0
50	423790	BE152393	115.23000,1	gb:CM2-HT0323-171199-033-a08 H	SS	7.0
	450688	AW272352	Hs.60450	ESTs	TM	7.0
	405928			Target Exon	SS,cystatin,Coprogen_oxid	7.0
26	454438	AA224053		cell division cycle 27	SS,TM,SPRY,7tm_3,ANF_rece	7.0
35	407281	A1307226	Hs.164421	ESTs	SS TOO	6.9
	423386	AW136098	Hs.314081	ESTS	SS,WD40,EPO_TPO	6.9 6.9
	459360 420187	BE384526 AK001714	Hs.25734 Hs.95744	gb:601277913F1 NIH_MGC_20 Homo hypothetical protein similar t	ank,TM	6.9
	431549	AA507036	Hs.170673	ESTs	ain, iii	6.9
40	423384	AL133632	Hs.127808	Homo sapiens mRNA; cDNA DKFZp4		6.9
••	454577	AW809272		gb:MR4-ST0118-040100-034-c08_1		6.9
	438118	AW753311		ESTs	SS, lipocatin	6.9
	416233	AA176633		gb:zp13g01.s1 Stratagene fetal		6.9
15	417012	N38970	Hs.194214	ESTs		6.9
45	452399	BE513301	Hs.29344	hypothetical protein, clone 24	SS, perilipin	6.9
	439963	AW247529	Hs.6793	platelet-activating factor ace	PAF-AH_lb,Lipase_GDSL,SS, E1-E2_ATPase,HMA,Hydrolas	6.9 6.9
	418416 404956	U11700	Hs.84999	ATPase, Cu transporting, beta C1003210*:gi 6912582fref NP_03	PI3_PI4_kinase,PI3K_C2,PI	6.9
	451606	AA018791	Hs.7945	AIE-75 binding protein protein	SS	6.9
50	438525	AW368528	Hs.100855	ESTs	SS	6.9
	400906			C18000324:gi 12229928 sp Q9PTW		6.9
	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA13	SS	6.8
	406834	Al318680	11. 30000	gb:ta49g09_x1 NCI_CGAP_Lu25 Ho	50 00-stores 60 00-store	6.8
55	414629	AA345824	Hs.76688 Hs.143026	carboxylesterase 1 (monocyte/m KIAA1087 protein	SS,COesterase,SS,COestera SS,TM,Na_Ca_Ex,Calx-beta,	6.8 6.8
55	424198 445873	AB029010 AA250970	Hs.251946	poly(A)-binding protein, cytop	SS,PABP,rm,pkinase,14-3-	6.8
	439605	AF086431	Hs.22380	ESTs	SS,TM	6.8
	432284	AA532807	Hs.105822	ESTs	SS,TM,pkinase	6.8
	421904	BE143533	Hs.109309	hypothetical protein FLJ20035		6.8
60	443136	NM_001440		exostoses (multiple)-like 3	Exostosin,SS,TM	6.8
	421758	BE397336	Hs.1422	Gardner-Rasheed feline sarcoma	SH2,SH3,pkinase	6.8
	448148 400205	NM_016578	HS.20509	HBV pX associated protein-8	PHD,Virus_HS,SS,ICIn_chan SS	6.8 6.8
	434315	AW196608		NM_006265*:Homo sapiens RAD21 ESTs	, 00	6.8
65	418184	AA367375		Homo sapiens cDNA FLJ14015 fis		6.8
	431898	AK000020	Hs.272018	hypothetical protein FLJ20013		6.7
	438527	Al087335	Hs.123473	ESTs	TM,Reticulon	6.7
	409649	AA159216	Hs.55505	hypothetical protein FLJ20442	Y_phosphatase,DSPc,TM	6.7
70	429712	AW245825	Hs.211914	ENSP00000233627*:NADH-ubiquino	oxidored_q6,SS,TM,rrm	6.7
70	456886	AW089093	Hs.144996	ESTs, Weakly similar to 138022	CC TH ACAT LED	6.7 6.7
	427461 434000	AA531527 BE002846	Hs.332040 Hs.112964	hypothetical protein MGC13010 ESTs	SS,TM,ACAT,LRR	6.7
	432530	AF131786	Hs.278303	Homo sapiens clone 25220 mRNA	SS,proteasome	6.7
	436141	AA970001	Hs.150319	Homo sapiens, clone IMAGE:3610	SS,TM	6.7
75	441794	AW197794		ESTs		6.7
	450287	AW291483	Hs.255909	ESTs		6.7
	441523	AW514263		ESTs, Weakly similar to ALUF_H	SS CO TATALED of	6.7
	452798	AI918771	Hs.257170	ESTS	SS,TM,TNFR_c6	6.7 6.7
80	451937 421417	AF119664 AA291004	Hs.27299 Hs.326088	transcriptional regulator prot ESTs	SS,integrin_B,fn3,Calx-be	6.7 6.7
Ö	440317	BE561888	ris20000	gb:601346093F1 NIH_MGC_8 Homo		6.7
	421321		Hs.103502	glutamic-pyruvate transaminase	aminotran_1_2,SS,TM,LRR	6.7
	444904	AW452054	Hs.161139	ESTs	-· ·	6.7
	449730	R72290	Hs.117557	ESTs, Weakly similar to 138022	RasGAP,thyroglobulin_1,Ri	6.7
					223	

	450622	AI660285	Hs.58210	ESTs, Highly similar to ITH4_H	SS,TM,vwa	6.7
	425424	NM_004954	Hs.157199	ELKL motif kinase	pkinase,KA1,UBA,SS	6.7
	435864	AL036499	Hs.188491	ESTs		6.7
_	410397	AF217517	Hs.63042	DKFZp564J157 protein	SS,homeobox,UPF0160,DUF23	6.7
5	454262	AW612232	Hs.254835	ESTs	SS,TM,voltage_CLC,CBS	6.7
	453023	AW028733	Hs.31439	serine protease inhibitor, Kun	Kunltz_BPTI,SS,TM,ion_tra	6.6
	419157	AA234540	Hs.23871	ESTs	pkinase	6.6
	412464	T78141	Hs.22826	ESTs, Weakly similar to 155214	SS,cadherin,crystall	6.6
10	407332	AI801565	Hs.200113	Homo sapiens cDNA FLJ11379 fis	SS,adh_short,Transglutami	6.6
10	456643	AW751497	Hs.98370	cytochrome P450, subfamily IIS		6.6
	411490	R39474		gb:yh95b09.r1 Soares placenta	SS	6.6
	455885	BE153524		gb:PMD-HT0339-241199-002-C03 H	SS,pkinase	6.6
	438857	A1627912	Hs.130783	Forssman synthetase	SS,RA,RasGEF,RasGEFN	6.6
	420307	AW502869	Hs.66219	ESTs	SS,TM	6.6
15	453496	AA442103	Hs.33084	solute carrier family 2 (facil	sugar_tr,SS,TM	6.6
	419182	AA234822	Hs.66147	ESTs	SS,TM,ion_trans,ion_trans	6.6
	406301	•	•	Target Exon	TM	6.6
	433938	AF161536	Hs.284292	ubiquinol-cytochrome c reducta	TM	6.6
_4	448980	AL137527	Hs.289038	hypothetical protein MGC4126		6.6
20	454095	AW178110	Hs.191705	gb:IL3-HT0061-010999-013-H04 H	SS,TM,homeobox,trypsin,PD	6.6
	459702	Al204995		gb:an03c03.x1 Stratagene schiz		6.6
	422201	NM_001505	Hs.113207	G protein-coupled receptor 30	7tm_1,SS,TM	6.6
	406779	AA412048	Hs.279574	CGI-39 protein; cell death-reg	SS,SS	6.6
	404149			C6002509*:gi[5031885 ref[NP_00	SS,TM,kringle	6.6
25	· 418576	AW968159	Hs.302740	Epithelial calcium channel 2,	SS,TM	6.6
	421363	NM_001381		docking protein 1, 62kD (downs	PH,IRS,TM,PH,IRS,trypsin,	6.6
	458919	AI681567	Hs.13349	KIAA0756 protein	TM	6.6
	427502	AI811865	Hs.7133	Homo sapiens, clone IMAGE:3161	SS,TM,ABC_tran,Glyco_tran	6.5
	412289	AW935967	Hs.170162	KIAA1357 protein	SS	6.5
30	447105	AW377610	Hs.11123	DKFZP564G092 protein	SS,TM	6.5
50					laminin_EGF,laminin_G,EGF	6.5
	444672	Z95636	Hs.11669	laminin, alpha 5	SS,TM,gla	6.5
	429299	AI620463	Hs.347408	hypothetical protein MGC13102		6.5
	420003	AA256906	Hs.111364	ESTs, Weakly similar to ubiqui	SS,TM	6.5
25	431849	A)670823	Hs.85573	hypothetical protein MGC10911	SS,TM	
35	430396	D49742	Hs.241363	hyaluronan-binding protein 2	trypsin,kringle,EGF,SS	6.5
	437662	AA765387		ESTs	WD40,RCC1,SPRY	6.5
	436543	NM_002212	Hs.5215	integrin beta 4 binding protei	elF6	6.5
	405375			CX000741*:gi 4885461 ref NP_00	SS,TM	6.5
40	430116	AA465350	Hs.119400	ESTs	SS,TM,adh_short	6.5
40	406109			Target Exon		6.5
	414871-	BE549179	Hs.29008	gb:601078714F1 NIH_MGC_12 Homo		6.5
	440656	Al979248	Hs.148221	ESTs		6.5
	438951	U51336	Hs.6453	inositol 1,3,4-triphosphate 5/	SS,oxidored_nitro,SS	6.5
4.0	405376			Target Exon	SS,TM	6.5
45	426925	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fi	SS	6.5
	400500			Target Exon		6.5
	408294	BE141732		gb:QV0-HT0101-061099-032-e07 H	Ammonium_transp	6.5
	447904	AW206303		ESTs		6.4
	439211	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fi	SS	6.4
50	426828	NM_000020	Hs.172670	activin A receptor type II-lik	pkinase,Activin_recp,SS,T	6.4
	446100	AW967109	Hs.13804	hypothetical protein dJ462O23.	SS,TM	6.4
	442146	R52599		gb:yg81g01.r1 Soares infant br	TM .	6.4
	425041	Al377150	Hs.150914	ESTs	SS	6.4
	457584	AA147979	Hs.285005	mitochondrial import receptor	Josephin	6.4
55	435449	AA682379	Hs.303460	EST		6.4
	406284			Homo sapiens mRNA full length		6.4
	425944	AK000664	Hs.164256	hypothetical protein FLJ20657		6.4
	453367	AW732847	Hs.70573	PKCI-1-related HIT protein	SS,TM	6.4
	419725	U66048	Hs.92683	Homo sapiens clone 161455 brea		6.4
60	412452	AA215731		suppression of tumorigenicity	SS	6.4
	421273	AJ245416	Hs.103106	U6 snRNA-associated Sm-like pr	Sm,SS,tRNA-synt_1,GST_C,G	6.4
	432746	AA564512	Hs.24301	polymerase (RNA) II (DNA direc	SS,TM,EF1BD	6.4
	429398	AA452239		KIAA0970 protein		6.4
	404430			C8000066*:gij10432395 emb CAC1	SS	6.4
65	427339	AI734109	Hs.97984	SRY (sex determining region Y)	•	6.4
	436389	AI811706		CHMP1.5 protein		6.4
	428890	AA525226	Hs.303293	ESTs, Moderately similar to 15		6.4
	445333	BE537641	Hs.44278	hypothetical protein FLJ12538	SS	6.4
	414756	AW451101	Hs.159489	ESTs, Moderately similar to JC	hexokinase2,hexokinase	6.4
70	423847	U16997	Hs.133314	RAR-related orphan receptor C	hormone_rec,zf-C4,SS,TM,h	6.4
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (mus	PGAM,BRCT,RNA_pol_L	6.4
	439569	AW602166	Hs.222399	CEGP1 protein	CUB,EGF,SS	6.4
	457274	AW674193	Hs.227152	mannan-binding lectin serine p	SS,TM,SS,TM,Clathrin_lg_c	6.4
	444550	BE250716	Hs.87614	ESTs	SS ·	6.4
75	407198	H91679	12.01017	gb:yv04a07.s1 Soares fetal liv	BIR	6.4
	423228	AL137491	Hs.125511	Homo sapiens mRNA; cDNA DKFZp4	SS,TM,sushi	6.4
	422682	W05238	Hs.94316	ESTs, Weakly similar to T31613	SS,TM,DEAD,helicase_C,Lam	6.3
	447887	AA114050	Hs.19949	caspase 8, apoptosis-related c	ICE_p20,DED,ICE_p10	6.3
	400137		110.10040	Eos Control		6.3
80	408784	AW971350	Hs.63386	ESTs	SS	6.3
00	435028	AW193035	Hs.187370	ESTs	<del></del>	6.3
	433026	AI467908	Hs.8882	ESTs	SS,TM,7tm_1	6.3
		D28419	Hs.82609	hydroxymethylbilane synthase	Porphobil_deam	6.3
	417810	Al057205	Hs.14584		· arkunaradan	6.3
	436050	71001200	113.17304	ESTs		0.0

	403672			C4001244:gi[539933]pir][A61275	tubulin,TM	6.3
	448269	BE622358	Hs.61260	hypothetical protein FLJ13164		6.3
	430217	N47863	Hs.180450	ribosomal protein S24	Ribosomal_S24e	6.3
	426675	AW084791	Hs.133122	hypothetical protein FLJ14524	SS,TM,aminotran_1_2	6.3
5	423510	AB000824	Hs.129712	trehalase (brush-border membra	Trehalase	6.3
	428573	AA430651	Hs.209249	ESTs		6.3
	457052	BE167242	Hs.47099	hypothetical protein FLJ21212	SS	6.3
	445099	BE163341		gb:QV3-HT0458-230200-099-b01 H		6.3
	450334	AF035959	Hs.24879	phosphalidic acid phosphatase	PAP2,SS	6.3
10	416000	R82342	Hs.79856	ESTs, Weakly similar to S65657	SS,TM,sugar_tr	6.3
	427880	AA436011	Hs.98187	ESTs	ool: witen 2	6.3
	426722	U53823	Hs.171952	occludin	Occludin, SS, TM, BIR	6.3
	452072	BE258857	Hs.27744	RAB3A, member RAS oncogene fam	ras,arf,SS,PDEase	6.2
	431161	AA493591	· IO.E/ · · · ·	gb:nh01a12.s1 NCI_CGAP_Thy1 Ho	SS	6.2
15	413055	AV655701	Hs.75183	cytochrome P450, subfamily IIE	p450	6.2
10	431250	BE264649	Hs.251377	taxol resistance associated ge	Pioc	6.2
	406373	DLL01010	110.201071	Target Exon	SS,TM,vwa,FG-GAP,integrin	6.2
	403003			NM_024944*:Homo sapiens hypoth	TM	6.2
	437834	AA769294		gb:nz36g03.s1 NCI_CGAP_GCB1 Ho	SS	6.2
20	406299	701703234		Target Exon	•	6.2
20	439327	AF086141	Hs.50760	ESTs, Highly similar to BirnL [	SS	6.2
	414246	BE391090	Hs.280278	EST		6.2
	427812	AA770424	Hs.98162	ESTs	SS	6.2
	420926	AA830402	Hs.221216	ESTs ·	UQ_con	6.2
25	443766	N91071	Hs.109650	ESTs	OCCUM	6.2
23	431082	AA491600	133.103000	gb:ne80a11.s1 NCI_CGAP_Ew1 Hom		6.2
	420530	AI218431		coagulation factor VIII-associ		6.2
	407360	X13075		gb:Human 2a12 mRNA for kappa-i		6.2
	449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)		6.2
30	409946	AW162263	Hs.312468	ESTs, Weakly similar to ALUC_H	RasGAP,C2,PH,BTK	6.2
50	413272	AA127923	115.512700	ESTs	SS	6.2
•	445050	AW205483	Hs.147260	ESTs	SS,trypsin,kringle,fn2,EG	6.2
	458130	AA115811	Hs.6838	ras homolog gene family, membe	ras,arf	6.2
	449940	AW291126	Hs.187520	Homo sapiens, clone IMAGE:3834	SS,zf-C2H2	6.2
35	440390	AW207385	Hs.36475	KIAA0493 protein	UU,ZFOZIIZ	6.2
55					•	6.2
	423106 402501	N52572	Hs.13702	ESTs, Moderately similar to AL	ig,MHC_I,SS	6.1
		AA832417	Un 1200E0	sperm specific antigen 2 ESTs	SS,ig,pkinase,LRR,LRRCT	6.1
	431470		Hs.139650		33,19,pallase,LTATLTATO	6.1
40	416597	H66891		gb:yr71c03.r1 Soares fetal liv	SS,WD40	6.1
<del>+</del> 0	412122	AW852707	th 77007	G-rich RNA sequence binding fa		6.1
	415056	AB004662	Hs.77867	adenosine A1 receptor	7tm_1,SS,TM	6.1
	400358	AF181286		Homo sapiens mutant dystrophin	COCasa I shais histin lin	6.1
	405473	AVANCOACOO	U- 455070	NM_001093°:Homo saplens acetyl	CPSase_L_chain,biotin_lip	
45	422625	AW504698	Hs.155976	cullin 4B	SS,SS,Cullin,Cullin	U.1
43	422262	AL022315	Hs.113987	lectin, galactoside-binding, s	Gal-bind_lectin	6.1
	401121	41/000000	11- 455074	C12001638*:gi 7291960 gb AAF47	714	6.1
	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	TM	6.1
	457216	AA452554	Hs.283697	ESTs, Weakly similar to A41796	bZIP_Maf,SS,P5CR,EF1BD	6.1
50	456021	BE246628	Hs.250726	gb:TCBAP1D5030 Pediatric pre-B	SS,TM,SS	6.1 6.1
50	420319	AW406289	Hs.96593	hypothetical protein	ras,arf	6.1
	410082	AA081594 AF129085	Hs.158311	Musashi (Drosophila) homolog 1	SS.HECT, phoslip	6.1
	450593		Hs.25197	STIP1 homology and U-Box conta	TPR,SS,TM,Rhomboid,lactam SS	6.1
	437050 458835	AA766420 Al868753	11- 70270	ESTs	SS	6.1
55			Hs.76372	ESTs	33	6.1
55	412777 454364	AI335773	Hs.323806	ESTS	CCTM	6.1
	448877	BE263928 AI583696	Hs.253313	gb:601191272F1 NIH_MGC_7 Homo	SS,TM	6.1
	413045	X92121	Hs.75180	ESTs	Metallophos, TPR	6.1
				protein phosphatase 5, catalyt	Metallopilos, (FIX	6.1
60	408054 417852	AW816490 AJ250562	Hs.8102 Hs.82749	ESTs transmembrane 4 superfamily me	transmembrane4,SS,TM	6.1
UU	410445	AA199830	NS.02/43	gb:zq75h01.r1 Stratagene hNT n	Uaisinchia anch, 30, 1 M	6.1
	415870	H15578	Hs.21017	ESTs		6.1
	438723	M34429	113.21017	gb:Human PVT-IGLC fusion prote		6.1
	441307	AW071696	Hs.209065	hypothetical protein FLJ14225	SS,TM	- 6.0
65	406575	711071030	113.203000	Target Exon	SS,pkinase,pkinase_C,RFX_	6.0
05	401488			Target Exon	Glyco_hydro_1	6.0
	437650	AA814338	Hs.292297	ESTs	G/30_1/4.0_1	6.0
	439827	AA846538	Hs.187389	ESTs	pkinase,DAG_PE-bind,PH	6.0
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, s	SS,TM	6.0
70	454513	BE159271	Hs.109731	gb:MR0-HT0407-180100-004-h05 H	30,1111	6.0
	414944	C15044		gb:C15044 Clontech human aorta	SS,TM	6.0
	451277	AK001123	Hs.26176	hypothetical protein FLJ10261	TM,SS,TM,death,DED	6.0
	421190	U95031	Hs.102482	mucin 5, subtype B, tracheobro	Cys_knol,vwc	6.0
	401215			C12000457*:gi]7512178[pir][T30	trypsin.SS.TM	6.0
75	408117	AL138255		ESTs, Weakly similar to 138022	SS,zf-C3HC4,BIR	6.0
. 5	426357	AW753757	Hs.12396	gb:RC3-CT0283-271099-021-a08 C	a contraction	6.0
	418630	AI351311	Hs.251946	poly(A)-binding protein, cytop	SS,pkinase .	6.0
	400389	AL135841		olfactory receptor, family 2,	7tm_1,SS,TM,CSD	6.0
	447128	AI271898		cyclin K		6.0
80	431297	AA651771	Hs.3076	ESTs		6.0
	431857	W19144	Hs.271742	ADP-ribosyltransferase (NAD; p	PARP,PARP_reg,SS,TM,Pepti	6.0
	430023	AA158243	Hs.227729	FK506-binding protein 2 (13kD)	SS,FKBP,SS,PDGF,C2,PI-PLC	6.0
	453101	AW952776	Hs.94943	ESTs	TM	6.0
	407383	AA532576		ESTs, Moderately similar to AL	SS,Patatin,ank	6.0
				,		0.0
					225	

	430132	AA204686	Hs.234149	hypothetical protein FLJ20647	SS,SS,TM,ig	6.0
	459111	AU077013	Hs.28757	transmembrane 9 superfamily me	EMP70	6.0
	405770			NM_002362:Homo sapiens melanom	MAGE	6.0
•	415611	T26376		gb:AB123C11R Infant brain, LLN	SS,TM,rmn,sushi	6.0
5	453413	AJ003294		gb:AJ003294 Selected chromosom	SS,Folale_carrier	6.0
	424415	NM_001975		enolase 2, (gamma, neuronal)	enolase, SS, Atrophin-1, Atr	5.9
	426048	AI768853	Hs.134478	ESTs	TM	5.9
	435750	AB029012	Hs.4990	KIAA1089 protein	SS,TM	5.9
10	439469	W69836		gbzd48a02r1 Soares_fetal_hea	SS,pkinase,C2,pkinase_C,D	5.9
10	445664	AW968638	Hs.237691	ESTs, Weakly similar to KIAA06		5.9
	418830	BE513731	Hs.88959	hypothetical protein MGC4816	TM,CDP-OH_P_transf	5.9
	452113	AI859393		gb:wm11a02.x1 NCI_CGAP_Ut4 Hom	actin	5.9
	449101	AA205847	Hs.23016	G protein-coupled receptor	7tm_1,SS,TM	5.9
16	437640	AA764893	Hs.272155	ESTs, Weakly similar to 138022		5.9
15	400748			NM_022122:Homo sapiens matrix	SS,Peptidase_M10,hemopexi	5.9
	442370	AI143593	Hs.129419	ESTs		5.9
	442419	Al749893	Hs.270532	ESTs, Wealthy similar to 138022	Adaptin_N,Alpha_adaptinC2	5.9
	439986	AW750272	Hs.128608	ESTs	SS,TM,ISK_Channel	5.9
20	407553	Z11168		gb:H.sapiens 5HT1A receptor re	SS,TM	5.9
20	431424	Al222969		ESTs	SS	5.9
	442297	NM_006202		phosphodiesterase 4A, cAMP-spe	PDEase	5.9
	457845	H93040	Hs.297729	ESTs	SS,TM,WD40	5.9
	446912	Al347650	Hs.128521	ESTs, Moderately similar to AL	SS	5.9
25	451381	BE241831	Hs.172330	hypothetical protein MGC2705	SS,Ribosomal_L28e	5.9
25	416024	AW886484	Hs.343522	ATPase, Ca transporting, plasm	E1-E2_ATPase,Hydrolase,Ca	5.9
	446329	NM_013272		solute carrier family 21 (orga	kazal,OATP_N,OATP_C	5.9
	431321	AW136372	Hs.1852	acid phosphatase, prostate	SS,TM,acid_phosphat	5.9
	420039	NM_004605		sulfotransferase family, cytos	Sulfotransfer, SS, DAGKc	5.9
20	428223	AA424313	Hs.98402	ESTs	HECT	5.9
30	433333	AI016521	Hs.71816	v-akt murine thymoma viral onc	homeobox,pkinase,PH,pkina	5.9
	450251	BE080483		gb:QV1-BT0630-280200-086-a05 B	SS	5.9
	408511	AW206404	Hs.27268	ESTs	00.019	5.9
	414348	AF041430	Hs.75922	brain protein 13	SS,SH3	5.9
35	456950	AF111170	Hs.306165	Homo sapiens 14q32 Jagged2 gen	SS,TM,DSL	5.9
33	412173	T71071		gb:yc50b05.r1 Stratagene liver	CPSase_L_chain	5.8
	404001	1157040	11- 40500	Target Exon	00	5.8
	445263	H57646	Hs.42586	KIAA1560 protein	SS	5.8
	441583	AI791499	Hs.205742	ESTs, Weakly similar to ALUA_H	CC TM aftered aftered	5.8
40	430168	AW968343		DKFZP434I1735 protein	SS,TM,efhand,efhand	5.8
70	454682	AW816029		gb:MR3-ST0220-151299-027-b10 S	filament CO-t-st-s	5.8
	453829	AL138200	Li- 000034	gb:DKFZp547N052_r1 547 (synony	SS,TM,ATP-synt_C,Gatactos	5.8
	437372	AA323968	Hs.283631	hypothetical protein DKFZp547G	SS	5.8
	421726	AK001237	Hs.319088	hypothetical protein FLJ10375	TM	5.8
45	451045	AA215672	U- cocos	gb:zr96e09.s1 NCI_CGAP_GCB1 Ho	SS,Peptidase_C1,zf-C2H2	5.8
73	439616	BE018635	Hs.58582	Homo sapiens cDNA FLJ12789 fis	SS,TM	5.8
	455679	BE066529	Un 124012	gb:RC3-BT0333-300300-017-a12 B	UBX	5.8 5.8
	457125 430600	AW444451 AW950967	Hs.134812	ESTS	SS white SS TM C paleb a	5.8
	421707	NM_014921	Hs.274348	HLA-B associated transcript-3	ubiquitin,SS,TM,G-patch,a	5.8
50	436127	W94824	Hs.107054 Hs.11565	lectomedin-2 RIKEN cDNA 2010100012 gene	Latrophilin,OLF,7tm_2,Gal	5.8
50	414347	BE275835	115.11303		Corona_7,SS,TM SS	5.B
	439910	H66765	Hs.339397	gb:601121639F1 NIH_MGC_20 Homo ESTs	SS ·	5.8
	410382	AW664971	Hs.259546	ESTs	LIM	5.8
	426391	AW161050	Hs.169611	second milochondria-derived ac	SS	5.8
55	423358	AI815474	Hs.343866	gb:au47f10.y1 Schneider fetal	SS	5.8
JJ	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fi	Peplidase_M1	5.8
	402189	711014201	113.30730	ENSP00000247423*:D-siglec prec	i cpadase_iii i	5.8
	439949	AW979197	Hs.292073	ESTs, Weakly similar to ALU7_H		5.8
	457978	AA776638	115.252015	gb:ae78g04.s1 Stratagene schiz	SS,PH,IQ,RasGEF,RasGEFN,R	5.8
60	436685	W28661	Hs.5288	Homo sapiens mRNA; cDNA DKFZp4	SS,TM,pkinase,Activin_rec	5.8
00	411602	L01406	Hs.767	growth hormone releasing hormo	7tm_2,HRM	5.8
	433357	T05639	115.701	gb:EST03528 Fetal brain, Strat	SS S	5.8
	404311	100000		Target Exon	TM	5.8
	428092	AW879141		ESTs	SS,TM	5.8
65	452620	AA436504	Hs.119286	ESTs	SS	5.8
05	401938	77430304	163.113200	Target Exon	SS,PHD,proteasome	5.7
	407202	N58172	Hs.109370	ESTs	SS,F5_F8_type_C,pkinase,E	5.7
	458882	R34993	Hs.226666	ESTs, Moderately similar to 15	SS,CRAL_TRIO,PKI	5.7
	452357	AI638176	Hs.283865		SS,TM,SS,TM	5.7
70	452625	AA724771	Hs.61425	ESTs	00,111,00,1111	5.7
. •	430281	AI878842	Hs.237924	CGI-69 protein	mito_carr,SS,TM	5.7
	430490	AW902951	Hs.301723	Homo sapiens cDNA FLJ12974 fis	TM	5.7
-	450122	BE313765	Hs.343443	ESTs, Weakly similar to 138022	SS,TM,Y_phosphatase,LON,A	5.7
	450801	AI739013	Hs.203348	ESTs	SS,TM,Hint,HH_signal	5.7
75	413413	D82520	Hs.132390	zinc finger protein 36 (KOX 18	SS,mm,DUF185	5.7
. •	445631	AK001822	102000	Homo sapiens cDNA FLJ10960 fis		5.7
	419390	AJ701162	Hs.90207	hypothetical protein MGC11138	SS,TM,PMP22_Claudin,PMP22	5.7
	423139	AW402725	Hs.288560	hypothetical protein FLJ21106		5.7
	426221	AB007881		KIAA0421 protein	PI3_PI4_kinase,FATC,SS,TM	5.7
80	443785	AW449952	Hs.190125	basic-helix-loop-helix-PAS pro	· ····································	5.7
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20,	WD40,SS,TM,fn3,EGF,fn3,ig	5.7
	446596	AW204515	Hs.156113	ESTs, Weakly similar to G01025		5.7
	432353		Hs.274411	SCAN domain-containing 1	SCAN	5.7
	427625	AF008216	Hs.285013	putative human HLA class II as	====	5.7
					226	

	421543	AK000519	Hs.105606	hypothetical protein FLJ20512	TM	5.7
	418087	AA961613	Hs.127838	ESTs		5.7
	432751	AF152099	Hs.278911	interleukin 17C	SS	5.7
_	433943	AA992805	Hs.44865	lymphoid enhancer-binding fact		5.7
5	414274	AW300961	Hs.334684	Homo sapiens, clone IMAGE:4127	SS,Vps26,Acyt-CoA_dh	5.7 5.7
	431328 451481	AA502999 AA300228	Hs.291591 Hs.295866	ESTs hypothetical protein DKFZp434N		5.7
	430344	AA476827	Hs.171012	hypothetical protein FLJ22349	HLH	5.6
	419516	H82550	10.17 1012	ATP-binding cassette, sub-fami	SS,TM,ABC_tran,ABC_membra	5.6
10	413564	BE260120	-	gb:601146990F1 NIH_MGC_19 Hamo		5.6
	415958	H10942		gb:ym06c11.r1 Soares infant br	SS,TM	5.6
	401402			Target Exon		5.6
	456145	BE299427	Hs.21446	KIAA1716 protein	SS,DIX,PDZ,DEP,Dishevelle	5.6
15	431536	AL133066	Hs.341906	ESTs	TM,SAM_decarbox,SS,pkinas	5.6 5.6
13	456266 435800	L29073 AI248285	Hs.198726 Hs.118348	cold shock domain protein A ESTs	CSD,homeobox,SS,TM,7tm_2, TM,ECH,chromo	5.6
	449285	AI912702	Hs.139135	ESTs .	interiorione	5.6
	418256	AW845318	Hs.12271	f-box and leucine-rich repeat	SS,SS,TM,HSF_DNA-bind	5.6
	417442	AA199940	Hs.124039	ESTs		5.6
20	405931			Target Exon	•	5.6
	455286	BE144384		gb:MR0-HT0166-191199-004-c11 H	SS	5.6
	446931	Al348856	Hs.21627	gb:tb05a05.x2 NCI_CGAP_Lu26 Ho	00 TI / D'L	5.6
	446548	AI769392	Hs.200215	ESTs	SS,TM,Ribosomal_S25,sugar	5.6 5.6
25	401984 404066			C17000146*:gi 2143629 pir  A57 Target Exon	pkinase,SS,TM,P2X_recepto SS,tRNA-synt_2b,HGTP_anti	5.6
23	418363	AA218628	Hs.202977	ESTs	Oo,Bab to Jin Cash To II Land	5.6
	458198	Al286100		ESTs		5.6
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	SS,TM,GNS1_SUR4,SS,TM,Rho	5.6
20	432328	Al572739	Hs.195471	6-phosphofructo-2-kinase/fruct	PGAM,6PF2K	5.6
30	421871	AK001416	Hs.306122	glycoprotein, synaptic 2	TM,Sterold_dh,SS	5.6
	415514	F11301 .	Hs.138329	ESTs	SS,TM	5.6
	426208 429367	AI370379 AB007867	Hs.132216 Hs.278311	ESTs plexin B1	SS,TM Sema,PSI,TIG,SS,TM,TIG,Se	5.6 5.6
	405939	ABOUTOUT	па.2/0011	Target Exon	38/18/13/110/33/11/110/36	5.6
35	457331	AV647405	Hs.18443	aldehyde dehydrogenase 8 famil	GTP_EFTU	5.6
	438705	AI049524	Hs.283390	ESTs, Weakly similar to 210926	SS,E2F_TDP,E2F_TDP	5.6
	428624	Al125222	Hs.98712	hypothetical protein DKFZp434H	SS,TM,ras,MSP_domain	5.6
	419389	Al074951	Hs.319095	ESTs	SS,DPPIV_N_term	5.6
40	447595	AW379130		phosphodiesterase 9A	PDEase	5.6
40	408015	AW136771		epidermal differentiation comp	SS	5.6 5.5
	413041 452849	BE061580 AF044924	Hs.61622 Hs.30792	gb:MR0-BT0249-091299-201-c07 B hook2 protein	bZIP,SS,AhpC-TSA	5.5 5.5
	434357	AW732284	Hs.3828	mevalonate (diphospho) decarbo	GHMP_kinases,SS,TM	5.5
	455274	BE151622		gb:PM0-HT0302-271099-001-a08 H	SS,TM,RNA_pol_L	5.5
45	453904	AW003821		ESTs		5.5
	424624	AB032947	Hs.151301	Ca2+dependent activator protei	Fork_head	5.5
	426576	AA381720		gb:EST94853 Activated T-cells	vwa.integrin_A,FG-GAP	5.5
	440682	AW362152	Hs.27181	nuclear receptor binding facto	SS	5.5 5.5
50	419125 450207	AA642452 T87615	Hs.130881 Hs.14716	B-cell CLL/lymphoma 11A (zinc ESTs	33	5.5 5.5
<b>J U</b> .	405211	10/010	110.17710	C7000900:gi 4508027 ref NP_003	SS	5.5
	413937	H65775	Hs.207915	ESTs		5.5
	426793	X89887	Hs.172350	HIR (histone cell cycle regula	WD40, Clathrin, Clathrin_pr	5.5
55	412091	R06185		gb:ye94d03.r1 Soares fetal liv	SS,TM,IBR,IBR	5.5
55	446536	W74413	Hs.15251	hypothetical protein	SS	5.5 5.5
	451117 409547	AA015752 AW409885	Hs.205173 Hs.335877	ESTS	TM	5.5 5.5
	412673	AL042957	Hs.31845	Homo sapiens, clone MGC 4558, ESTs		5.5
	426440	BE382756	Hs.169902	solute carrier family 2 (facil	sugar_tr,SS,TM,sugar_tr	5.5
60	449225 .	R39108	Hs.6777	ESTs	SS,TM,Na_sulph_symp	5.5
	403938			Target Exon	Ephrin	5.5
	441197	BE244638	Hs.166	sterol regulatory element bind	KLH	5.5
	455604	BE011183 AW971345	Un 202745	gb:PM3-BN0218-100500-003-d09 B		5.5 5.5
65	457468 447677	Al419235	Hs.292715 Hs.344456	ESTs gb:tt21d02.x1 NCI_CGAP_Brn23 H	SS,zf-C2H2,SCAN,SCAN,zf-C	5.5
05	415473	R39986	Hs.12778	ESTs	TM,ion_trans	5.5
	408422	AW977031	Hs.143554	ESTs, Highly similar to B45036		5.5
	442780	Al017521		ESTs	SS,TM,7tm_1	5.5
70	451558	NM_001089		ATP-binding cassette, sub-fami	ABC_tran,SRP54,SS,TM,ECH	5.5
70	439422	AW452791		ESTs	SS,TM	5.5
	423479		Hs.129208	death-associated protein kinas	pkinase SS	5.5 5.5
	459558 441187	AI539821 AW195237	Hs.298799	ESTs, Wealty similar to 210926 hypothetical protein FLJ22174	SS,TM, bubulin	5.5 5.5
	420894	AA744597	Hs.7734 Hs.88854	ESTs	SS,ank	5.5
75	404710			C9001584:gi[7499208[pir][T2099		5.5
-	447827	U73727	Hs.19718	protein tyrosine phosphatase.	Y_phosphatase,fn3,ig,MAM,	5.5
	448387	AI874402	Hs.292590	ESTs		5.5
	419541	AW749617		tankyrase, TRF1-interacting an		5.5
80	449686	AW072813		ESTs, Moderately similar to AL	SS coverage	5.5 5.5
30	426315 451312	AA854219 AI769831	Hs.348137 Hs.337054	Homo sapiens, clone IMAGE:3542 ESTs	SS,crystafl SS	5.5 5.5
	432538	BE258332	Hs.278362	mate-enhanced antigen	SS,TM,AAA,Ribosomal_L2	5.5
	446790	AW452105		ESTs	SS,zf-C2H2	5.5
	448682	T09471	Hs.250820	hypothetical protein FLJ14827		5.5

	425234	AW152225	Hs.165909	ESTs, Weakly similar to 138022	SS	5.5
	411219	AW832917		gb:QV2-TT0003-161199-013-h06 T		5.5
	439742	AI827721	Hs.284298	Homo sapiens mRNA full length	SS	5.5
5	432004	BE018302	Hs.2894	placental growth factor, vascu	PDGF,SS	5.5 5.5
J	402916 405346			ENSP00000202587*:Bicarbonate ( Rag C protein	HCO3_cotransp,SS RCC1	5.5
	415976	R43144	Hs.21919	ESTs	TM	5.4
	435064	T70740	Hs.31433	ESTs	SS,MDM2	5.4
	440024	AA969333	Hs.160098	ESTs	O , mone	5.4
10	431525	AA506656	Hs.6185	KIAA1557 protein		5.4
	458644	AW270149		ESTs, Moderately similar to GG		5.4
	410895	AW809679		gb:MR4-ST0124-261099-015-f05 S		5.4
	441350	AB020690	Hs.7782	paraneoplastic antigen MA2		5.4
• -	413034	BE392896	Hs.129126	Homo sapiens, clone MGC:10992,	SS	5.4
15	444664	N26362	Hs.11615	map kinase phosphatase-like pr	DSPc,Rhodanese,SS,TM	5.4
	443887	NM_004729	Hs.9933	Ac-like transposable element	zf-BED	5.4
	445871	AI702901	Hs.145582	ESTs, Weakly similar to FOR4 M	SS,TM,efhand,efhand	5.4 5.4
	411992 458341	AW816214 AW373583	Hs.143055 Hs.221994	ESTs gb:QV4-BT0534-281299-053-e08 B	SS,TM	5.4
20	451677	AA059222	Hs.33538	ESTs, Weakly similar to oxygen		5.4
20	432656	NM_000246		MHC class II transactivator	LRR	5.4
	417739	Z43995	1.0.00.0	gb:HSC1QB121 normalized infant	SS,ArfGap,wwa,TSPN,fn3,Co	5.4
	424618	L29472	Hs.1802	major histocompatibility compl	TM,ig,MHC_II_beta,SS,TM,A	5.4
	446847	T51454	Hs.82845	Homo sapiens cDNA: FLJ21930 fi	SS,TM,BNR,fn3,ltdl_recept_	5.4
25 ·	436094	AI798701		ESTs		5.4
	433168	AI085436		gb:ow84g06.s1 Soares_fetal_tiv	SS,TM,PID	5.4
	417359	T99264	Hs.191117	ESTs 40	Diller Bu Diller Bu C 00 TC	5.4
	436014	AF281134	Hs.283741 Hs.301637	exosome component Rrp46	RNase_PH,RNase_PH_C,SS,TG	5.4 5.4
30	435154 431630	AA668764 NM 002204	Hs.265829	ESTs integrin, alpha 3 (antigen CD4	SS,TM integrin_A,FG-GAP,Rhabd_g	5.4 5.4
50	444064	W85970	Hs.16292	ESTs	SS,TM,Dihydroorotase	5.4
	415970	H23333	Hs.29002	KIAA1706 protein	ou, in parjurous and	5.4
	445303	AW362198	Hs.12503	Interleukin 15 receptor, alpha	SS,sushi,SS	5.4
	421542	AA411607	Hs.118964	ESTs, Weakly similar to KIAA11	SS,SS	5.4
35	459704	AA719572	Hs.274441	Homo sapiens mRNA; cDNA DKFZp4		5.4
	402285			sclerostin	SS,TM	5.4
	431543	AW969619	Hs.259768	adenylate cyclase 1 (brain)	TM	5.4
	431534	AL137531	Hs.258890	Homo sapiens mRNA; cDNA DKFZp4	SS,TM,ras	5.4
40	417516	AA203473	Hs.81529	ESTS	TM	5.4 5.4
70	423233 420733	BE048021 AW291446	Hs.11067 Hs.88651	ESTs, Highly similar to T46395 ESTs	SS	5.4
	404807	711251440	10.0001	Target Exon	UPF0027	5.4
	436483	AJ272063	Hs.283010	vaniiloid receptor subtype 1	SS,TM,ank,ion_trans,SS,TM	5.4
	425316	AA354977	Hs.99010	ESTs, Moderately similar to T1	SS,pkinase,ig	5.4
45	425565	AA359485	Hs.173084	gb:EST68511 Fetal lung II Homo		5.4
	413341	H78472	Hs.191325	ESTs, Weakly similar to T18967		5.4
	401203	A1 4400FF	U- 440000	Target Exon	filament .	5.4
	422452 436718	AL110255 AW015227	Hs.116808 Hs.289053	Homo sapiens mRNA; cDNA DKFZp5 hypothetical protein FLJ14733	SS,asp,PGAM SS,TM	5.4 5.4
50	428501	AL041162	Hs.98587	ESTs	TM	5.4
	439695	W28548	Hs.285050	ESTs	TM,ion_trans,K_tetra,Kv2c	5.3
	417514	AA203445	Hs.325819	ESTs	· · ·	5.3
	441358	AW173212		ESTs		5.3
55	401722			Target Exon	TM,PLAT,SS	5.3
55	408905	AV655783	Hs.661	Target CAT		5.3
	454453	AW752781	U- 75350	hypothetical protein FLJ12614	Vineville	5.3 5.3
	410312 437926	AW850953 BE383605	Hs.75350 Hs.300816	gb:IL3-CT0220-150200-058-A11 C small GTP-binding protein	Vinculin SS,TM,TPR	5.3
	457520	AV659151	Hs.282961	ESTs	55,1m,1FK	5.3
60	411605	AW006831	1101202001	ESTs	TM.synantobrevin	5.3
	409164	AA706639		gb:ag90e09.r1 Stratagene hNT n	SS,TM,Hint,HH_signal,tubu	5.3
	438868	AW246243	Hs.334800	hypothetical protein FLJ20974	•	5.3
	439034	AF075083		gb:Homo saplens full length in	filament, filament	5.3
65	411426	BE141714		gb:QV0-HT0101-061099-032-c04 H	SS	5.3
65	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A,	Glyco_hydro_38,SS,TM,Pept	5.3
	438470	AW936329	Hs.227823	pM5 protein hypothetical protein FLJ23093	SS,TM	5.3 5.3
	427789 430230	AA412428 BE257724	Hs.48642 Hs.236361	seb4D	rrm,SS,2-Hacid_DH,WD40	5.3
	434314	BE392921	Hs.3797	RAB26, member RAS oncogene fam	ras,arf,SS	5.3
70	428539	AW410063	Hs.184877	solute carrier family 25 (mito	mito_carr,SS,TM,profilin,	5.3
	414927	T83587	Hs.186476	ESTs	SS, Sulfatase	5.3
	404596			Target Exon	SS	5.3
	454151	AA047169	Hs.154088	hypothetical protein FLJ22756	SS,TM,Glycos_transf_4	5.3
75	431627	AW609720	U_ 49900 *	HSPC042 protein		5.3
75	422379 426765	AA932860 AA743603	Hs.133864	ESTs	MAM33	5.3 5.3
	426765 433325	AA743603 AW206986	Hs.172108 He 1/3905	nucleoportn 88kD ESTs	SS	5.3
	403128	V11500200	Hs.143905	KIAA1033 protein	SS,TM,tubulin,EGF,F5_F8_1	5.3
	447730	AI421251	Hs.114085	Homo sapiens mRNA for KIAA1755	SS,Transglutamin_C,Transg	5.3
80	405085			Target Exon	SS,SS,SNF2_N,helicase_C	5.3
	438080	AA777381	Hs.291530	ESTs, Weakly similar to ALUC_H		5.3
	439091	AA830144	Hs.135613	ESTs, Moderately similar to 13	KH-domain	5.3
	427326 427859	Al287878 AA416856	Hs.98170	gb:qv23f06.x1 NCI_CGAP_Lym6 Ho ESTs	SS,TM,7tm_1,SS,TM SS,TM,DUF60,bypsin,CUB,u	5.3 5.3
	721003	rvm 10030	111000110	2010		J.J
					228	

	421779	Al879159	Hs.108219	wingless-type MMTV integration	SS.wnt,SS	5.3
	408270	AW177805		gb:IL3-HT0059-180899-007-806 H		5.3
	418437	AA771738	Hs.348000	ESTs, Moderately similar to AL		5.3
5	409879	BE083422	Hs.56851	hypothetical protein MGC2668	SS,TM	5.3
3	428304 418678	AI743177	Ue 167370	ESTs cancerflestis antigen (NY-ESO-	SS,TM	5.3 5.3
	436540	NM_001327 8E397032	Hs.14468	hypothetical protein MGC14226	SS,TM,zf-C2H2 SS,TM	5.2
	437161	AA054477	Hs.25391	ESTs	SS,TM	5.2
• •	400171			ENSP00000211797:Helicase SKI2W	SS,proteasome	5.2
10	431461	BE299671	Hs.256310	likely ortholog of mouse ZFP28		5.2
	402197	A1A8070440	U= 22042	Target Exon	SS,TM,ATP1G1_PLM_MAT8,ig,	5.2 5.2
	449514 442472	AW970440 AW806859	Hs.23642	protein predicted by clone 236 gb:MR0-ST0020-081199-004-c03 S	SS,PX,arf,lipocatin,PHD,z SS,TM,tnos-1-P_synth,Occl	5.2 5.2
	409679	BE250521		ras homolog gene family, membe	SS,homeobox,CUT	5.2
15	439150	AF086006		gb:Homo sapiens full length in	SS	5.2
	412934	BE011437		gb:CM4-BN0220-080500-170-f03 B		5.2
	435186	AL119470		ESTs	SS	5.2
	400668	D47000	II- AJOECT	Target Exon	CARD,ICE_p20,SS,ICE_p20,I	5.2
20	409125 445904	R17268 AW449920	Hs.343567 Hs.248855	axonal transport of synaptic v ESTs	SS,kinesin,PH,FHA,kinesin SS,homeobox	5.2 5.2
20	414567	BE281057	Hs.184519	hypothetical protein FLJ12949	SS,TM,ank,Adap_comp_sub	5.2 5.2
	414551	Al815639	Hs.76394	enoyl Coenzyme A hydratase, sh	ECH,Peptidase_U7,SS,TM	5.2
	432872	A1908984	Hs.279623	selenoprotein X, 1	DUF25,SS,Ribosomal_L3,PDZ	5.2
25	419492	AA243547	Hs.19447	PDZ-LIM protein mystique	LIM,SS,SH3,Sorb,Metalloph	5.2
25	407478	L77559		gb:Homo sapiens DGS-B partial		5.2
	457892 457228	AA744389 U15177	Hs.206984	gb:ny51e10.s1 NCI_CGAP_Pr18 Ho Human cosmid CRI-JC2015 at D10	6PF2K,PGAM	5.2 5.2
	437536	X91221	Hs.144465	ESTs .	SS,TM,Na_Ca_Ex	5.2 5.2
	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN	00,111,110_00_01	5.2
30	431275	T56571	Hs.10041	ESTs	SS,HLH	5.2
	428021	AI022287	Hs.111991	ESTs, Weakly similar to T33900	SS	5.2
	422400	AA974434	Hs.128353	ESTs		5.2
	446442	BE221533 R59946	Hs.257858	ESTs	cc	5.2 5.2
35	415585 438429	D16918	Hs.184852 Hs.12547	KIAA1553 protein Homo sapiens cDNA: FLJ23388 fi	SS TM	5.2 5.2
55	401677	210310	110.12047	BAI1-associated protein 3	SS,TM,zf-C2H2,kinesin,Vau	5.2
	405637			Target Exon		5.2
	450437	X13956	Hs.24998	hypothetical protein MGC10471	SS	5.2
40	408215	BE614290		syntaxin 10	SS,SS,TM,HLH,TRM,zf-CCCH	5.2
40	452666	AW194601	Hs.13219	ESTs	PI-PLC-X,PI-PLC-Y,C2,PH	5.2
	401553 447541	AK000288	Hs.18800	Target Exon hypothetical protein FLJ 20281	zf-CCHC	5.2 5.2
	453434	AJ271378	Hs.333243	ESTs	2POSITO	5.2
	450351	BE547267	Hs.59791	hypothetical protein MGC13183	SS,TM	5.2
45	411456	AW847588		gb:fL3-CT0213-161299-038-G09 C	SS,TM	5.2
	445634	A1624849	Hs.344612	ESTs, Weakly similar to NEL1_H	vwd	5.2
	453740 426318	AL120295	Hs.311809	ESTs, Moderately similar to PC	CC TM COU the abises of 2	5.2 5.1
	416470	AA375125 N90464	Hs.147112 Hs.303023	Homo sapiens cDNA: FLJ22322 fi beta tubulin 1, class VI	SS,TM,EPH_lbd,pkinase,fn3 SS,tubulin,SS	5.1
50	432022	AL162042	Hs.272348	Homo sapiens mRNA; cDNA DKFZp7	Olimpanilag	5.1
	457579	AB030816	Hs.36761	HRAS-like suppressor	TM	5.1
	438484	AW021671	Hs.293330	ESTs, Weakly similar to p40 [H		5.1
	422802	NM_004278	Hs.27008	phosphatidylinositol glycan, c	DUF158,ank	5.1
55	401724 438670	AI275803	Hs.123428	C16001374:gij6755086 ref NP_03 ESTs	TM,PLAT,SS	5.1 5.1
"	414757	U46922	Hs.77252	fragile histidine triad gene	HIT	5.1
	425098 -	AW295349	Hs.8038	ESTs	SS,TM	5.1
	431896	AW297844	Hs.101428	ESTs	SS	5.1
60	416732	H81066	Hs.285017	hypothetical protein FLJ21799	SS	5.1
OU	404571	AMEG77653	U- 75240	NM_015902*:Homo sapiens proges ribonucleolide reductase M2 po	HECT,zf-UBR1,PABP SS	5.1 5.1
	433675 426358	AW977653 AA376438	Hs.75319	gb:EST88856 HSC172 cells II Ho	TM	5.1
	456767	AI086412	Hs.129064	Homo sapiens chromosome 19, co	SS,TM,trypsin,kringle,UPA	5.1
	412915	AW087727	Hs.74823	NM_004541:Homo sapiens NADH de		5.1
65	443553	AL040535	Hs.9573	ATP-binding cassette, sub-fami	ABC_tran,SS	5.1
	415886	Z42737		gb:HSC0SE081 normalized infant	SS SAR MARKET	5.1
	401674 424266	AA337810	Hs.149152	C16001417":gi[7500345[pirl][T21 ESTs, Weakly similar to RHOP M	FAD-oxidase_C,FAD_binding	5.1 5.1
	455035	AW851734	113.143132	gb:MR2-CT0222-011199-007-e10 C		5.1
70	408567	S72921		ciliary neurotrophic factor	CNTF	5.1
-	436616	AW799109	Hs.226755	ESTs	14-3-3	5.1
	409078	AW327515		ESTs		5.1
	447976	AW972653	Hs.293691	ESTs, Highly similar to CR2_HU		5.1
75	457720 400528	AA992835	Hs.186776	ESTs NM_020975*:Homo sapiens ret pr	cadherin,pkinase,SS	5.1 5.1
, ,	400526	BE048414	Hs.165215	hypothetical protein MGC5395	SS,EF1G_domain,GST_C,GST_	5.1
	452446	AA086123	Hs.297856	ESTs	mm,NTF2	5.1
	450807	A1739262		gb:wi17b08.x1 NCI_CGAP_Co16 Ho		5.1
00	432540	Al821517	Hs.105866	ESTs	SS,TM	5.1
80	449324	AI638706	Un 0044	ESTs, Weakly similar to A47582	ECE curbi An accordant	5.1
	426434 407652	M17755 W27953	Hs.2041 Hs.292911	thyroid peroxidase ESTs, Highly similar to \$60712	EGF,sushi,An_peroxidase,p Troponin	5.1 5.1
	443952	AI149106	, 15.202311	ESTs	SS_pkinase	5.1
	448869	AI792798	Hs.12496	ESTs, Wealty similar to ALU4_H	SS,TM	5.1
				·	229	

	422837	U25441	Hs.121478	doparnine receptor D3	7tm_1,SS,TM,7tm_1	5.1
	407143	C14076	Hs.332329	EST	SS,TM	5.1
	442296	NM_007275		lung cancer candidate	SS,TM,Glyco_hydro_56,Glyc	5.1
5	407722	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin	pfkB,SS	5.1
)	427336	NM_005658		TNF receptor-associated factor	MATH,SS,MATH,A2M_N,A2M,NT	5.1 5.1
	447960 400863	AW954377	HS.20412	ring finger protein 26 C11002296:gi 11692557 gb AAG39	SS,TM,Cbl_N,Cbl_N2,Cbl_N3 SS,TM	5.1 5.1
	409034	Al684149	Hs.172035	hypothetical protein similar (	SS	5.1
	421696	AF035306	Hs.106890	Homo sapiens clone 23771 mRNA	<b>55</b>	5.1
10	427587	BE348244	Hs.284239 ·		SS,UDPGT	5.1
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_H	SS histone histone	5.1
	454219	X75042	Hs.44313	v-rel avian reticutoendothelio	RHD,TIG	5.1
	430513	AJ012008	Hs.241586	G6C protein	SS,TM,GST_C,abhydrolase	5.1
1.5	435902	AA701867	Hs.297726	ESTs		5.1
15	442743	AI801351	Hs.302110	ESTs, Weakly similar to MUC2_H	SS,fibrinogen_C,Rhodanese	5.1
	454923	AW897236		gb:CM0-NN0057-150400-335-c06 N	SS,Caldesmon	5.1
	440518	AA888046	Hs.233235 Hs.309386	ESTs ESTs	SS,TM TM,Ribosomal_S7	5.1 5.1
	448237 428924	AI471790 AI016405	Hs.98959	ESTs, Weakly similar to JC5314	SS,TMJectin_c	5.1
20	412081	Z24895	Hs.293818	gb:HSB67F122 STRATAGENE Human	SS,TM,SQS_PSY,GATA	5.1
	437141	BE304917	Hs.31097	hypothetical protein FLJ21478	SS,TM,Glycos_transf_4	5.1
	421658	X84048	Hs.301760	frequenin (Drosophila) homolog	efhand	5.1
	423467	AK000214	Hs.129014	hypothetical protein FLJ20207	SS,TM,GDPD,SS,TM,SH3,PDZ,	5.0
0.5	417151	AA194055	Hs.293858	ESTs	PH	5.0
25	408307	AJ761786	Hs.204674	ESTs	Armadillo_seg	5.0
	404752			NM_024778:Homo sapiens hypothe		5.0
	453126	AA032155	Hs.61622	ESTs		5.0
	413983	BE348384	Hs.279194	ESTs		5.0
30	405366	*********		NM_003371*:Homo sapiens vav 2	SS	5.0 5.0
20	412425 437036	AW949156 AI571514	Hs.133022	gb:QV4-FT0005-110500-205-b06 F	SS TM Change Imper 2	5.0 5.0
	437030 448455	AI252625	Hs.269860	ESTs ESTs, Moderately similar to S6	SS,TM,Glycos_transf_2 SS,TM	5.0
	411413	BE379438	Hs.211573	heparan sulfate proteoglycan 2	ig,laminin_B,laminin_EGF,	5.0
	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis	CARD,SS,HSF_DNA-bind,E2F_	5.0
35	424874	AA347951		Homo sapiens cDNA FLJ20812 fis	SS	5.0
	408023	BE018269	Hs.279688	ESTs		5.0
	411758	AW860667		gb:QV0-CT0383-210400-204-d03 C	homeobox,homeobox	5.0
	410660	AI06111B	Hs.65328	Fanconi anemia, complementatio		5.0
40	427411	AA402242		ESTs		5.0
40	437018	AA889078		ESTs	SS,TM,ERG4_ERG24	5.0
	427029	AA397596	Un 42510	ESTs	SS,ras SS	5.0 5.0
	452047 432093	N35953 H28383	Hs.43510	ESTs, Weakly similar to BOX B gb:yl52c03.r1 Soares breast 3N	Band_41,ERM	5.0 5.0
	453099	H62087	Hs.31659	thyroid hormone receptor-assoc	SS .	5.0
45	441456	AI458911	Hs.127765	ESTs		5.0
	414356	AW505085	Hs.335147	gb:UI-HF-BN0-als-a-10-0-UI.r1	SS,TM	5.0
	434067	H18913	Hs.124023	Homo sapiens cDNA FLJ14218 fis		5.0
	436393	AW022213		ESTs	Galactosyl_T_2	5.0
	409227	AA806165	Hs.130323	Homo sapiens, clone IMAGE:3960		5.0
50	448680	AW245890	Hs.21753	JM5 protein	WD40,SS,TM,KOW,HLH	5.0
	439343	AF086161	Hs.114611	hypothetical protein FLJ11808		5.0
	428079	AA421020	Hs.208919	ESTs	SS.TM,trypsin	5.0
	421951	BE327432	Hs.109804	H1 histone family, member X	00.00	5.0
55	427204 409690	AA405404 W45393	Hs.215725 Hs.55888	ESTs activating transcription facto	SS,SS	5.0 5.0
55	436574	AW293527	Hs.126465	ESTs		5.0
	457761	AW401809	Hs.4779	KIAA1150 protein	SS,LIM,SS	5.0
	435294	T84084	Hs.196008	Homo sapiens cDNA FLJ11723 fis	HMG_box	5.0
	445372	N36417	Hs.144928	ESTs	SS,PID,PDZ	5.0
60	440511	AF132959	Hs.7236	eNOS interacting protein	SS,TM,MAGE,Ribosomal_S17,	5.0
	424437	BE244700	Hs.147049	cut (Drosophila)-like 1 (CCAAT	CUT,homeobox,beta-lactama	5.0
	401539			NM_002675:Homo sapiens promyel	zf-B_box,zf-C3HC4,SS	5.0
	417903	NM_002342		lymphotoxin beta receptor (TNF	TNFR_c6,SS	5.0
65	442451	Al498080	Hs.129616	ESTs	SS	5.0
65	450536	AI699529	11- 400544	gb:tt17a02.x1 NCI_CGAP_GC6 Hom	SS,G-alpha,arf	5.0
	425169	AW292500	Hs.128514	ESTs	SS	5.0
	435262	AA677088	Do 12004	ESTs	GTP_EFTU.GTP_EFTU_D3.GTP_	5.0 5.0
	444855 433507	BE409261 AI817336	Hs.12084 Hs.191791	Tu translation elongation fact ESTs	pkinase	5.0
70	432396	AW295956	Hs.11900	hypothetical protein FLJ14972	SS S	5.0
. •	438395	AA017514	Hs.6211	methyl-CpG binding domain prot	MBD,zf-CXXC,SS,zf-CXXC	5.0
	446603	NM_014835		oxysterol-binding protein-rela	Oxysterol_BP,SS	5.0
	400762			Target Exon		5.0
76	440133	AI056255	Hs.133349	ESTs		5.0
75	445903	AJ347487	Hs.132781	class I cytokine receptor	SS,TM,EF1BD	5.0
	412940	BE295701	Hs.819	homeo box B7	homeobox,SS,homeobox,home	5.0
	419269	AA235838		gb:zs41b04.s1 Soares_NhHMPu_S1	TM	5.0
	~.~ = 000					

TABLE 208:
Pkey: Unique Eos probeset identifier number
CAT number: Gene duster number
Accession: Genbank accession numbers

	~		
	Pkey	CAT Number	Accession
	408117	104000_1	AL138255 BE380045 AA047314 D82381 T18585 H64978 T10798
	408215	10478_1	BE614290 AA307674 N35629 AA338538 A193603 AA781096 A1680061 A1613258 AWZ76647 BE221263 A1348910 A1985031 A1090078 A1359617
_			AA666391 AI160210 AI446461 AI355345 AI343638 AI343640 AI275091 M78746 AW262795 AW250002 AA503756 AI934519 AW272086 N26520
5			AA626639
	408270	1049980_1	AW177805 AW177895 AW177816 AW177901 BE141597 BE141584 AW177822 AW177818 AW177899
	408294	1050553_1	BE141732 U75823 BE141331 AW178416 AW178430 BE141343 BE141298 BE141702 BE141285
	408567	10663_1	S72921 NM_000614 X55889 X60542 X60477
	409078	1098756_1	
10	409164	110421_1	AA708639 AA084707 AL038920 Al651598
10	409679	114787_1	BE250521 AA076837 BE249870 AA984291 AW502442 AW501551 AI221491 AA194239 D63046 AA193426 AA773243 AA193293
	409832	115564_1	AW953293 AI866310 AA077791 AA362540
	410445	120374_2	AA199830 AJ143895 AW961629 AA322482
15	410471	1204721_1	T88872 AW749857 AW809679 AW809678 AW810113 AW810182 AW809900 AW809851 AW810110 AW810228 AW810342 AW810181 AW809632 AW809745
13	410895	1220031_1	
			AW810372 AW809681 AW809792 AW809806 AW810452 AW809675 AW809964 AW810033 AW810111 AW809846 AW809847 AW809717
	411219		AW832917 AW832913 AW832906 AW832788 AW832915 AW832776
	411298	1237955_1	
20			AW835848 AW835851 AW835852 AW835862 AW835855 AW835825 AW835847 AW835838
20	411426	1245515_1	
	411456	1246706_1	AW847588 AW847716 AW847664 AW847592
	411490	1247426_1	R39474 AW848420 R76943
	411605		AW006831 AA678298 R12579 W86152 Al123683 AA699780 Al672155 BE092587 AA094230 Al633815 AA526153 W86151
	411758	1256751_1	AW860667 AW860665
25	412091	1276564_1	R06185 AW891805 AW901892 AW901895
	412122	127838_2	AW852707 N57282 AA725075 AI703492 AW612137 Al696372 Al879394 Al653605 W26914
	412128	1278726_1	AW894709 N78140
	412173		T71071 AW902279 AW897608
	412425	1293726_1	AW949156 AW949003 AW949008
30	412452	129707_1	AA215731 N48523 AA307559 AA130794 BE296746 BE378396 AA190411 AI904194 AA311805 AI356291 AA446714 AI818924 AI609152
50	712702	120.0	AW771476 BE298184 AA295023 AA13070B A10783B1 AA114156 A1198283 AA215665 AI201085 AI594848 AI077572 AA102778 AW016425
			A1923123 AA577072 A1671
	417777	122572 1	A335773 A1288496 AA120880
	412777	132672_1	
35	412934		BE011437 BE011402 BE011395 BE011428 BE011407 BE011421 BE011401 BE011406
22	413272	135718_1	AA127923 AA127846 AA534131 N53566 AA533669 AW511251 AI174441 AA127875 AI685293 AA127913 N72525 AW770386 N69010 AW070312
			H80275 H80289 AA972923
	413534	1375357_1	BE146961 BE146780 BE146788 BE146967 BE146774 BE146963 BE146907
	413564		BE260120 BE148538
40	414347	1437406_1	
40	414371	14388_8	AI905865 BE294801 BE562308 BE297957 AW157051 AI815883 AW162529 BE439610 AW157225 AW157210 AW162675 AW161998 AI816168
			AW162599 AI816004 AI815820 AW162158 AW162339 M17733 AW157639 AI879416 BE258811 AW157436 AW162433 AW161633 AW162155
			AW157410 AW157269 AW162
	414391	1441921_1	BE409872 BE281460
	414413	1443696_1	BE294877 BE294759
45	414593	1464909_1	BE386764 BE387560
	414944	1509480_1	C15044 D80943 C15696
	415126	1523506_1	D60945 D61346 D81568 D80539
	415611	1540555_1	T26376 F12852 T75058
	415886	1560411_1	Z42737 T08986 H07956
50	415958		H10942 Z42911 R60453
	416233	158010_1	AA176633 AW961842 AA309418
	416597		H66891 R98149 H68467
	417739		Z43995 R12357 R34740
	418184	172744_1	AA367375 AA486701 BE152479 BE152800 AW816961 AA214097
55	418304	173658_2	AA215702 AA368006 AA215703 BE066555 BE006876
55	419269	183444_1	AA235838 BE180775
	419516	185533_1	H82550 N43802 AA243820 AL040762 N24315 U66692
	420530	19446_1	AI218431 AA432232 AW183040 X86012 AA868831 AI191788 AA912999 AI204297 AI205744 AI218259 AA428596 AA993742 AA703660 AI018669
	420000	13410_1	A8579431
60	424070	200040 4	
00	421879 423790	208649_1 232031_1	AW959607 AA299654 AA579966 BE152393 AA330984 BE073904
	424874	244523_1	AA347951 A1688463 AA883123 APROTEIN HOOGEN HOOGEN HOOGEN HOUSE A 1002045 TREED AND 100404 A1002034 A10
	426221	26281_1	AB007881 U32581 AW131202 AW995994 W31964 N24261 Al033045 H98694 AW364848 Al222031 AA907216 Al215730 AA776981 AW473826
65	400050	-05504 4	W31373
UJ	426358	265504_1	AA376438 AA376324 AW963848 AW834782
	426576	269378_1	AA381720 AA382040 AW963564
	427029	274544_1	AA397596 A1198827 AA435832
	427326	277229_1	AJ287878 AJ804160 AA400787
70	427411	278474_1	AA402242 AA813659 AI150316 AA412054
70	428092	286920_1	AW879141 AA421182 AI734104 AI733923 AA430600
	428304	289603_1	A1743177 AA425743 AI804283 AI743189
	428948	29737_1	BE514352 AI879343 BE272870 BE616390 AW163444 AW161588 AW378754 AW238803 BE267205 BE047746 BE207213 BE312782 BE266301
			BE266413 BE278348 BE280885 BE278833 BE281417 BE407786 BE378176 BE392818 AW377597 BE395951 BE393978 AW327483 BE394175
~~			BE385795 BE275663 BE3
75	429398	303954_1	AA452239 Al262173 Al925886 Al469041 H96628 Al768463 Al671422 Al915624 AA766891 AA521087 AA814103 AW993151 AW005927
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	431424	333110_1	AI222969 AA806560 AA504839 AA805261
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	432093	341283_1	H28383 AW972670 H28359 AA525808
	432945	356589_1	AL043683 AA570698 AA907496 AL043682 AW362288
	433168	360235_1	A1085436 AA579438 AA579002
	433357	35402_1	T05639 AF024702
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	404140	3320_1	AW505595 AF086096 N90340 N63271 AA131836 AW607273 AA527132 T32215 AA421961 T34951 AW966080 M76807 N31947 AA521151
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	435262	403605_1	AA677088 AI022246 AA677107
	435339	404485_1	AI358300 AI762981 AA678073 AA988621
10	436094	414444_1	AI798701 AW008826 AA704731
10	436389	41894_1	AIB11706 AW297940 AJ227887 AA875850 AA228803 AI610234 AI921618 AI768606 N37039 AA081104 BE172693 D56503 Z28585 T95651
			AA292389 AA293502 N28751
	436393	41903_1	AW022213 AJ274032 AJ227898 AJ160412 AJ084451
	437018	431333_1	AA889078 AA907263 AA742199
	437050		AA766420 AA743319 AW976442 .
15	437215	43473_1	AL117488 AL044479
10	437662	440374_1	AA765387 AA832241 Al222134 Al216405 Al685043
	437834	443674_1	AA769294 AW749299 AW749302 AW749295 AW749304 AW749293 AW749298 AW749294 AW749268 AW749291 AW749297 AW749292
	101001	410014_1	AW749296 AW749289 AW749287 BE535498
	420440	450293_1	
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20	438723	46392_1	M34429 M34431 M34432 M25802 AW938720
	439034	46802_1	AF075083 H52291 H52528
	439150	46919_1	AF086006 H64722 H65212 H66282
	439469	47274_1	W69836 AF086287 W69657
	440317	49187_1	BE561888 BE560615 BE562102
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	441358	515468_1	AW173212 AA983948 Al080705 AA931334
	441523	519049_1	AW514263 Al567908 Al299828 Al299043 N51706 AA936483
	441794	526289_1	AW197794 AW195867 AW197787 AA968466
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30	447904	741913_1	AW206303 AW207644 AI765705
			AL03649 AW016705 Al492482
	448330	758690_1	ALUSSARIS AWO16705 ARIS2462 AL471630 BE540637 BE265481 AW407710 BE513882 BE546739 AA053597 BE140503 BE218514 AW956702 Al656234 Al636283 Al567265
	448993	79225_1	A47 (030 B590837 BE203401 AVV407 (0 BE313002 BE340733 AAUS333) BE140740 BE210314 AVV33010 A 2004234 AUG422 AUG42 AUG422 AUG42 AUG42 AUG422 AUG422 AUG422 AUG42 AUG422 AUG42 AU
55			AW340858 BE207794 AA053085 R59173 AA292343 AA454908 AA293504 Al659741 Al927478 AA399460 Al760441 AA346416 BE047245
22			AA730380 AA394063 AA454
	449324	804806_1	Al638706 BE550292 R11026
	449495	808345_1	AI652833 AI695904 AW888916
	450251	829987_1	BE080483 BE080416 Al689298
	450536	837848_1	AI699529 BE161564 BE077251
60	450807	847591_1	A1739262 R28418
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	434103	120102_1	AA161386 AA205211 AA167824 AA084940 AA223625 AA191190 AA309486 AW961804
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	454577	1225673_1	AW809250 AW809199 AW809259 AW809239 AW809273 AW809270 AW809147 AW809188 AW809245
	454000	4000000 4	
	454682	1228976_1	AW816029 AW813292 AW816156 AW813333 AW816159 AW813302 AW813344 AW813172
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	455286	1273576_1	DC 144004 A44001414 A44001400 DC 144000
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80	455286		AW995839 AW995907 BE011183 BE011170 BE011333 BE011188 BE011181 BE011324 BE011161 BE011169
80	455286 455557	1325974_1	AW995839 AW995907 BE011183 BE011170 BE011333 BE011188 BE011181 BE011324 BE011161 BE011169
80	455286 455557 455604 455679	1325974_1 1337197_1 1349914_1	AW995839 AW995907 BE011183 BE011170 BE011333 BE011188 BE011181 BE011324 BE011161 BE011169 BE066529 BE066274 BE066390 BE066356 BE066419 BE066345 BE066298 BE066292 BE066359
80	455286 455557 455604	1325974_1 1337197_1 1349914_1 1364506_1	AW995839 AW995907 BE011183 BE011170 BE011333 BE011188 BE011181 BE011324 BE011161 BE011169

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AA744389 AA744270 AA744284 AA744299 AA745380 AA744337 AA846905 AA847698
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                        448900_1
           457978
                                     AJ286100 AA952934 AA918305
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           458198
                        670856_1
                                     AW270149 AW664628 AI285912
           458644
          TABLE 20C:
          Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L et al." refers to the publication entitled "The DNA sequence of
10
                 human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
           Strand: Indicates DNA strand from which exons were predicted
          Nt position: Indicates nucleofide positions of predicted exons
15
                                                   Nt_position
          Pkey
                                     Strand
           400460
                        8389428
                                     Plus
           400500
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                                     Minus
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                                                  472381-472528,474170-474277,475328-475542,475878-476000
121756-122043
84237-84398
           400528
                        6981824
                                     Plus
           400668
                        8118719
                                     Phis
20
           400748
                        8119063
                                     Plus
                                                   7235-7605
           400762
                        8131616
                                     Plus
           400772
                        8131629
                                                   34896-35021,41078-41197
                                     Minus
           400833
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                                     Minus
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112863-112989,120162-120286
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9966290
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                                     Minus
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                        8099284
                                     Minus
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                                     Plus
           401677
                        9965537
                                     Minus
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401822
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45
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                        3808091
                                                   46329-46473
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60
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           403748
                        7658423
                                                    129503-130344
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                        7711795
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                                      Minus
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                                      Minus
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404365
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50151-50319,50859-51098
                         9802821
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                                      Plus
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                                      Ptus
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           404676
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           404710
                         9801097
                                      Minus
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                         7109522
                                      Minus
                                                    120168-120326
            404807
                         4165210
                                                    124246-124422
                                      Minus
80
            404956
                         7387343
                                      Plus
                                                    55883-56203
44045-44230
                         8072509
            405085
                                      Minus
            405113
                         8096927
                                                    170073-170894
                                      Plus
                         9438278
            405143
                                                    5894-5983,7355-7427
                                      Plus
            405159
                                                    79659-79804
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	405211	6692345	Minus	31340-32609
	405247	7249301	Minus	65578-65778,68088-68234
•	405346	2981263	Plus	101982-102171
	405366	2182280	Plus	22478-22632
5	405371	2078469	Minus	47657-47766,48461-48596
	405375	1552539	Plus	11646-12050,12207-12485
	405376	1552533	Plus	28875-29099
	405473	8439781	Plus	153074-153343, 154501-154598, 156879-156999, 158863-159051, 159910-160053, 161109-161229, 163035-163131, 165163-
		0.00.01		165259,165868-166003,167375-167552,169252-169364,171127-171281
10	405474	8439781	Plus	172005-172175
	405557	1621108	Plus	39883-40047
	405637	6289229	Phis	189852-189978
	405770	2735037	Plus	61057-62075
	405928	7717155	Minus	2923-3209
15	405931	6758795	Minus	148233-148705
	405939	6758795	Plus	170500-170654
	406109	9127147	Minus	58328-58485
	406230	4760409	Plus	71716-72515
	406284	7549620	Plus	74002-74199
20	406299	5686278	Minus	35655-36119
	406301	8575868	Plus	57291-57494
	406373	9256130	Phus	188922-189152
	406495	7711328	Minus	174661-174978
	406575	7711679	Plus	142034-142473
25				

Table 21A lists about 933 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 20A, except that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 3.0, the "average" ovarian cancer level was set to the 95th percentile value amongst various ovarian cancer specimens, the "average" normal adult tissue level was set to the 75th percentile value amongst variou normalignant tissues, the "average" ovarian cancer value was greater than or equal to 400 units (this selects for the most abundant of the up-regulated genes), and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g., ig, fn3, efg, 7tm domains, signal sequences, transmembrane domains). The predicted order of domains are noted.

TABLE 21A:
Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UG ID: Unigene number
Title: UniGene gene title
Pred. Protein Dom.: Predicted protein domain

R1: Ratio of tumor to normal body tissue

40

Pred. Protein Dom. UGID Pkey ExAcon Title H96850 gb:yw03b12.s1 Soares melanocyt SS,TM,SS,TM,DDOST\_48kD 407223 Hs.103253 perilipin,SS 47.6 421296 NM\_002666 perilipin 45 milo\_carr,SS,TM SS,TM,IdI\_recept\_a,trypsi PH,SS,LIM,Troponin 430281 AJ878842 Hs.237924 CGI-69 protein 46.7 transmembrane protease, serine pleckstrin homology-like domai CA125 antigen; mucin 16 41 N 410418 D31382 Hs.63325 37.1 BE409442 431773 Hs.268557 428758 AA433988 Hs.98502 35.6 SS 438424 Al912498 Hs.25895 hypothetical protein FLJ14996 SS,TM 35.3 50 450461 BE408081 Hs.46736 hypothetical protein FLJ23476 SS 34.4 33.9 hypothetical protein FLJ22969 ESTs, Weakly similar to ALU5\_H cytochrome P450, subfamily IIS SS.TM.zf-DHHC AA770561 AW452434 437897 Hs.146170 SS,PAS,HLH 32.5 Hs 58006 452554 422310 AA316622 Hs.98370 SS,TM,pkinase,fn3,ig 30.5 452849 AF044924 Hs.30792 hook2 protein bZIP,SS,AhpC-TSA 29.6 55 407722 BE252241 Hs.38041 pyridoxal (pyridoxine, vitamin pfkB,SS 28.2 pim-2 oncogene bicarbonate transporter relate pkinase,SS,TM,OTU,K\_tetra 27.9 416819 **U77735** Hs.80205 HCO3\_cotransp,SS,TM AJ924533 27.7 430397 Hs.105607 27.5 U66839 Hs.180533 mitogen-activated protein kina 427725 454017 AW023617 Hs.347130 hypothetical protein FLJ22709 SS,TM,myosin\_head,RA,DAG\_ 60 445434 BE391690 Hs.9265 hypothetical protein FLJ20917 SS,PWWP,Exonuclease,lipoc 26.8 452399 BE513301 Hs.29344 hypothetical protein, clone 24 SS,perilipin 26.5 syntaxin binding protein 2 prostaglandin E synthase Homo sapiens, Similar to hypot 419451 Al907117 BE614743 Sec1.SS.TM 25.1 Hs.90535 Hs.146688 25.1 MAPEG.SS,TM, MAPEG SS,SS,arf,ras,fn3,ras efhand,SS,CAP\_GLY Hs.43621 407893 BE408359 65 X04106 24.4 24.3 412674 Hs.74451 calpain 4, small subunit (30K) SS,FKBP,SS,PDGF,C2,PI-PLC larminin\_EGF,larminin\_G,EGF 430023 AA158243 Hs.227729 FK506-binding protein 2 (13kD) 24.0 444672 413726 taminin, alpha 5 annexin A11 Z95636 Hs.11669 AJ278465 23.1 annexin,SS,annexin Hs.75510 438951 U51336 Hs.6453 inositol 1,3,4-triphosphate 5/ SS,oxidored\_nitro,SS 23.0 70 23.0 22.4 429099 BE439952 Hs.196177 phosphorylase kinase, gamma 2 pkinase, SS, SNF2\_N, helicas 422645 L40027 Hs.118890 glycogen synthase kinase 3 alp pkinase.SS.Ets serum amyloid A1 gb:zo71c07.s1 Stratagene pancr SS,SAA\_proteins,SS,SAA\_pr AA829286 22.2 427899 Hs.332053 21.3 AA146625 407117 ENSP00000202587°:Bicarbonale t HCO3\_cotransp,SS 20.8 402916 75 D17629 galactosamine (N-acetyl)-6-sul Sulfatase, SS, TM 20.7 425760 Hs.159479 similar to mouse neuronal prot ESTs, Weakly similar to A47582 DKFZP586G1722 protein 422098 H03117 Hs.111497 TM 20.6 SS,TM,TGFb\_propeptide,TGF 442232 AI357813 Hs.337460 20.1 SS,Tropomyosin WD40,SS 20.0 453157 AF077036 Hs.31989 dynein, axonemal, intermediate 20.0 AF091619 Hs.112667 422179 80 Hs.90443 Target CAT fer4,SS,TM,V\_ATPase\_sub\_a 19.5 419444 NM 002496 416893 Hs.62406 hypothetical protein FLJ22573 SS,mm,SS 19.2 AA455588 434030 AW162336 Hs.3709 low molecular mass ubiquinone-19.1 411813 NM 014931 Hs.72172 KIAA1115 protein SS,TM,Y\_phosphatase 18.9 ESTs, Highly similar to AF1984 18.8 422305 A1928242 Hs.293438

	419167	AI589535	Hs.94875	ESTs Woods similar to A35363	SS	18.6
	406663	U24683	HS.54013	ESTs, Weakly similar to A35363 immunoglobulin heavy constant	SS SS	18.5
	429712	AW245825	Hs.211914	ENSP00000233627*:NADH-ubiquino	oxidared_q6,SS,TM,rrm	18.5 -
	425848	BE242709	Hs.159637	valyl-tRNA synthetase 2	GST_C,GST_N,Tropomyosin,S	18.4
5	447151	AI022813	Hs.92679	Homo sapiens clone CDABP0014 m	SS,TM,LRR,aminotran_1_2	18.4
	413343	BE392026	Hs.334346	hypothetical protein MGC13045	SS,DnaJ	18.2
	450029	AW073380	Hs.267963	hypothetical protein FLJ 10535	SS.Pyridox_oxidase.zf-C2H	17.7
	427721	AI582843	Hs.180455	RAD23 (S. cerevisiae) homolog	ubiquitin,UBA,integrin_B,	17.6 17.2
10	443780 421612	NM_012068 AF161254	Hs.9754 Hs.106196	activating transcription facto 8D6 antigen	bZIP,NTP_transf_2,SS,TBC tdl_recept_a,SS,TM	17.1
10	444607	AW405635	Hs.293687	ESTs	SS.PI-PLC-X.PH.PI-PLC-Y,C	16.7
	406621	X57809	Hs.181125	immunoglobulin lambda locus	SS	16.6
	443496	AJ006973	Hs.9482	target of myb1 (chicken) homol	VHS,GAT,TM,Heme_oxygenase	16.6
	440104	AA132838 ·	Hs.239894	hypothetical protein MGC2803	SS,DS	16.3
15	427640	AF058293	Hs.180015	D-dopachrome tautomerase	MIF, Late_protein_L2, SS, GS	16.2
	445625	BE246743		hypothetical protein FLJ22635	SS,TM	16.1
	427461	AA531527	Hs.332040	hypothetical protein MGC13010	SS,TM,ACAT,LRR	15.9
	423366 409017	Z80345 T86957	Hs.127610	acyl-Coenzyme A dehydrogenase, hypothetical protein RP4-622L5	Acyl-CoA_dh,Acyl-CoA_dh_M SS,TM	15.7 15.6
20	428167	AA770021	Hs.272299 Hs.16332	ESTs	SS,ig,fn3	15.5
20	420029	BE258876	Hs.94446	polyamine-modulated factor 1	aldo_ket_red,SS,TM,gla	15.5
	400460	DELLOCATO	1100 1110	C11002253*:gi[129091 sp[P23267	SS,TM,SCAN,zf-C2H2,KRAB	15.4
	407767	W15398	Hs.38628	hypothetical protein	SS,Zf-CCCH	15.4
~ -	406918	M88357		gb:Homo sapiens DNA-binding pr	zf-C2H2,SS	15.4
25	435158	AW663317	Hs.65588	DAZ associated protein 1	rm,SS,rm	15.3
	407619	AL050341	Hs.37165	collagen, type IX, alpha 2	SS,Collagen,SS,Collagen	15.3
	421273 402365	AJ245416	Hs.103106	U6 snRNA-associated Sm-like pr Target Exon	Sm,SS,IRNA-synt_1,GST_C,G SS,SS,TM,ig	15.1 14.9
	450503	R35917	Hs.301338	hypothelical protein FLJ12587	SS SS, TM, NG	14.8
30	427502	AI811865	Hs.7133	Homo sapiens, clone IMAGE:3161	SS,TM,ABC_tran,Gtyco_tran	14.6
-	432872	A1908984	Hs.279623	selenoprotein X, 1	DUF25,SS,Ribosomal_L3,PDZ	14.5
	439233	AA831893	Hs.292767	hypothetical protein FLJ23109	zf-C3HC4,TM,Sulfate_trans	14.5
	416897	M78146	Hs.324700	hypothetical protein MGC2663	SS	14.3
25	447304	Z98883	Hs.18079	phosphalidylinositol glycan, c	SS,Peptidase_C2	14.2
35	431543	AW969619	Hs.259768	adenylate cyclase 1 (brain)	TM	14.0
	447544 417595	AA401573 AA424317	Hs.288284 Hs.6259	hypothetical protein FLJ22378 KIAA1698 protein	SS,TM SS,TM,Gtyco_hydro_31,Gtyc	14.0 13.8
	436127	W94824	Hs.11565	RIKEN cDNA 2010100O12 gene	Corona_7,SS,TM	13.8
	412623	R28898	Hs.74170	metallothionein 1E (functional	SS,TM,metalthio,DEAD,meta	13.7
40	448133	AA723157	Hs.73769	fotate receptor 1 (adult)	Folate_rec,SS	13.5
	453367	AW732847	Hs.70573	PKCI-1-related HIT protein	SS,TM .	13.5
	431462	AW583672	Hs.256311	granin-like neuroendocrine pep	SS	13.2
	408724	AI685842	Hs.294143	ESTs, Weakly similar to T22914	SS,pkinase,tubulin	13.2
45	423464 428539	NM_016240 AW410063	Hs.128856 Hs.184877	CSR1 protein solute carrier family 25 (mito	Collagen,SS mito_carr,SS,TM,profilin,	13.1 13.0
73	436014	AF281134	Hs.283741	exosome component Rrp46	RNase_PH,RNase_PH_C,SS,TG	12.9
	438857	Al627912	Hs.130783	Forssman synthetase	SS,RA,RasGEF,RasGEFN	12.8
	444410	BE387360	Hs.33719	ESTs, Moderately similar to S6	SS	12.8
	427527	AJ809057	Hs.153261	immunoglobulin heavy constant	SS,TM,ig	12.6
50	430168	AW968343		DKFZP434I1735 protein	SS,TM,efhand,efhand	12.5
	437543	H16443	Hs.7117	glutamate receptor, ionotropic	SS,TM,lig_chan,ANF_recept	12.4
	413711 422625	AW291765 AW504698	Hs.75486 Hs.155976	heat shock transcription facto cullin 4B	NA,SS,E2F_TDP SS,SS,Cullin,Cullin	12.3 12.2
	443136	NM_001440	Hs.9018	exostoses (multiple)-like 3	Exostosin, SS, TM	12.1
55	407143	C14076	Hs.332329	EST	SS,TM	12.1
	424707	BE061914	Hs.10844	Homo sapiens cDNA FLJ14476 fis	SS,SS,TM,Sema	12.1
	425251	Z22521	Hs.155342	protein kinase C, delta	pkinase,DAG_PE-bind,pkina	12.0
	427336	NM_005658	Hs.2134	TNF receptor-associated factor	MATH,SS,MATH,A2M_N,A2M,NT	12.0
60	421572	- AA531607	Hs.165827	hypothetical protein FLJ22678 ESTs	SS,TM,TGF-beta,ASC SS.PTN_MK.7tm_1.DAGKc.DAG	12.0 11.9
oo	447946 425954	AI566164 AK000633	Hs.164476	hypothetical protein FLJ20626	SCAN,zi-C2H2,KRAB,SS,KRAB	11.7
	427273	AW139032	Hs.107376	hypothetical protein DKFZp434N	SS,SS,TM	11.7
	427397	AJ929685	Hs.177656	calmodulin 1 (phosphorylase ki	efhand,RrnaAD,SS,efhand	11.7
	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	enolase, SS, Atrophin-1, Atr	11.7
65	417852	AJ250562	Hs.82749	transmembrane 4 superfamily me	transmembrane4,SS,TM	11.6
	447451	AL379925	Hs.207525	ESTs	SS.pkinase,PH.pkinase_C	11.5
	410397	AF217517	Hs.63042	DKFZp564J157 protein	SS,homeobox,UPF0160,DUF23	11.4
	430354	AA954810	Hs.239784 Hs.90207	human homolog of Drosophila Sc hypothetical protein MGC11138	SS,TM,ig SS,TM,PMP22_Claudin,PMP22	11.3 11.3
70	419390 422682	AJ701162 W05238	Hs.94316	ESTs, Weakly similar to T31613	SS,TM,DEAD,helicase_C,Lam	11.3
70	422178	AL122083	Hs.112645	Homo sapiens mRNA; cDNA DKFZp4	SS.TM	11.2
	450122	BE313765	Hs.343443	ESTs, Weakly similar to I38022	SS,TM,Y_phosphatase,LON,A	11.1
	453968	AA847843	Hs.62711	High mobility group (nonhiston	SS,HMG_box	11.1
75	444744	BE394732	Hs.147562	ESTs	SS	10.9
75	423220	BE394920	Hs.125262	aladin	WD40,TM,Activin_recp,pkin	10.9
	417116	Z43916	Hs.7634	hypothetical protein FLJ12287	SS,TM,filament,IF_tail	10.9
	406779 450593	AA412048 AF129085	Hs.279574 Hs.25197	CGI-39 protein; cell death-reg STIP1 homology and U-Box conta	SS,SS TPR,SS,TM,Rhomboid,lactam	10.8 10.7
	430333	R70292	Hs.156110	immunoglobulin kappa constant	SS S	10.7
80	452434	D30934	Hs.29549	C-type lectin-like receptor-1	lectin_c,SS,TM	10.7
	440150	AW975738	Hs.7001	Homo sapiens, clone IMAGE:3940	SS,TM,SS,TM,Peptidase_M22	10.6
	418641	BE243136	Hs.86947	a disintegrin and metalloprote	disintegrin, Reprotystn, Pe	10.6
	414313	NM_004371	Hs.75887	coatomer protein complex, subu	WD40,SS,WD40,Ribosomat_S2	10.6
	420307	AW502869	Hs.66219	ESTs	SS,TM	10.6
				. 225		

						40.0
	414918 -	Al219207	Hs.72222	hypothetical protein FLJ13459	SS,TM,efhand	10.6
	446562	BE272686	Hs.15356	hypothetical protein FLJ20254	hormone,SS,pfkB	10.5
	419846	NM_015977	Hs.285681	Williams-Beuren syndrome chrom	SS,HLH,SS,TM,WD40	10.4
~	453023	AW028733	Hs.31439	serine protease inhibitor, Kun	Kunitz_BPTI,SS,TM,ion_tra	10.4
5	438800	AB037108	Hs.6418	seven transmembrane domain orp	SS,TM	10.3
	431275	T56571	Hs.10041	ESTs	ss,hlh	10.3
	407241	M34516		gb:Human omega light chain pro	SS,ig,PH,ig,PH	10.3
	441238	Al372555	Hs.322456	hypothetical protein DKFZp761D	homeobox,SS,TM,Rho_GDI,th	10.3
	436325	AL390088	Hs.7393	hypothetical protein from EURO	SS,Synapsin_C,SS	10.3
10	435605	AF151815	Hs.4973	hypothetical protein	SS,TM,SS,TM,ABC_tran,ABC_	10.3
	444202	AL031685	Hs.12785	KIAA0939 protein	SS,TM,Na_H_Exchanger,ABC2	10.3
	425597	U28694	Hs.158324	chemokine (C-C motif) receptor	7tm_1	10.3
	415200	AL040328	Hs.78202	SWI/SNF related, matrix associ	SNF2 N.helicase C.bromodo	10.2
	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	Nol1_Nop2_Sun,SS,SNF2_N,h	10.2
15	414874	D26351	Hs.77515	inositol 1,4,5-triphosphate re	TM,RYDR_ITPR,ion_trans,MI	10.2
10	423524	AF055989	Hs.129738	potassium voltage-gated channe	ion_trans,K_tetra,thaumat	10.2
	434552	AA639618	Hs.325116	Homo sapiens, clone MGC:2962,	SS	10.2
	406836	AW514501	Hs.156110	immunoglobulin kappa constant	SS	10.1
	420233	AA256714	Hs.194864	hypothetical protein FLJ22578	SS	10.1
20		BE208364				10.1
20	427458		Hs.29283	ESTs, Weakly similar to LKHU p	SS,F5_F8_type_C,EGF,TGT SS,BTB,abhydrolase_2,RasG	10.1
	427672	AA356615	Hs.336916	death-associated protein 6		
	423218	NM_015896	Hs.167380	BLu protein	zf-MYND,SS,TM,Glyco_hydro	10.0
	403028	**** 04 1707	11. 74500	Target Exon	SS,trefoil	10.0
25	412790	NM_014767	Hs.74583	KIAA0275 gene product	kazal,thyroglobulin_1,zf-	10.0
25	419823	AW271708	Hs.118918	-ESTs, Weakly similar to M2OM_H	SS,TM	10.0
	433886	AA613596	Hs.28412	ESTs	SS	9.9
	428092	AW879141		ESTs	SS,TM	9.8
	450493	M93718	Hs.166373	nitric oxide synthase 3 (endot	flavodoxin,FAD_binding,NO	9.7
20	420423	AA827718	Hs.88218	ESTs	SS	9.7
30	452302	AF173867	Hs.28906	glucocorticoid modulatory elem	SAND,SS	9.7
	444681	AJ243937	Hs.288316	chromosome 6 open reading fram	notch,EGF,ank,GoLoco,SS,T	9.7
	414249	A1797994	Hs.279929	gp25L2 prolein	SS,TM,EMP24_GP25L,SS,TM,G	9.6
	424263	M77640	Hs.1757	L1 cell adhesion molecule (hyd	fn3,ig,lRK,SS,TM,fn3,ig,R	9.6
	438627	AI087335	Hs.123473	ESTs	TM,Reticulon	9.6
35 ·	407065	Y10141		gb:H.sapiens DAT1 gene, partia	SNF,SS,TM	9.6
	441307	AW071696	Hs.209065	hypothetical protein FLJ14225	SS,TM	9.6
	409649	AA159216	Hs.55505	hypothetical protein FLJ20442	Y_phosphatase,DSPc,TM	9.6
	424487	T08754	Hs.6259	KIAA1698 protein	SS,SS,TM,Glyco_hydro_31,G	9.5
	444633	AF111713	Hs.286218	junctional adhesion molecule 1	ig,SS,TM,HLH	9.4
40	427747	AW411425	Hs.180655	serine/threonine kinase 12	pkinase,SS,TM,synaptobrev	9.4
•••	450437	X13956	Hs.24998	hypothetical protein MGC10471	SS	9.4
	415169	W42913	Hs.78089	ATPase, vacuolar, 14 kD	ATP-synt_F,SS,TM,CH,Filam	9.4
	400201	***************************************	110.1 0000	NM_006156°:Homo sapiens neural	ubiquitin,SS,TM,Transglut	9.4
	454319	AW247736	Hs.101617	ESTs, Weakly similar to T32527	SS	9.4
45	421680	AL031186	Hs.289106	Human DNA sequence from clone	SS,SS,rm,zf-RanBP,rm,GA	9.4
	445143	U29171	Hs.75852	casein kinase 1, delta	pkinase,SS	9.4
	407507	U73799	113.10002	gb:Human dynactin mRNA, partia	SS,TM,HCO3_cotransp,CAP_G	9.4
	450883	NM_001348	Hs.25619	death-associated protein kinas	pkinase,GTP_EFTU,EFG_C,GT	9.4
	411674	AW861123	(13.25013	gb:RC3-CT0297-120200-014-a05 C	SS SS	9.3
50	414625	AA335738	Hs.76686	glutathione peroxidase 1	GSHPx,SS,ras,HLH	9.3
50	456950	AF111170	Hs.306165	Homo sapiens 14q32 Jagged2 gen	SS,TM,DSL	9.3
	445333	BE537641	Hs.44278	hypothetical protein FLJ 12538	SS	9.2
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_H	SS,histone,histone	9.1
	412338	AA151527	Hs.69485	hypothetical protein FLJ 12436	SS,TM,TIG,Sema,PSI	9.1
55	439963				PAF-AH_Ib,Lipase_GDSL,SS,	9.1
55		AW247529	Hs.6793	platelet-activating factor ace		9.1
	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN	SS,TM	
	443553	AL040535	Hs.9573	ATP-binding cassette, sub-fami	ABC_tran,SS	9.1
	448984	AW751955	Hs.22753	hypothetical protein FLJ22318	SS SO THE THE	9.0
60	418776	A1401004	Hs.88411	lymphocyte antigen 117	SS,TNF,TNF	9.0 9.0
00	418843	AJ251016	Hs.89230	potassium intermediate/small c	TM,CaMBD,SK_channel,TM	
	419244	AJ436567	Hs.89761	ATP synthase, H transporting,	ATP-synt_DE,SS,mm,Ephrin	8.9
	451855	R54913	Hs.175804	ESTs	SS,TM,wa	8.9
	424825	AF207069	Hs.153357	procollagen-lysine, 2-oxogluta	20G-Fell_Oxy,Glycos_trans	8.9
65	447374	AF263462	Hs.18376	KIAA1319 protein	SS,Myosin_tail,M	8.9
05	430167	Y08976	Hs.234759	FEV protein	Ets, SS, crystall	8.8
	409936	AK001691	Hs.57655	hypothetical protein FLJ 10829	SS,TM	8.7
	437926	BE383605	. Hs.300816	small GTP-binding protein	SS,TM,TPR	8.7
	430037	BE409649	Hs.227789	mitogen-activated protein kina	pkinase	8.7
70	424919	BE314461	Hs.153768	U3 snoRNP-associated 55-kDa pr	WD40,SS,KH-domain	. 8.7
70	414534	BE257293	Hs.76366	BCL2-antagonist of cell death	SS,harmone_rec,zf-C4	8.7
	433333	AJ016521	Hs.71816	v-akt murine thyrnoma viral onc	homeobox,pkinase,PH,pkina	8.7
	423228	AL137491	Hs.125511	Homo sapiens mRNA; cDNA DKFZp4	SS,TM,sushi	8.7
	419493	AF001212	Hs.90744	proteasome (prosome, macropain	PCI,SS,CDK5_activator	8.7
75	420160	AI492840		ESTs	SS,TM	8.6
75	421871	AK001416	Hs.306122	glycoprotein, synaptic 2	TM,Steroid_dh,SS	8.6
	447827	U73727	Hs.19718	protein tyrosine phosphatase,	Y_phosphatase,fn3,ig,MAM,	8.6
	417193	Al922189	Hs.288390	hypothetical protein FLJ22795	SS	8.6
	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-	SS,TM,zf-C2H2	8.5
	458963	AJ701393	Hs.278728	Rad and Gem-related 2 (rat hom	ras,SS,Peptidase_M10,hemo	8.5
80	406868	AA505445	Hs.300697	immunoglobulin heavy constant	SS,TM,ig	8.3
	434105	AW952124	Hs.13094	presentlins associated rhombol	TM,Rhombold,SS,TM	8.3
	421726	AK001237	Hs.319088	hypothetical protein FLJ10375	TM	8.3
	421707	NM_014921	Hs.107054	lectomedin-2	Latrophilin, OLF, 7tm_2, Gal	8.2
	453898	AW003512	Hs.232770	arachidonate lipoxygenase 3	SS,TM,lipoxygenase,PLAT,s	8.2
				006	• • • •	

	456672	AK002016	Hs.114727	Homo sapiens, clone MGC:16327,	SS,PK,PK_C,myosin_head,Rh	8.2
	430072 421592	AK002016 s AF009801	Hs.105941	baggipe homeobox (Drosophila)	homeobox,SS	8.2
	409829	M33552	Hs.56729	lyπphocyte-specific protein 1	Caidesmon,SS,Ribosomal_S2	8 <u>-</u> 4 ·
	444341		Hs.146650	ESTs	SS,TM,Reprolysin,Pep_M12B	8.0
5	413762	AI142027	Hs.848	FK506-binding protein 4 (59kD)	FKBP,TPR,SS	8.0
,	436685	AW411479 • W28661	Hs.5288	Homo sapiens mRNA; cDNA DKFZp4	SS,TM.pkinase,Activin_rec	8.0
	420932	AW374605	Hs.11607	ESTs, Weakly similar to T21697	SS,bZIP_Maf	8.0
	431493	AI791493	Hs.129873	ESTs, novel cytochrome P450	SS,p450,SS	7.9
	447598	AI791493 AI799968	Hs.199630	ESTs	SS,TM	7.9
10	415758	BE270465	Hs.78793	protein kinase C, zeta	pkinase,DAG_PE-bind,pkina	7.8
10	457022	AW377258	15.70750	gb:MR2-CT0222-261099-003-a10 C	SS,Ribosomal_L7Ae	7.8
			Hs.169902	solute carrier family 2 (facil	sugar_tr,SS,TM,sugar_tr	7.8
	426440 432747	BE382756	Hs.278907	calcium channel, voltage-depen	PMP22_Claudin,SS,TM,PMP22	7.8
		NM_014404 W24563	Hs.9911	hypothetical protein FLJ11773	SS.TM.hormone_rec,zf-C4	7.8
15	441084 424443	AI751281	Hs.284161	hypothetical protein from EURO	SS,TM,SS,TM	7.7
13		AB029010	Hs.143026	KIAA1087 protein	SS,TM,Na_Ca_Ex,Caix-beta,	7.6
	424198		Hs.241586	G6C protein	SS,TM,GST_C,abhydrolase	7.6
	430513	AJ012008	Hs.82906	CDC20 (cell division cycle 20,	WD40,SS,TM,fn3,EGF,fn3,lg	7.6
	417900 432891	BE250127 AF161483	Hs.279761	HSPC134 protein	SS,TM,ubiquitin,Transglut	7.5
20	432234		Hs.115803	ESTs	SS S	7.5
20		AA531128	Hs.33026	hypothetical protein PP2447	SS,TM	7.5
	453485	BE620712	Hs.7778	hypothetical protein FLJ10751	SS,TM,7tm_1	7.5
	441327 436540	AK001706 BE397032	Hs.14468	hypothetical protein MGC14226	SS,TM	7.5
	438340	AW845318	Hs.12271	f-box and leucine-rich repeat	SS,SS,TM,HSF_DNA-bind	7.5
25		AW674193	Hs.227152	-mannan-binding lectin serine p	SS,TM,SS,TM,Clathrin_lg_c	7.5
23	457274 437141	BE304917	Hs.31097	hypothetical protein FLJ21478	SS,TM,Glycos_transf_4	7.5
	425428	AL110261	Hs.157211	DKFZP586B0621 protein	· C1q,Collagen,SS	7.4
	431934	AB031481	Hs.272214	STG protein	SS	7.4
	418349	NM_001383	Hs.84183	dipheria toxin resistance pro	Diphthamide_syn,SS	7.4
30	430600	AW950967	Hs.274348	HLA-B associated transcript-3	ubiquitin,SS,TM,G-patch,a	7.3
50		BE397336	Hs.1422	Gardner-Rasheed feline sarcoma	SH2,SH3,pkinase	7.3
	421758 412841	AI751157	Hs.101395	hypothetical protein MGC11352	SS,TM	7.3
	418313	BE244231	Hs.84038 .	CGI-06 protein	SS,wap	7.3
		AB007867	Hs.278311	plexin B1	Sema,PSI,TIG,SS,TM,TIG,Se	7.3
35	429367	U48263	Hs.89040	prepronociceptin	Opiods_neuropep,SS	7.2
55	418837		Hs.123034	G protein-coupled receptor 12	TM	7.2
	423015 440188	U18548 AK001812	Hs.7036	N-Acetylglucosamine kinase	ROK,SS,TM	7.2
	421975	AW961017	Hs.6459	hypothetical protein FLJ11856	SS,TM,ACAT	7.2
	423858	AL137326	Hs.133483	Homo sapiens mRNA; cDNA DKFZp4	SS,TM	7.2
40	446143	BE245342	Hs.306079	sec61 homolog	secY,SS,TM	7.2
70	417704	NM_001747	Hs.82422	capping protein (actin filamen	Gelsotin, SS, Gelsotin	7.2
	440869	NM_014297	Hs.7486	protein expressed in thyroid	lactamase_B,SS,XRCC1_N,BR	7.1
	435099	AC004770	Hs.4756	flap structure-specific endonu	XPG_N,XPG_L,5_3_exonuclea	7.1
	438856	N40027	Hs.7473	ESTs	SS,TM,connexin	7.1
45	426268	AF083420	Hs.168913	serine/threonine kinase 24 (St	pkinase,pkinase	7.1
73	418373	AW750770	Hs.84344	CGI-135 protein	SS,TM,PMP22_Claudin,2OG-F	7.1
	445087	AW893449	Hs.12303	suppressor of Ty (S.cerevisiae	S1,SH2,Ribosomal_L23,pkin	7.1
	421748	NM_014718	Hs.107809	KIAA0726 gene product	cadherin,TM,TPR	7.1
	413837	AW163525	113.101003	tifin-cap (telethonin)	SS,Methyltransf_3	7.0
50	426691	NM_006201	Hs.171834	PCTAIRE protein kinase 1	pkinase,SS,UCH-2,UCH-1,rr	7.0
50	409125	R17268	Hs.343567	axonal transport of synaptic v	SS,kinesin,PH,FHA,kinesin	7.0
	424251	AA677466	Hs.143696	coactivator-associated arginin	SS,SNF2_N,helicase_C,brom	7.0
	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD4	integrin_A,FG-GAP,Rhabd_g	7.0
	428156	8E269388	Hs.182698	mitochondrial ribosomal protei	SS SS	7.0
55	459255	Al493244	Hs.239500	hypothetical protein MGC13114	SS	7.0
55	441323	AA928413	Hs.159089	ESTs, Weakly similar to ALU7_H	SS,Peptidase_C1,zf-C2H2	6.9
	455928	BE170313	113.1133003	gb:QV4-HT0536-040500-193-g02 H	SS	6.9
	420856	BE513294	Hs.205736	HLA class II region expressed	kazal,SS,TM,ig,pkinase	6.9
	421543	AK000519	Hs.105606	hypothetical protein FLJ20512	TM	6.9
60	442296	NM_007275	Hs.8186	tung cancer candidate	SS,TM,Glyco_hydro_56,Glyc	6.9
.00	445937	Al452943	Hs.321231	UDP-Gal:betaGlcNAc beta 1,4- g	Galactosyl_T_2,SS,TM,tsp_	6.9
	439732	AW629604	Hs.167641	hypothetical protein from EURO	SS,TM,SS,TM,A2M,A2M_N,NTR	6.8
	429542	AF038660	Hs.206713	UDP-Gal:betaGlcNAc beta 1,4- g	Galactosyl_T_2,ig,SS,TM,A	6.8
	420190	A1816209	Hs.95867	hypothetical protein EST00098	SS,dynamin_2,dynamin,PH,G	6.8
65	408215	BE614290	113.35001	syntaxin 10	SS,SS,TM,HLH,TRM,zf-CCCH	6.7
05	410277	R88621	Hs.26249	ESTs, Weakly similar to T2D3_H	SS.TM.SS	6.7
	419667	AU077005	Hs.92208	a disintegrin and metalloprote	disintegrin, Reprolysin, Pe	6.7
	448677	AI560769	INCLES	ESTs	SS,TM	6.7
	425228	NM_005253	Hs.301612	FOS-like antigen 2	bZIP,SS	6.6
70	432538	BE258332	Hs.278362	male-enhanced antigen	SS,TM,AAA,Ribosomal_L2	6.6
70	421864	BE387198	Hs.108973	dolichyl-phosphate mannosyltra	SS,TM,SS,TM	6.6
	421004	M69113	Hs.226795	glutathione S-transferase pi	GST_C,GST_N,SS,efhand	6.6
	429302 406867	AA157857	Hs.182265	keratin 19	filament,bZIP,SS,filament	6.6
	426068	AF029778	Hs.166154	jagged 2	OSLEGF,vwc,granulin,SS,T	6.5
75	419344	U94905	Hs.277445	diacylglycerol kinase, zeta (1	ank,DAGKa,DAGKc,DAG_PE-bi	6.5
, 5	424681	AA054400	Hs.151706	KIAA0134 gene product	helicase_C.PRK,SS,TM,7tm_	6.5
	417903	NM_002342	Hs.1116	lymphotoxin beta receptor (TNF	TNFR_c6,SS	6.5
	423876	BE502835	Hs.15463	Homo sapiens, done IMAGE:2959	SS efhand	6.4
	433439	AA431176	Hs.133230	ribrito sapieris, cione nuncicizzada ribosomal protein S15	TM,SS,TM,TPR,ras	6.4
80	441379	AW175787	Hs.334841	selenium binding protein 1	SS,RFX_DNA_binding	6.4
30	432968	BE614192	Hs.279869	melanoma-associaled antigen re	SS,TM,RGS,DIX	6.4
	456863	T16837	Hs.4241	ESTs	fusion_gly,homeobox,TM	6.4
	432269	NM_002447	Hs.2942	macrophage stimulating 1 recep	pkinase,Sema,PSI,TIG,A4_E	6.4
	432269 425676	AW410656	Hs.2942 Hs.159161	Rho GDP dissociation inhibitor	Rho_GDI,homeobox,SS,Cytid	6.4
	450010		160.100101	NIC GOP dissociation minimize		-

	442420	DOCUTE.	Hs.191208	ECT.	22	6.4
	443420 436322	R06846 AL355092	Hs.120243	ESTs parvin, gamma	SS CH.SS,TM,CTF_NFI	6.4
	440088	BE559877	Hs.183232	hypothetical protein FLJ22638	SS_zf-C3HC4,SPRY_zf-B_box	6.4
	447665	BE044245	Hs.30011	hypothetical protein MGC2963	SS.TM	6.3
5	431785	AA292385	Hs.268763	Breakpoint cluster region prot	BAF,kazal,TM	6.3
,	422714	AB018335	Hs.119387	KIAA0792 gene product	DUF221,SS,TM,TGFb_propept	6.3
	434916	AF161383	Hs.284207	Homo saplens, Similar to RIKEN	TM	6.3
	414551	AI815639	Hs.76394	encyl Coenzyme A hydratase, sh	ECH,Peptidase_U7,SS,TM	6.3
	413254	U40272	Hs.75253	isocitrate dehydrogenase 3 (NA	isodh,SS	6.3
10	458367	AA088470	Hs.83135	Homo sapiens, Similar to RIKEN	SS,tRNA-synt_2d	6.3
10	415010	NM_004203	Hs.77783	membrane-associated tyrosine-	pkinase,SS,PMP22_Claudin	6.3
	410076	T05387	Hs.7991	ESTs	SS	6.3
	412940	BE295701	Hs.819	homeo box 87	homeobox,SS,homeobox,home	6.2
	440042	AI073387	Hs.133898	ESTs	SS	6.2
15	414023	BE243628		gb:TCBAP1D1053 Pediatric pre-B	SS	6.2
	414513	AW239400	Hs.76297	G protein-coupled receptor kin	pkinase,RGS,pkinase_C,SS,	6.2
	446662	NM_013323	Hs.15827	sorting nextn 11	PXSS	6.2
	409882	AJ243191	Hs.56874	heat shock 27kO protein family	HSP20,SS,TM,zf-C2H2,BTB,E	6.2
	414576	AK000405	Hs.76480	ubiquitin-like 4	ubiquitin,SS,TM,G6PD,G6PD	6.2
20	447507	H59696	Hs.18747	POP7 (processing of precursor,	SS,TM,WD40,vwd,MAM,EPO_TP	6.2
	453447	AW771318	Hs.326586	hypothetical protein MGC11134	SS,TPR	6.1
	435968	AW161481	Hs.111577	integral membrane protein 3	TM	6.1
	424441	X14850	Hs.147097	H2A histone family, member X	histone,CBFD_NFYB_HMF,SS,	6.1
25	434558	AW264102	Hs.39168	`ESTs	SS,TM,LRRCT,LRR	6.1
25	434202	BE382411	Hs.3764	.guanylate kinase 1	Guanylate_kin,CoaE,Viral_	6.1
	432183	AW151952	Hs.46679	hypothetical protein FLJ20739	SS	6.0
	444416	AW288085	Hs.11156	hypothetical protein	zf-C3HC4,SpoA,PHD,TM,syna	6.0
	447205	8E617015	Hs.11006	ESTs, Moderately similar to T1	SS,TM,LRRCT,Sema	6.0 6.0
20	407704	BE315072	Hs.78768	malignant cell expression-enha	TM,MBOAT,SS,TM PH,PHD,RUN,SS	6.0
30	453190	AB002354	Hs.32312	KIAA0356 gene product	Ham1p_like,SS	6.0
	439975	AW328081	Hs.6817	inosine triphosphatase (nucleo protein predicted by clone 236	SS,PX,arf,lipocalin,PHD,z	6.0
	449514 432805	AW970440 X94630	Hs.23642 Hs.3107	CD97 antigen	SS.TM.7tm_2.GPS.EGF.SS.TM	6.0
	414362	AI347934	Hs.75932	N-ethylmateimide-sensitive fac	NSF,SS,TM	6.0
35	417483	BE549343	Hs.82208	acyl-Coenzyme A dehydrogenase,	Acyl-CoA_dh,Acyl-CoA_dh_M	6.0
33	427988	AA789333	Hs.181349	hypothetical protein 628	SS,SS	6.0
	423473	H49104	Hs.129888	hypothetical protein FLJ14768	zf-C2H2,SS,rm,ENTH	6.0
	406773	AA812424	Hs.76067	heat shock 27kD protein 1	HSP20.SS	5.9
	409938	AW974648	11011 0001	gb:EST386752 MAGE resequences,	SS,Adap_comp_sub,GYF	5.9
40	424959	NM_005781	Hs.153937	activated p21cdc42Hs kinase	pkinase, SH3	5.9
	453082	H18835	Hs.31608	hypothetical protein FLJ20041	SS,TM,ion_trans	5.9
	452094	AF049105	Hs.27910	centrosomal protein 2	hZIP,5_3_exonuclease,M,SS	5.9
	451524	AK001466	Hs.26516	hypothetical protein FLJ 10604	SS,SS,TM,pkinase,pkinase_	5.9
	427438	AW328515	Hs.178011	hypothetical protein FLJ20257	SS,TM	5.9
45	439685	AW956781	Hs.293937	ESTs, Weakly similar to FXD2_H	SS,PWWP,TSC22	5.9
	440511	AF132959	Hs.7236	eNOS interacting protein	SS,TM,MAGE,Ribosomal_S17,	5.9
	417334	AA337572	Hs.157240	hypothetical protein MGC4737	SS,TM,ion_trans	5.9
	425976	C75094	Hs.334514	NG22 protein	SS,TM,pkinase,SH2,SH3,BNR	5.8
50	433173	Z35093	Hs.3196	surfeit 1	SURF1,SS,TM,SURF1,SURF4	5.8
50	437891	AW006969	Hs.6311	hypothetical protein FLJ20859	TM,SET	5.8
	410239	A1568350	Hs.61273	hypothetical protein MGC2650	SS,ART,TM	5.8 5.8
	458060	R95860	Hs.293629	hypothetical protein MGC3121	SS CS TM Mild homoshay	5.8
	409591	AA532963	Hs.9100	Homo sapiens cDNA FLJ13100 fis	SS,TM,LIM,homeobox	5.8
55	409686	AK000002	Hs.55879 Hs.25450	Homo sapiens mRNA; cDNA DKFZp4 solute carrier family 29 (nucl	SS,ABC_tran,SS,TM Nucleoside_tran,SS,TM,HSP	5.8
55	450778	U81375	Hs.1686	guanine nucleolide binding pro	G-alpha,arf,SS,G-alpha	5.8
	423612	NM_002067	Hs.119273	KIAA0296 gene product	zi-C2H2,GST_C,PHD,SS,TM,H	5.8
	422701 412958	NM_014699 BE391579	Hs.75087	Fas-activated serine/threonine	SS.nkinase	5.8
	436957	AA902488	Hs.122952	ESTs	SS,DAGKc,DAGKa,RA,DAG_PE-	5.8
.60	423158	H97991	Hs.193313	Target CAT	MoaA_NifB_PqqE,SS,TM	5.8
.00	414788	X78342	Hs.77313	cyclin-dependent kinase (CDC2-	pkinase	5.8
	420904	AL035964	Hs.100221	nuclear receptor subfamily 1,	hormone_rec,zf-C4,SS,DNA_	5.7
	410431	BE261320	Hs.158196	transcriptional adaptor 3 (ADA	pkinase	5.7
	420508	AJ270993	Hs.98428	homeo box B6	homeobox,SS,homeobox,home	5.7
65	435593	R88872	Hs.4964	DKFZP586J1624 protein	Herpes_HEPA.SS	5.7
	433064	D79991	Hs.30002	SH3-containing protein SH3GLB2	TM	5.7
	451920	AA224483	Hs.27239	DKFZP586K0524 protein	SS,TM,SS,TM	5.7
	453054	A1878908	Hs.31547	Target CAT	SS	5.7
	415117	AF120499	Hs.78016	polynucleotide kinase 3'-phosp	Viral_helicase1,SS,Amino_	5.7
70	413163	Y00815	Hs.75216	protein tyrosine phosphatase.	fn3.ig,Y_phosphatase,SS,T	5.7
	425246	AI085561	Hs.155321	serum response factor (c-fos s	SRF-TF,flavodoxin,SS,TM,p	5.7
	433271	BE621697	Hs.14317	nucleolar protein family A, me	SS,TM	5.7
	448484	BE613340	Hs.334725	Homo sapiens, Similar to RIKEN	TM,SS,TM,Kunitz_BPTI	5.7 5.7
75	449139	BE268315	Hs.23111	phenylalanine-tRNA synthetase-	neur,SS,zf-C2H2,DNase_II	5.7
75	449181	X96783	Hs.23179	synaptotagmin V	C2,SS,TM,Y_phosphatase,Tr	5.6
	414457	AW514320	Hs.76159	ATPase, H transporting, lysoso	ATP-synt_C,SS,TM,pkinase	5.6 5.6
	424964	AW161271	Hs.153961	ARP1 (actin-related protein 1,	actin,SS	5.6
	415193	AL048891	Hs.12185	hypothetical protein MGC14333 Homo sapiens cDNA FLJ14105 fis	SS,TM,aminotran_1_2,LRR SS,TM,SS,TM,TSPN,tsp_3,SE	5.6
80	407754	AA527348 NM_002151	Hs.288967	hepsin (transmembrane protease	typsin,SS,TM,ATP1G1_PLM_	5.6
30	413049	H50256	Hs.823	ribosomal protein S15a	SS	5.6
	454252 431787	AW972024	Hs.63236 Hs.343661	ret finger protein	SS,WD40,pkinase	5.6
	431607	AB033097	Hs.183669	KIAA1271 protein	SS,TM .	5.6
	406782	AA430373	110.100000	gb:zw20f11.s1 Soares ovary turn	SS	5.6
	700102		•	v		

	444364	AL137294	Hs.10964	hypothetical emisin EL 122351	SS,TM,pkinase	5.6
	427834	AA506101	Hs. 285813	hypothetical protein FLJ22351 hypothetical protein FLJ11807	SS,TM,	5.5
	443759	BE390832	Hs.134729	FXYD domain-containing ion tra	SS.TM.ATP1G1_PLM_MAT8.ATP	5-5 ·
_	416322	BE019494	Hs.79217	pyrroline-5-carboxylate reduct	PSCR,Octopine_DH_N,SS,thi	5.5
5	406673	M34996	Hs.198253	major histocompatibility compl	SS,TM,MHC_II_alpha,ig,SS,	5.5
	415351	U44755	Hs.78403	small nuclear RNA activating c	SS,TM.pkinase	5.5
	411030	BE387193	Hs.67896	7-60 protein	SS,Collagen,Collagen	5.5
	410653 433012	BE383768 NM_004045	Hs.65238 Hs.279910	95 kDa retinoblastoma protein ATX1 (antioxidant protein 1, y	zf-C3HC4,SS,SNF2_N,helica HMA,SS,TM	5.5 5.5
10	437741	BE561610	Hs.5809	putative transmembrane protein	SS,TM,SS,TM,RA,VPS9,SH2	5.5
10	421883	X55079	Hs.1437	glucosidase, alpha; acid (Pomp	trefoil, Glyco_hydro_31,SS	5.4
	427361	AW732480	Hs.7678	cellular retinote acid-binding	SS,TM,aminotran_1_2,LRR	5.4
	411574	BE242842	Hs.6780	protein tyrosine kinase 9-like	cofilin_ADF,SS,TM	5.4
1.0	457313	AF047002	Hs.241520	transcriptional coactivator	SS,rm,SS,Cytidylyltransf	5.4
15	428345	AJ242431	Hs.118282	PAP-1 binding protein	SS,TM	5.4
	434845	BE267057	Hs.325321	hypothetical protein R32184_1	SS,TM,CH,calponin,ARID	5.4
	427162 447402	AB011133 H54520	Hs.173864 Hs.18490	KIAA0561 protein hypothetical protein FLJ20452	SS,pkinase,PDZ,SS,SH2,Rho SS,TM	5.4 5.4
	433676	AW371389	Hs.250173	hypothetical protein FLJ13158	SS	5.4
20	424373	AJ133798	Hs.146219	copine VII	C2,SS	5.4
	423402	BE167615	Hs.141556	Homo sapiens cDNA FLJ12976 fis	SS	5.4
	409983	D50922	Hs.57729	Kelch-like ECH-associated prot	BTB,Kelch,SS,TM	5.4
	450184	W31096	Hs.237617	Homo sapiens, done IMAGE:3447	SS	5.3
25	431629	AU077025	Hs.265827	Interferon, alpha-inducible pr	pkinase,SH2,SH3	5.3
23	430413 440333	AW842182 Al378424	Hs.241392 Hs.288761	.şmali inducible cytokine A5 (R hypothetical protein FLJ21749	IL8,SS SS,TM,IP_trans,pkinase,pk	5.3 5.3
	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	SS,TM	5.3
	412276	BE262621	Hs.73798	macrophage migration inhibitor	MIF,SS,TM,MIF,sugar_tr	5.3
	416181	AA174126	Hs.332163	ESTs	SS,TM,GalP_UDP_transf,Gal	5.3
30	440609	Al287585	Hs.7301	G protein pathway suppressor 2	SS,Acyl-CoA_dh,Acyl-CoA_d	5.3
	435327	BE301871	Hs.4867	mannosyl (alpha-1,3-)-glycopro	SS,HLH,Myc_N_term,Myc-LZ,	5.2
	421139	AW953933	Hs.301372	KIAA1552 protein	SS,TM	5.2
	453449	W16752	Hs.32981	sema domain, immunoglobulin do	SS,Sema,ig,PSI,SS,TM,G-al	5.2
35	414411 440906	X54079 AW161556	Hs.76067	heat shock 27kD protein 1 hypothetical protein MGC2731	HSP20,SS SS,TM,Furin-like,pkinase,	5.2 5.2
55	421899	AJ011895	Hs.240170 Hs.109281	Nef-associated factor 1	Virus_HS,bZiP,G-gamma,Myo	5.2
	439473	AI215529	Hs.144787	ESTs	SS SS	5.2
	451585	AK001171	Hs.326422	hypothetical protein MGC4549	SS,Metallophos	5.2
40	407191	AA608751		gb:ae56h07.s1 Stratagene lung	SS,Peptidase_C1	5.2
40	427515	T79526	. Hs.179516	integral type I protein	EMP24_GP25L,SS	5.2
	405325	15100011		C14000786*:gi[7023514[dbj]BAA9	SS .	5.2
	434119	AF193844	Hs.3758	COP9 complex subunit 7a	SS THESE TH	5.1 5.1
	413052 445109	BE249841 AF039916	Hs.12330	gb:600942857F2 NIH_MGC_15 Homo ectonucleoside triphosphate di	TM,SS,TM SS,TM,GDA1_CD39,SS,TM,pho	5.1 5.1
45	409323	H2B855	Hs.53447	Homo sapiens mRNA; cDNA DKFZp7	TPR,SS,TM,pkinase,ig	5.1
	438707	L08239	1.0.00111	amino acid system N transporte	SS,TM,ACAT,MBOAT,SS,TM,TB	5.1
	442599	AF078037	Hs.324051	RelA-associated inhibitor	SH3,ank,SS,TM,HHH,ig	5.1
	420372	AW960049	Hs.293660	Homo sapiens, clone IMAGE:3535	SS	5.1
50	436576	A1458213	Hs.77542	ESTs	SS,TM,7tm_1,DnaJ	5.1
50	439012	BE383814	Hs.6455	RuvB (E coli homolog)-like 2	AAA,DnaB,UPF0079,SS,Cys_k	5.1
	418910 414849	Z25821 AW372721	Hs.89466 Hs.291623	Homo sapiens, Similar to dodec ESTs, Weakly similar to unname	ECH,SS,TM,aminotran_3,ABC TM,pkinase	5.1 5.1
	425743	BE396495	Hs.159428	BCL2-associated X protein	Bcl-2,SS, ferritin, Bcl-2,e	5.1
	418231	AA326895	Hs.83848	triosephosphate isomerase 1	TIM,SS,TM,zf-UBP,UCH-2,UB	5.0
55	419238	AW959538	Hs.321214	hypothetical protein DKFZp564D	SS,TM,WH2	5.0
	441917	A1989925	Hs.24891	ESTs, Highly similar to unknow	SS,TM,Ammonium_transp	5.0
	437617	AI026701	Hs.5716	KIAA0310 gene product	SS,zf-C3HC4,Peptidase_M16	5.0
	412867	AU076861	Hs.74637	testis enhanced gene transcrip	UPF0005,SS,TM	5.0 5.0
60	419579 425824	W49529 Al939563	Hs.296200 Hs.159589	hypothetical protein AF053356_ ESTs, Moderately similar to RE	MSP_domain,SS,TM,CUB,NTR, . SS,PHD	5.0
-0	439414	NM_001183	Hs.6551	ATPase, H transporting, lysoso	SS,SS,TM,GDI,Sema,TIG,PSI	5.0
	436042	AF284422	Hs.119178	cation-chloride cotransporter-	SS,TM,aa_permeases,SS,TM,	5.0
	410775	AB014460	Hs.66196	nth (E.coli endonuclease III)-	HhH-GPD,SS,TM,REJ,PLAT,PK	5.0
65	453350	AI917771	Hs.61790	hypothetical protein FLJ23338	SS,SS,TM,EMP70,PA28_alpha	4.9
65	400300	X03363	11. 470000	HER2 receptor tyrosine kinase	pkinase	4.9
	426811 421179	BE259228 U72664	Hs.172609 Hs.148495	nucleobindin 1 proteasome (prosome, macropain	efhand,SS,TM,GFO_IDH_MocA UIM,SS,TM,PMP22_Claudin,P	4.9 4.9
	421119	Al346255	Hs.216354	ring finger protein 5	SS.zf-C3HC4.Palm_thioest	4.9
	419250	AW770185	113.210004	U5 snRNP-specific protein, 116	SS,TM,7tm_1,BAH,zf-CXXC,D	4.9
70	426831	BE296216	Hs.172673	S-adenosylhomocysteine hydrola	AdoHcyase,SS	4.9
	442103	AA333367	Hs.8088	similar to S. cerevisiae Sec6p	SS	4.9
	414820	AA371931	Hs.77422	proteolipid protein 2 (colonic	SS	4.9
	426347	AA454912	Hs.169407	SAC2 (suppressor of actin muta	SS,RasGEF,RA,RasGEFN,horm	4.9
75	423880 429545	BE278111 AI824164	Hs.134200	DKFZP564C186 protein lymphocyte antigen 6 complex.	UPF0120,SS,TM SS,TM	4.9 4.9
, 5	443044	N28522	Hs.8935	quinolinate phosphoribosyltran	QRPTase, QRPTase_N, SS, TM	4.9
	417080	BE392846	Hs.1063	small nuclear ribonucleoprotei	SS,S10_plectin	4.8
	441455	AJ271671	Hs.7854	zinc/iron regulated transporte	Zip,SS,TM,Cytidylyltransf	4.8
00	410182	NM_0019B3	Hs.59544	excision repair cross-compleme	HHH,SS,SH3,ank	4.8
80	456062	AI866286	Hs.71962	ESTs, Weakly similar to B36298	SS 20 THURSD I	4.8
	439270	8E268278	Hs.28393	hypothetical protein MGC2592	SS,TM,HCO3_cotransp	4.8
	408985	BE267317 BE243985	Hs.332040	hypothetical protein MGC13010 major vault protein	SS,TM,ACAT,LRR Vauli,SS,TM,kinesin,zf-C2	4.8 4.8
	416976 436057	AJ004832	Hs.80580 Hs.5038	neuropathy target esterase	cNMP_binding,SS,TM,cNMP_b	4.8 4.8
	100001		. 10.0000			7.0

						4.0
	424501	Al470163	Hs.323342	actin related protein 2/3 comp	SS,HhH-GPD	4.8 4.8
	409214	AW405967	Hs.333388	Homo saplens, clone IMAGE:3957	SS,EF1BD,P5CR	
	432716	AI762954	Hs.205180	ESTs	SS,TM	4.8 4.8
5	414460	L00727	Hs.898	dystrophia myotonica-protein k	pkinase,SS,WD40	4.0
3	443329	BE262943	Hs.9234	hypothetical protein MGC1935	SS,TM,SS,TM,gpdh,gpdh_C	4.7
	426120	AA325243	Hs.166887	copine I ENSP00000247029*:SEBOX.	C2,SS,aminotran_5 SS,TM,hemopexin,Somatomed	4.7
	405356	AD0270E7	Hs.300591	CD9 partner 1	TM,ig,SS,TM	4.7
	437118	AB037857		dimethylarginine dimethylamino	SS,TM,GST_C,abhydrolase	4.7
10	430609	AA302921	Hs.247362			4.7
10	447131	NM_004585	Hs.17466	relinoic acid receptor respond	SS,TM,pkinase Band_7,Flotilin,TM	4.7
	428469	BE549205	Hs.184488	flotillin 2	SS S	4.7
	405189			Target Exon	SS,TM,SPRY,SPRY,ig	4.7
	404256	*1000000	11- 404047	NM_024018*:Homo sapiens butyro	SS,zf-B_box,SPRY,SS,NoI1_	4.7
15	457955	Al208986	Hs.121647	ESTs	SS,SH2,RhoGAP,SH3,GILT	4.7
13	413201	BE275378	Hs.13972	hypothetical protein MGC12972	zi-C2H2,SS	4.7
	431115	AB015427	Hs.250493	zinc finger protein 219	ribonuclease_T2,SS,ribonu	4.7
	442414	BE408758	Hs.8297	ribonuclease 6 precursor	SS	4.6
	418289	AW403103	Hs.83951	Hermansky-Pudlak syndrome	SS	4.6
20	436730	AA045767	Hs.5300	bladder cancer associated prol		4.6
20	444596	BE560662	Hs.11417	Rab acceptor 1 (prenylated)	SS,TM,lig_chan,ANF_recept zf-Tim10_DDP,SS	4.6 4.6
	433019	AI208513	Hs.279915	translocase of inner mitochond	fn3,Y_phosphatase,SS,TM	4.6
	431522	AI625859	Hs.258609	protein tyrosine phosphatase,		4.6
	400846	T70045	11- 400040	sortilin-related receptor, L(D	ldl_recept_a,fn3,ld1_rece SS	4.6 4.6
25	422154	T79045	Hs.168812	ESTs		
23	420321	D78761	Hs.96657	_fryothelical protein	SS,tsp_1,SS	4.6
	439921	AL110209	Hs.6770	LCAT-like lysophospholipase	SS,LACT,SS,TM,aa_permease	4.6
	427122	AW057736	Hs.323910	HER2 receptor tyrosine kinase	pkinase,Furin-like,Recep_ WD40,TPR.SS.TM	4.6 4.6
	426899	AL043221	Hs.172825	KIAA1037 protein		4.6 4.6
30	408116	AA251393	Hs.289052	Homo saplens, Similar to RIKEN	SS,TM SS,TM,SS,TM,TBC,rrm,FtsJ	4.6 4.6
30	412974	R18978	Hs.75105	emopamil-binding protein (ster	TM	4.6 4.6
	426510	AW861225	Hs.110613	BANP homolog, SMAR1 homolog		4.6
	414702	L22005	Hs.76932	cell division cycle 34	UQ_con,SS,trypsin,ig	4.6 4.6
	408135	AA317248	Hs.42957	methyltransferase-like 1	Methyltransf_4,SS,p450,Ge SS	4.6
35	445637	W58459	Hs.8949	hypothetical protein MGC4172	SS	4.6
22	452190	H26735 .	Hs.91668	Homo sapiens clone PP1498 unkn		4.6
	409680	W31092	Hs.55847	mitochondrial ribosomal protei	SS,TM,synaptobrevin Herpes_UL3,SS,TM,Sema,pki	4.6
	421140	AA298741	Hs.102135	signal sequence receptor, dell	SH2,SAM,SS,Folate_rec	4.6 4.6
	413407	Al356293	Hs.75339	Inositol polyphosphate phospha		4.5
40	402463	0.0303333	11-00475	NM_014624:Homo sapiens S100 ca	efhand,S_100,SS,efhand,S_ SS,PGAM	4.5 4.5
40	426402	BE387327	Hs.80475	polymerase (RNA) II (DNA direc		4.5 4.5
	406939	M34515	11- 02007	gb:Human omega light chain pro	SS,ig,PH SS,TFiIS	4.5
	417891	W79410	Hs.82887	protein phosphalase 1, regulat	SS SS	4.5 4.5
	426207	BE390657	Hs.30026	HSPC182 protein	= =	4.5 4.5
45	423664	NM_004714	Hs.130988	dual-specificity tyrosine-(Y)-	pkinase,SS,Fibrillarin,CK	4.5 4.5
43	432562	BE531048	Hs.278422	DKFZP586G1122 protein	zf-C2H2,SS,TM,FG-GAP,inte	4.5
	427391	W60675	D- 070774	hypothetical protein FLJ10350	SS,SS	4.5
	432893	NM_016154	Hs.279771	Homo sapiens clone PP1596 unkn	ras,arf,SS,2OG-Fell_Oxy,2 P53.SS	4.5
	424954	NM_000546	Hs.1846	tumor protein p53 (U-Fraumeni		4.5 4.5
50	413815	AL046341	Hs.75562	discoidin domain receptor fami	F5_F8_type_C,pkinase,SS,T SS,TM	4.5 4.5
50	448963	AA459796	Hs.331247	Homo sapiens, clone IMAGE:3610	mito_carr,SS	4.5 4.5
	416297	AA157634	Hs.79172	solute carrier family 25 (mito		4.5 4.5
	421962	D82061 AA488915	Hs.288354	FabG (beta-ketoacyl-[acyl-carr	SS,adh_short,SS,TM,zf-C3H SS	4.5
	426726		Hs.171955	trophinin associated protein (	SS,TM	4.5 4.5
55	414427	L19711	Hs.76111	dystroglycan 1 (dystrophin-ass		4.5 4.5
55	435891	AW249394	Hs.5002	copper chaperone for superoxid	sodcu,HMA,SS,TM,spectrin,	4.5 4.5
	453997	AW247615	Hs.37003	v-Ha-ras Harvey rat sarcoma vi	ras,SS	4.5
	449029	N28989	Hs.22891	solute carrier family 7 (callo	aa_permeases,SS,TM,bZIP	4.5
	432078	BE314877	Hs.24553	hypothetical protein FLJ12541 .	SS,TM SS.SS,WD40	4.5
60	409650 412833	T08490 AW960547	Hs.288969 Hs.298262	HSCARG protein ribosomal protein S19		4.5 4.4
OU		,		······································	SS,TM,ig,ITAM,Ribosomal_S SS,TM	4.4 4.4
	424133	AA335721	Hs.213628	ESTs	SS_Anti_proliferat	4.4
	414787	AL049332	Hs.77311	BTG family, member 3	SS SS	4.4
	433046	AA229553	Hs.279945	HSPC023 protein	SS,TM	4.4
65	417068	AA451910	Hs.85852	hypothetical protein MGC3169 farnesyl diphosphale synthase	polyprenyl_synt,SS,TM	4.4
05	414814	D14697	Hs.77393			
	418267	BE389537	Hs.83919	glucosidase I histone deacetylase 6	Glyco_hydro_63,SS,PH Hist_deacetyl,zf-U8P,SS,G	4.4 4.4
	439902	AF174499	Hs.6764	Homo sapiens, Similar to RIKEN	TM,SS	4.4
	448847	AI587180	Hs.110906	cysteine sulfinic acid decarbo	SS S	4.4
70	452160	BE378541	Li- 70004			4.4
70	416121	X92762	Hs.79021	tafazzin (cardiomyopathy, dila	Acyltransferase,SS,TM,GDI	4.4
	449717	AB040935	Hs.23954	cerebral cell adhesion molecul	SS,SS SS,aldo_ket_red	4.4
	425069	AA687465	Hs.298184	potassium voltage-gated channe	Band_7,SS,Band_7,SH3	4.4
	413380	AI904232	Hs.75323	prohibitin	SS,SS,TM,Sec1	4.4
75	452911	AA541537	Hs.112619	metallothlonein 1E (functional	Peptidase_M24,SS,TM,Pepti	4.4 4.4
13	436415	BE265254	Hs.343258	proliferation-associated 2G4,	SS,Nop	4.4
	429218	AA225065	Hs.198269	Target CAT	SS,NDK,LRRNT,LRRCT,LRR	4.4
	447987	BE621544	Hs.157160	hypothetical protein MGC2616	filament,bZIP,SS,filament	4.4
	407230	AA157857	Hs.182265	keratin 19	SS,PH,RhoGEF,SS,maseA	4.3 4.3
80	448886	AL137291	Hs.22451	hypothetical protein FLJ10357	zi-C2H2,SS,TM	4.3 4.3
00	421178	BE267994	Hs.102419	zinc finger protein	TM	4.3 4.3
	454031	R36772	Hs.71941	hypothetical protein MGC15577	SS,ig,fn3	4.3 4.3
	450126	BE018138	Hs.24447	sigma receptor (SR31747 bindin		
	446557	U68566	Hs.15318	HS1 binding protein	SS,TM,MIP,UBA	4.3
	413781	J05272	Hs.850	IMP (mosine monophosphate) de	IMPDH_C,IMPDH_N,CBS,NPD,S	4.3

				1714.4.500		
	433251	AB040955	Hs.322735	KIAA1522 protein	SS,SS,zf-C3HC4,SPRY	4.3
	420531	AI652069	Hs.98614	ribosome binding protein 1 (do	bzip,ss	4.3
	432179	X75208	Hs.2913	EphB3	EPH_lbd,fn3,pkinase,SAM	4.3
_	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA)	Neur_chan_LBD,Neur_chan_m	4.3
5	426626	Al124572	Hs.323879	inhibitor of kappa light polyp	zf-C2H2,SS	4.3
	432956	AL037895	Hs.279861	CGI-31 protein	thiored,SS,TM	4.3
	428970	BE276891	Hs.194691	retinoic acid induced 3	7tm_3,SS,TM	4.3
	428953	AA306610	Hs.348183	tumor necrosis factor receptor	TNFR_c6,SS	4.2
	401128	1000000	10.010100	C12000644:gi[5729785]ref[NP_00	SS	4.2
10	446899	NM_005397	Hs.16426	podocałyxin-like		4.2
10					SS,TM,SS,TM	
	407151	H25836	Hs.301527	ESTs, Moderately similar to un	SS,TNF	4.2
	426613	U96132	Hs.171280	hydroxyacyl-Coenzyme A dehydro	adh_short,SS	4.2
	408616	R51604	Hs.300842	KIAA1608 protein	SS,DENN,DENN	4.2
	446616	R65964	Hs.334873	ESTs, Weakly similar to ALU8_H	SS,Zn_carbOpept	4.2
15	414467	AW903820	Hs.85752	copine II	SS	4.2
	455857	T70192		gb:yc18d03.s1 Stratagene lung	SS,TM,isodh	4.2
	401751			RAN binding protein 3	SS, Orexin, SH2, STAT	4.2
	400563			Target Exon	SS,Pep_M12B_propep	4.2
	430237	A1272144	Hs.236522	DKFZP434P106 protein	abhydrolase,TM	4.2
20	406101	PULL E 177	113.200022	C11000273*:gi 12656107 gb AAK0	SS,TM,7tm_1	4.2
20	421661	DE201202	Hs.299148			4.2
		BE281303	NS.233140	hypothetical protein FLJ21801	SS,VHP	
	444590	AA457456		hypothetical protein FLJ20435	SS	4.2
	408187	AF034373	Hs.43509	ataxin 2 related protein	SS ·	4.2
25	437696	Z83844	Hs.5790	hypothetical protein dJ37E16.5	SS,Hydrolase,SS,Gal-bind_	4.2
25	400278			"ENSP00000243264:Dolichyl-dipho	SS,TM	4.2
	407394	AF005081		gb:Homo sapiens skin-specific	SS	4.2
	447407	BE387301	Hs.18528	Siggren's syndrome nuclear aut	SS,HLH,ras,GSHPx	4.2
	410237	AI750589	Hs.61258	argininosuccinate lyase	lyase_1,SS	4.1
	415410	AF037332	Hs.278569	sorting nexin 17	PX,fn3,pkinase,SAM,EPH_tb	4.1
30	457757	AA434109	Hs.12271	f-box and leucine-rich repeat	SS,F-box,SS,TM,HSF_DNA-bi	4.1
50	446388	AA292979	Hs.7788	NPD007 protein	SS,TM	4.1
	412825	AW167439	Hs.190651	Homo sapiens cDNA FLJ 13625 fis	SS	4.1
	439737	AI751438	Hs.41271	Homo sapiens mRNA full length	SS,C1q,Collagen	4.1
0.5	422256	M64673	Hs.1499	heat shock transcription facto	NA,SS,TM,F-box	4.1
35	441164	AB023180	Hs.7724	KIAA0963 protein	helicase_C,SS,RNA_pol_H	4.1
	401727			Target Exon	A_deamin,SS	4.1
	411142	NM_014256	Hs.69009	transmembrane protein 3	GalactosyLT,SS,Ribosomal	4.1
	458176	Al961519	Hs.140309	Homo sapiens, clone IMAGE:3677	SS,pkinase,pkinase_C	4.1
	432178	BE265369	Hs.272814	hypothetical protein DKFZp434E	SS,serine_carbpept	4.1
40	421537					4.1
70		BE383488	Hs.105547	neural proliferation, differen	SS,TM,Glyco_hydro_47	
	421380	D31833	Hs.1372	arginine vasopressin receptor	7tn_1	4.1
	422702	AJ011373	Hs.119285	chromosome 9 open reading fram	SS,TM,SS,TM	4.1
	434142	U47927	Hs.3759	ubiquitin specific protease 5	zf-UBP,UCH-2,UBA,UCH-1,SS	4.1
	423696	Z92546		Sushi domain (SCR repeat) cont	SS,TPR,vwd,sushi,Somatome	4.1
45	427407	BE268649	Hs.177766	ADP-ribosyltransferase (NAD; p	BRCT,PARP,zf-PARP,PARP_re	4.1
	413749	Al929320	Hs.75516	tyrosine kinase 2	pkinase,SS,TM,ig	4.1
	411927	BE274009	Hs.772	glycogen synthase 1 (muscle)	Glycos_transf_1,SS	4.1
	433320	D60647	Hs.250879	ESTs, Highly similar to CTXN R	SS,TM,mn	4.1
50	433890	AF103801	Hs.16361	hypothetical protein	DAO,SS	4.1
50	452603	AW410601	Hs.30026	HSPC182 protein	SS	4.1
	444496	BE302472	Hs.11314	DKFZP564N1363 protein	SS,GKAP,Band_41	4.1
	422556	NM_006245	Hs.118244	protein phosphatase 2, regulat	B56,SS,TM,Atrophin-1,Exo_	4.1
	447347	AA570056	Hs.122730	ESTs, Moderately similar to KI	TM,SS	4.1
	428284	AA535762	Hs.183435	NM_004545:Homo sapiens NADH de	SS,TM,Josephin,UIM,Joseph	4.1
55	426551	AA381268	Hs.323947	ESTs	SS, sushi	4.0
	417782	T10149	Hs.4243	hypothetical protein FLJ12650	SS,TM	4.0
	443639	BE269042	Hs.9661	proteasome (prosome, macropain	proteasome, SS,TM, LACT, try	4.0
	410039	AF207989	Hs.58014	Homo sapiens, Similar to G pro	SS,TM,7tm_3,SS,TM	4.0
	452715	Z21093	Hs.30352	ribosomal protein S6 kinase, 5	pkinase	4.0
60						
UU	442549	AI751601	Hs.8375	TNF receptor-associated factor HBV associated factor	zf-C3HC4,MATH,zf-TRAF,SS,	4.0
	430603	AA148164	Hs.247280		SS,zf-C3HC4,zf-RanBP,pkin	4.0
	427239	BE270447		ubiquitin carrier protein	UQ_con,SS,TM	4.0
	402665			Target Exon	SS,TM,ig,DSPc	4.0
	413818	BE161405	Hs.79	hypothetical protein MGC15429	SS,KH-domain,WD40,Ribosom	4.0
65	406919	M88359		gb:Homo saptens DNA-binding pr	SS,rm	4.0
	412656	AF006011	Hs.74375	dishevelled 1 (homologous to D	SS,PDZ,DEP,DIX,Dishevelle	4.0
	437546	AW074836	Hs.173984	T-box 1	SS,TM,T-box,GTP_CDC,LRRCT	4.0
	419489	AW411280	Hs.90693	replication initiation region	zf-C2H2,LIM,TM	4.0
	410043	D30612	Hs.58167	zinc finger protein 282	zi-C2H2,KRAB,SS,zi-C2H2,K	4.0
70						
70	430067	U79458	Hs.231840	WW domain blinding protein 2	GRAM,SS	4.0
	408449	NM_004408	Hs.166161	dynamin 1	PH,GED,dynamin,dynamin_2,	4.0
	448099	BE621839	Hs.61976	Homo sapiens cDNA FLJ12947 fis	SS	4.0
	436656	N35568	Hs.5245	hypothetical protein FLJ20543	SS,TM,sugar_tr,PID	4.0
7.5	424512	X53002	Hs.149846	Integrin, beta 5	integrin_B,EGF,SS,TM	4.0
75	440346	AI923985	Hs.59621	ESTs, Wealdy similar to A40815	SS,TM,ig,pkinase	3.9
	420065	AW140093	Hs.129926	ESTs	SS,TM	3.9
	426636	BE242634	Hs.2055	ubiquitin-activating enzyme E1	ThiF,UBACT,SS,pkinase,UCH	3.9
	421579	NM_002975	Hs.105927	stem cell growth factor, lymph	lectin_c,SS,TM	3.9
80	427498	NM_003926	Hs.178728	methyl-CpG binding domain prot	SS,HLH	3.9
οU	457820	AA341497	Hs.31408	RAR (RAS like GTPASE)	SS,TM,Rhomboid	3.9
	439998	BE559554	Hs.61790	hypothetical protein FLJ23338	SS,SS,TM,EMP70,PA28_alpha	3.9
	438662	AA223599	Hs.6351	cleavage and polyadenylation s	zf-OCHC,zf-CCCH,thaumatin	3.9
	414303	NM_004427	Hs.165263	early development regulator 2	SAMSS	3.9
	435406	F26698	Hs.4884	calcium/calmodulin-dependent p	pkinase, SS, hexokinase, hex	3.9
				0.45		

	414168	AW793295	Hs.103845	ESTs, Moderately similar to 15	SS .	3.9
	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp5	SS .	3.9
	418181	U37012	Hs.83727	cleavage and polyadenylation s	CPSF_A,SS,TM	3:9
	402793			Target Exon	SS,TM,cyclin,cyclin_C	3.9
5	418681	AA287786	Hs.23449	insulin receptor tyrosine kina	SS,SH3	3.9
	412621	L40397	Hs.74137	transmembrane trafficking prot	EMP24_GP25L,SS,TM	3.9
	420631	AW976530	Hs.28355	hypothetical protein FLJ22402	SS,TM	3.9
	438483	AW966735	Hs.321635	ESTs, Weakly similar to A46302	SS,TM,IP_trans	3.9
	431472		Hs.256549	nucleotide binding protein 2 (	fer4_NifH,ParA,APS_kinase	3.9
10		AK001023				3.8
10	447800	AL080092	Hs.19610	DKFZP564N1362 protein	SS,TM,SS,TM	
	436686	AW450205	Hs.305890	BCL2-like 1	TM,Bcl-2,BH4	3.8
	408815	AW957974	Hs.25485	hypothetical protein FLJ22341	SS,TM	3.8
	441196	BE397802	Hs.7744	NM_007103°:Homo sapiens NADH d	Complex1_51K,SNF2_N,helic	3.8
	433030	AW068857	Hs.279929	gp25L2 protein	ss,tm,emp24_gp25l,ss,tm,g	3.8
15	408721	BE515274	Hs.47062	polymerase (RNA) II (DNA direc	RNA_POL_M_15KD,SS,COX7a	3.8
	435049	AL122067	Hs.4746	hypothetical protein FLJ21324	SS,pfkB	3.8
	431347	AJ133461	Hs.251664	insufin-like growth factor 2 (	SS,Insulin,Insulin	3.8
	450835	BE262773	Hs.25584	hypothetical protein FLJ10767	ArfGap,SS,vwa,TSPN,fn3,Co	3.8
	414134	X60188	Hs.861	mitogen-activated protein kina	pkinase,SS,pkinase,T-box	3.8
20	418090	U57059	Hs.83429	tumor necrosis factor (ligand)	TNF,SS	3.8
20				ECSIT	SS,rm	3.8
	448832	AW245212	Hs.22199			3.8
	447256	AW593008	Hs.6126	hypothetical protein dJ1141E15	SS,TM,SS,TM	
	448107	D45853	Hs.20313	protein tyrosine kinase 2 beta	Focal_AT,pkinase,SS,Pepti	3.8
~~	426433	L38969	Hs.169875	thrombospondin 3	TSPN,tsp_3,SS,TM,SEA,TSPN	3.8
25	431626	AL035681	Hs.265327	-hypothetical protein DKFZp761I	SS	3.8
	430956	Al183529	Hs.2706	glutathione peroxidase 4 (phos	GSHPx,SS,TM,ABC_tran	3.8
	450998	BE387614	Hs.25797	splicing factor 3b, subunit 4,	SS,TM,sugar_tr,histone	3.8
	434899	BE613631	Hs.283565	FOS-like antigen-1	bZIP,SS,bZIP,cofilin_ADF,	3.8
	444734	NM_001360	Hs.11806	7-dehydrocholesterol reductase	ERG4_ERG24,SS,TM	3.8
30	411090	BE165650	Hs.339697	VPS28 protein	SS,TM,CPSF_A	3.8
50	452135	Al492175	Hs.21446	KIAA1716 protein	SS,DIX,PDZ,DEP,Dishevelle	3.8
					SS , DISTRICTED , DISTRICTED	3.7
	421339	AA070224	Hs.103561	SRp25 nuclear protein		
	406535	4.4047040		Target Exon	SS,TM,Ribosomal_S19e,ig,I	3.7
25	447281	AA017018	Hs.18021	hypothetical protein FLJ20446	SS,SS,Tektin,Piwi,PAZ	3.7
35	433126	AB021262	Hs.99816	beta-catenin-interacting prote	SS,TM	3.7
	425215	AF030291	Hs.155165	zinc finger protein-like 1	PHD,SS,TM,DnaJ,ERG4_ERG24	3.7
	420536	AL117455	Hs.275438	histone deacetylase 7A	Hist_deacetyl,SS,Hist_dea	3.7
	417998	AW967420		gb:EST379495 MAGE resequences,	SS,TM	3.7
	430890	X54232	Hs.2699	glypican 1	Glypican, SS	3.7
40	427863	AF189712	Hs.181002	MLL septin-like fusion	SS,GTP_CDC,SS,TM	3.7
. •	448606	BE613362	1101101000	Homo sapiens ubiquitin conjuga	SS,TM	3.7
	421961	AB032993	Hs.109929	likely homolog of rat GRIP-ass	TM,K_tetra,ion_trans,HLH,	3.7
	410293		Hs.61960	hypothetical protein	K_tetra,SS	3.7
		AK000047				3.7
45	425233	Z17861	Hs.155218	E1B-55kDa-associated protein 5	SPRY,SAP,SS,TM,SPRY,SAP,p	
43	423683	BE388699	Hs.4188	hypothetical protein MGC10812	SS,Peptidase_C15,TGF-beta	3.7
	415697	Al365603	Hs.78605	DKFZP566I1024 protein	SS,cpn60_TCP1	3.7
	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3	SS	3.7
	418052	AA350659	Hs.83347	angio-associated, migratory ce	WD40,Bacterial_PQQ,TM,UPF	3.7
	444706	AK000398	Hs.11747	hypothetical protein FLJ20391	SS,SS,TM	3.7
50	407381	AA420659	Hs.183110	ESTs, Weakly similar to ALUC_H	SS,TM	3.7
	423432	BE252996	Hs.44067	ESTs	TM	3.7
	444982	AK002182	Hs.12211	GDP-fucose transporter 1	SS,TM,DUF6,SS,TM	3.7
	407777	AA161071	Hs.71465	squalene epoxidase	SS,TM,Monooxygenase	3.7
	422715	AA332178	Hs.119403	hexosaminidase A (alpha polype	Glyco_hydro_20,Glyco_hydr	3.7
55	422609	Z46023	Hs.118721	sialidase 1 (lysosomal sialida	SS,TM,BNR,SS,TM,SET,HSP70	3.7
55				minichromosome maintenance def	MCM,RIP,SS,zf-C2H2,KRAB	3.7
	414732	AW410976	Hs.77152	ESTs		3.7
	452579	AA131657	Hs.23830		SS,CN_hydrolase	
	419032	W81330	Hs.58643	ESTs, Highly similar to JAK3B	SS,pkinase,SH2,Insulin,pk	3.6
60	411165	NM_000169	Hs.69089	galactosidase, alpha	Melibiase, Ribosomal_L44,z	3.6
UU	444000	A1095034	Hs.135528	ESTs	SS,HLH	3.6
	441174	BE312775	Hs.294005	Homo sapiens, clone IMAGE:3050	SS,TM	3.6
	429491	NM_012111	Hs.204041	chromosome 14 open reading fra	SS	3.6
	438433	AB018274	Hs.6214	KIAA0731 protein	· SS	3.6
	425162	BE514851	Hs.154886	choline kinase-like	Carn_acyltransf,Choline_k	3.6
65	429671	BE379335	Hs.211594	proteasome (prosome, macropain	AAA,NB-ARC,TM	3.6
	421018	Al569028	Hs.129888	hypothetical protein FLJ14768	zf-C2H2,SS,rm,ENTH	3.6
	433604	NM_013442	Hs.3439	stornatin-like 2	Band_7,SS,TM,AAA,cdc48_N,	3.6
	451544	AK000429	Hs.26570	hypothetical protein FLJ20422	SS,TM,COX3,SS,TM,SRF-TF	3.6
	444369	AV649296	Hs.282793	ESTs	SS	3.6
70					= =	3.6
, 0	406660	X65371	Hs.172550	polypyrimidine tract binding p	mm,beta-lactamase,SS,try	3.6
	456503	AW977779	Hs.194613	ESTs	SS,TM,bromodomain,abhydro	
	451711	AK000461	Hs.26890	cat eye syndrome chromosome re	SS,SS,TM,A_deaminase	3.6
	425394	AA356730	Hs.323949	kangai 1 (suppression of tumor	SS,TM,transmembrane4	3.6
~-	428011	BE387514	Hs.181418	KIAA0152 gene product	Acyl-CoA_dh,SS,efhand	3.6
75	407627	Al419020	Hs.62620	chromosome 6 open reading fram	SS	3.6
	436437	F12200	Hs.5811	chromosome 21 open reading fra	SS,Syja_N,Exo_endo_phos	3.6
	419418	X75621	Hs.90303	tuberous sclerosis 2	Rap_GAP,Tuberin,Peptidase	3.6
	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN	SS	3.6
	448136	AA036680	Hs.20447	protein kinase related to S. c	okinase.PBD	3.6
80	435977	AL138079		brain-specific membrane-anchor	SS,TM,SS,TM,utbiquitin,Rib	3.6
90			Hs.5012			
	419095	AA234009	Hs.188715	ESTs	pkinase,PH,pkinase_C	3.6
	447267	AL360143 ·	Hs.17936	DKFZP434H132 protein	SS	3.6
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	SRCR,Lysyl_oxidase,SS,TM,	3.6
•	444354	AA847582	Hs.10927	hypothetical protein R33729_1	SS	3.6

	429098	AF030249	Hs.196176	encyl Coenzyme A hydratase 1,	ECH, Herpes_V23, SS, Gal-bin	3.6
	430622	BE616971	Hs.247478	Homo sapiens, Similar to DNA s	G-patch, SS, TM, ubiquitin, a	3.6
	440675	AW005054	Hs.47883	ESTs, Weakly similar to KCC1_H	pkinase	3.6 ·
_	409678	NM_005632	Hs.55836	small optic lobes (Drosophila)	TM,Peptidase_C2	3.6
5	413097	BE383876	Hs.75196	ankyrin repeat-containing prot	ank,SET,SS,TM,pkinase,SH2	3.6
	427579	AA366143	Hs.179669	hypothetical protein FLJ20637	HECT,SS,HECT	3.6
	409154	U72882	Hs.50842	Interferon-induced protein 35	SS,ras,Ribosomal_L27e,KOW	3.5
	448528	BE613248	Hs.172084	Homo sapiens, clone IMAGE:3627	SS,PID,SH2	3.5
	444426	AL121105	Hs.11170	RNA binding motif protein 14	rm,SS,spectrin,PH,rm,so	3.5
10	409297	R34662	Hs.53066	hsp70-interacting protein	SS	3.5
	441138	T56785	Hs.10101	hypothetical protein FLJ12875	SS	3.5
	435169	AF148509	Hs.279881	mannosidase, alpha, class 1B,	TM,Głyco_hydro_47	3.5
	422575	AK000546	Hs.118552	hypothetical protein FLJ20539	TM,SS,TM,SRCR,Glyco_trans	3.5
	403325			C2000428*:gi[7705383]ref[NP_05	SS	3.5
15	437895	AB014568	Hs.5898	KIAA0668 protein	TM,UL21,Lipoprotein_6,GBP	3.5
	449030	Al365582	Hs.57100	Homo sapiens mRNA for FLJ00016	SS,Synuclein	3.5
	426542	AF190746	Hs.170310	cat eye syndrome chromosome re	A_deaminase,SS,TM,Hydrola	3.5
	439873	BE159253	Hs.300638	ESTs	SS	3.5
	428950	BE311879	Hs.194673	phosphoprotein enriched in ast	DED,SS,TM,Calsequestrin	3.5
20	421564	AB007864	Hs.105850	KIAA0404 protein	SS SS	3.5
20					SS,zf-C2H2,LIM,PHD,TFIIS,	3.5
	441094	U33819	Hs.7647	MYC-associated zinc finger pro		
	450007	BE270693	Hs.24301	polymerase (RNA) II (DNA direc	NA,SS	3.5
	422898	AL043101	Hs.127401	DKFZP434A163 protein; selectiv	SS,TM	3.5
25	444914	AA046947	Hs.12142	WD repeat domain 13	WD40,SS,TBC,rrm	3.5
23	420178	D50550	Hs.95659	Jethal giant larvae (Drosophil	WD40,SS,TM	3.5
	418984	AA421401		ribosomal protein L18	SS,TM	3.5
	414166	AW888941	Hs.75789	N-myc downstream regulated	Ndr,abhydrolase,SS	3.5
•	409944	BE297925	Hs.57687	four and a half LIM domains 3	LIM,SS	3.5
20	421458	NM_003654	Hs.104576	carbohydrate (keratan sulfate	SS	3.5
30	423599	Al805664	Hs.31731	peroxiredoxin 5	AhpC-TSA,SS,hormone_rec,z	3.5
	427715	BE245274	Hs.180428	KIAA1181 protein	TM,SS,TM,KOW	3.5
	405496			Target Exon	SS,tubulin,SS	3.5
	417911	AA333387	Hs.82916	chaperonin containing TCP1, su	cpn60_TCP1,SS,cpn60_TCP1	3.5
	433620	AA604520	Hs.269468	ESTs, Moderately similar to AL	SS,UCH-2,UCH-1	3.5
35	430053	AF052155	Hs.227949	SEC13 (S. cerevislae)-like 1	WD40,SS,TM,E1-E2_ATPase,C	3.5
	458687	AW024815	Hs.170088	GLUT4 enhancer factor	SS	3.5
	424679	AL117477	Hs.119960	DKFZP727G051 protein	chromo,SS	3.5
	417360	AW651703	Hs.82023	hypothetical protein similar t	SS,TM,GDA1_CD39,GDA1_CD39	3.5
	439641	Al251317	Hs.33184	ESTs	SS,TM,GYF,actin,PA	3.5
40	426437	BE076537	Hs.169895	ubiquitin-conjugating enzyme E	UQ_con,SS,TM,Armadillo_se	3.5
. •	427117	BE258946	Hs.173611	Target CAT	complex1_49Kd,SS,TM,ITAM,	3.4
	422051	AW327546	Hs.111024	solute carrier family 25 (mito	SS,mito_carr,SS,mito_carr	3.4
	422759	AA316582	Hs.224571	ESTs	SS	3.4
	417230	U40998	Hs.81728	unc119 (C.elegans) homolog	SS,glycolytic_enzy	3.4
45	450158	AK001999	Hs.24545	hypothetical protein FLJ11137	SS,zf-C2H2,SCAN,TFIIS,SS	3.4
	425421	L11669	Hs.157145	tetracycline transporter-like	SS,TM,SS,TM	3.4
	415515	F11327	Hs.167406	gb:HSC2VD101 normalized infant	SS	3.4
	427868	Al360119.comp	Hs.181013	phosphoglycerate mutase 1 (bra	PGAM,SS,TM,ldh	3.4
	413503	BE410228	Hs.75410	heat shock 70kD protein 5 (glu	SS,HSP70,homeobox,Hydanto	3.4
50	413014	AW250533	Hs.75139	partner of RAC1 (arfaptin 2)	SS,hemopexin,Filamin,NHL,	3.4
50	457655	AA622968	Hs.71574	hypothetical protein FLJ14926	SS,P5CR,EF1BD	3.4
	419432	AK001459	Hs.90375	hypothetical protein FLJ10597	PEP-utilizers.PEP-utilize	3.4
	421066	AU076725	Hs.101408	branched chain aminotransferas	aminotran_4,TM	3.4
	428038	AW134756	Hs.192477	ESTs	SS,Exonuclease,zf-C2H2	3.4
55	430352				TM	3.4
55		AW750535 Al807481	Hs.50742	Homo sapiens cDNA: FLJ23331 fi		3.4
	432647		Hs.278581	fibroblast growth factor recep	ig,pkinase,SS,TM,ig,pkina	3.4
	421310	AW630087	Hs.103315	trinucleotide repeat containin	TM,zf-C2H2,SS,PHD	3.4
	420999	AA338903	Hs.100915	peroxisomal biogenesis factor	SS	
60	409561	U58048	Hs.183138	procollagen (type III) N-endop DKFZP564O243 protein	SS,TM Herpes_env,SS,TM,Peptidas	3.4 3.4
UU	419727	AW160796	Hs.92700			
	421267	BE314724	Hs.103081	ribosomal protein S6 kinase, 7 KIAA0370 protein	pkinase,pkinase_C,SS	3.4 3.4
	411501	AB002368	Hs.70500		SS,TM,SS,TM	3.4
	448741	BE614567	Hs.19574	hypothetical protein MGC5469	SS .	
65	407103	AA424881	Hs.256301	hypothetical protein MGC13170	SS,TM,trypsin	3.4
05	422808	AA449014	Hs.121025	chromosome 11 open reading fra	SS,TM,trypsin,CUB,ubiquil	3.4
	448173	N95657	Hs.6820	ESTs, Moderately similar to YO	SS SS TM become beautiful	3.4
	416535	H61851	11 404000	gb:yr80e10.r1 Soares fetal liv	SS,TM,homeobox,LIM	3.4
	406656	M16714	Hs.181392	major histocompatibility compl	MHC_1,ig,SS,TM	3.4
70	435669	AI867781	Hs.31819	HT014	SS,abhydrolase_2	3.4
70	411077	AW977263	Hs.68257	general transcription factor I	SS,TM,TGF-beta	3.4
	427062	AW327785	Hs.173421	KIAA1564 protein	SS,Peptidase_M24	3.4
	421890	AW959486	Hs.21732	ESTs	SS,zf-C3HC4,SPRY	3.4
	412968	AW500508	Hs.75102	alanyl-tRNA synthelase	DHHA1,SS,tRNA-synt_2c,DHH	3.4
7Ė	439496	BE616501	Hs.32343	Homo sapiens, Similar to RIKEN	SS MEDIA OR THE COMMON COMMON	3.4
75	433659	AK001301	Hs.3487	hypothetical protein FLJ10439	WD40,SS,TM,Syntaxin,Synta	3.3
	447578	AA912347	Hs.136585	ESTs, Weakly similar to JC5314	SS	3.3
	441722	AW960504	Hs.173103	FE65-LIKE 2	SS,TM	3.3
	452345	AA293279	Hs.29173	hypothetical protein FLJ20515	DSPc,SS,imiC,F-box	3.3
0.0	451714	AK000344	Hs.26898	hypothetical protein FLJ20337	SS,TBC,FHA,zf-C3HC4	3.3
80	410633	BE546789	Hs.346742	hypothetical protein MGC3260	SS,TM	3.3
	410609	BE298441	Hs.287361	ADP-ribosylation factor relate	arf,ras,SS,arf,Stathmin	3.3
	414775	AA992036	Hs.172702	ESTs, Weakly similar to (defli	SS,PCI	3.3
	428495	NM_013279	Hs.184640	hypothetical protein MGC10781	SS,TM,XPG_N,XPG_I,5_3_exo	3.3
	429215	NM_005341	Hs.2364	GLI-Kruppel family member HKR3	zf-C2H2,BTB,TP2,K_tetra,S	3.3
		_			· · · ·	-

	446618	AL110307	Hs.15591	COP9 subunit 6 (MOV34 homolog,	Mov34,SS,zf-C2H2,SCAN	3.3
	44486B	BE560471	Hs.12101	hypothetical protein	SS.PCI	3.3
	430041	AW247237	Hs.227835	KIAA1049 protein	SS,TM,7tm_1,tubulin	3.3 ·
_	416950	AL049798	Hs.80552	dermatopontin	SS	3.3
5	431203	AW248421	Hs.250758	proteasome (prosome, macropain	AAA,Sigma54_activat,SS,TP	3.3
	432714	Y12059	Hs.278675	bromodomain-containing 4	bromodomain,SS,TM,SNF2_N,	3.3
	415674	BE394784	Hs.78596	proteasome (prosome, macropain	SS,proteasome,SS,TM,Cadhe	3.3
	426152	BE299190	Hs.167246	P450 (cytochrome) oxidoreducta	flavodoxin,FAD_binding,SS	3.3
10	418440	NM_006936	Hs.85119	SMT3 (suppressor of mif two 3,	ublquitin,SS,UQ_con	3.3 3.3
10	410545 409428	U32324 M33680	Hs.64310 Hs.54457	interleukin 11 receptor, alpha CD81 antigen (target of antipr	ig,fn3,SS,TM,GalP_UDP_tra transmembrane4,cyclin,SS,	3.3
	443121	Z19267	Hs.9006	VAMP (vesicle-associated membr	TM,MSP_domain	3.3
	453856	AA804789	Hs.19447	PDZ-LIM protein mystique	LIM,SS,SH3,Sorb	3.3
	430137	NM_005456	Hs.234249	mitogen-activated protein kina	SS,SH3,PID,SS,PID	3.3
15	446427	AW295863	Hs.119632	ESTs	SS	3.3
	400747			Target Exon	fn3,ig	3.3
	445580	AF167572	Hs.12912	skb1 (S. pombe) homolog	SS,SS	3.3
	452568	AA805634	Hs.300870	Homo sapiens mRNA; cDNA DKFZp5	SS,mm,Ephrin,pkinase,ATP	3.3
20	418558	AW082266	Hs.86131	Fas (TNFRSF6)-associated via d	death,DED,SS,TM	3.3
20	401655			Target Exon	SS	3.3
	429460	D56263	Hs.203238	phosphodiesterase 1B, calmodul	PDEase,SS,PDEase	3.3
	416448	L13210	Hs.79339	lectin, galactoside-binding, s	SRCR,SS,TM	3.3 3.3
	433038 440251	AF192559 AW796016	Hs.279939 Hs.332012	mitochondrial carrier homolog	TM,mito_carr,TM SS,TM,SS,TM,IRK	3.3
25	412922	M60721	Hs.74870	'Homo sapiens, clone IMAGE:3687 _H2.0 (Drosophila)-like homeo b	SS, homeobox, SS	3.3
23	432941	W04803	Hs.279851	hypothetical protein FLJ10241	SS,RNase_PH,RNase_PH_C	3.3
	441244	BE612935	Hs.184052	PP1201 protein	SS,TM,WD40	3.3
	438175	Al376727	Hs.122110	ESTs	SS,TM,trypsin,kringle,fn2	3.3
	423024	AA593731	Hs.325823	ESTs, Moderately similar to AL.	SS,TM,CD36,CD36	3.3
30	430120	AW675298	Hs.233694	hypothetical protein FLJ11350	SS	3.3
	419571	AW674962	Hs.91146	protein kinase D2	pkinase,DAG_PE-bind,PH,DC	3.3
	413019	BE281604	Hs.75140	low density lipoprotein-relate	SS	3.3
	400299	X07730	Hs.171995	kallikrein 3, (prostate specif	trypsin,SS,trypsin,trypsi	3.3
35	433519	BE263901	11. 4000	ESTs, Weakly similar to S37431	SS,TM	3.2
22	434702	AL039734	Hs.4099	nardilysin (N-arginine dibasic	Peptidase_M16,HCO3_cotran	3.2 3.2
	422242 430480	AJ251760	Hs.273385 Hs.241543	guanine nucleotide binding pro DKFZP586F1524 protein	G-alpha,arf,SS,G-alpha SS,TM,hemopexin,Somatomed	3.2
	452438	AL079399 BE514230	Hs.29595	JM4 protein	SS,TM,KOW,HLH	3.2
	456939	AA431633	Hs.163867	NM_002488*:Homo sapiens NADH d	SS,tRNA-synt_2b,WHEP-TRS,	3.2
40	421009	AL049709	Hs.343357	Human DNA sequence from clone	TM	3.2
	411969	X12458	Hs.72980	Protein P3	SBF,SS,TM,G6PD,G6PD_C,hex	3.2
	409197	N54706	Hs.303025	chromosome 11 open reading fra	SS	3.2
	417896	AA379770	Hs.82890	defender against cell death 1	DAD,SS,TM	3.2
15	418026	BE379727	Hs.83213	fatty acid binding protein 4,	lipocalin,SS,lipocalin	3.2
45	409057	AA702305	Hs.180060	ESTs	SS,TGFb_propeptide,TGF-be	3.2
	437869	W91976	Hs.290834	ESTs	SS,TM,SH3,zf-C3HC4	3.2
	413211 425080	AW967107 AJ393498	Hs.109274	hypothetical protein MGC4365 inositol 1,4,5-biphosphate re	ss,TM ss,CTF_NFI	3.2 3.2
	445363	NM_005993	Hs.12570	tubulin-specific chaperone d	ATP-synt_B,HEAT_PBS,SS,TM	3.2
50	421943	BE616520	Hs.343912	Homo sapiens, Similar to RIKEN	SS,TM,SS,TM	3.2
•	443337	Y07604	Hs.9235	non-metastatic cells 4, protei	NDK,SS,adh_short,NDK	3.2
	418885	D17530	Hs.89434	drebrin 1	cofilin_ADF,SS,cofilin_AD	3.2
	411817	BE302900	Hs.72241	mitogen-activated protein kina	pkinase,SS	3.2
	413891	BE271020		turnor suppressor delated in or	SS,TM	3.2
55	449455	T60748	Hs.278408	hypothetical protein	TM .	3.2
•	419193	D29643	Hs.34789	dolichyl-diphosphooligosacchar	SS,TM,DDOST_48kD,VP7,SS,T	3.2
	406701	AA780613	Hs.62954	ferritin, heavy polypeptide 1	SS,TM,UDPGT	3.2
	436467	AW450278	Hs.91681	ESTs, Weakly similar to DCHUO	SS,tRNA-synt_1b,tRNA_bind	3.2
60	446334	U52427	Hs.14839	polymerase (RNA) II (DNA direc	S1,SS SS TM EGE lostin, o cuchi	3.2 3.2
UU	410270	AF279142	Hs.195727	tumor endothelial marker 1 pre hypothetical protein FLJ22693	SS,TM,EGF,lectin_c,sushi, SS,hormone_rec,zf-CCCH	3.2
	445411 458018	AL137255 Al199575	Hs.12646 Hs.37716	ESTs	SS,TM,Oxysterol_BP	3.2
	426530	U24578	Hs.278625	complement component 4A	SS,A2M,NTR,A2M_N,prenyitr	3.2
	445604	T08566	Hs.12956	Tax interaction protein 1	PDZ,SS,TM,P2X_receptor,FG	3.2
65	443402	U77846		elastin (supravalvular aortic	SS,PDZ,LIM,pkinase	3.2
•	432416	BE410937	Hs.2985	emerin (Emery-Dreifuss muscula	LEM,SS,Ribosomal_L10e,Acy	3.2
	429662	Al929701	Hs.211586	phosphoinositide-3-kinase, reg	SH2,SH3,RhoGAP,SS,GILT,SH	3.2
	429150	AF120103	Hs.197365	smoothened (Drosophila) homolo	SS,TM,Fz,Frizzled,7tm_2,S	3.2
70	427729	AB033100	Hs.300646	KIAA1274 protein (similar to m	SS	3.2
70	418151	AA864238.comp	Hs.83583	actin related protein 2/3 comp	RhoGEF,REV,PH,SS,TM,Ribos	3.2
	448250	NM_016034	Hs.20776	mitochondrial ribosomal protei	Ribosomal_S2,SS,lipocalin	3.2
	431158	AW859138	Hs.136280	Homo sapiens cDNA: FLJ22288 fi ubiquitin-conjugating enzyme E	SS,Exonuclease UQ_con,SS,TM,SAM_PNT	3.2 3.2
	414292 406307	BE388407	Hs.75875	Target Exon	SS,TM,7tm_2,SS,TM,7tm_2,G	3.2
75	423325	R55565	Hs.347286	hypothetical protein FLJ22427	SS,TM,Surp,ubiquitin,TBC	3.2
	423525	BE410293	Hs.179718	v-myb avian myeloblastosis vir	NA,SS	3.1
	419069	AA233801		ESTs, Weakly similar to CA13_H	SS	3.1
	431717	BE396150	Hs.6945	mitochondrial ribosomal protei	SS,TM	3.1
	448381	D61580	Hs.21036	Homo sapiens mRNA; cDNA DKFZp4	RhoGAP,SS,TM,SET,zI-CXXC,	3.1
80	419394	AB011124	Hs.90232	KIAA0552 gene product	SS,ig	3.1
	436240	BE388673	Hs.5086	hypothetical protein MGC10433	SS,TM,Ets,COX6B,transmemb	3.1
	413900	AW409747	Hs.75612	stress-induced-phosphoprotein	TPR,SS,TM,DnaJ	3.1
	417920	S47833	Hs.82927	adenosine monophosphate deamin	A_deaminase,SS,G-alpha,GS	3.1
	421819	NM_013403	Hs.108665	zinedin	WD40,pkinase,pkinase	3.1
				244		

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				Diggraph (0.40) - 1-1-	15 00 00 DD00	24
	426362	BE267158	Hs.169474	OKFZP586J0119 protein	IF-2B,SS,PP2C	3.1
	408917	AW249025	Hs.7768	fibroblast growth factor (acid	SS.bZIP.coffin_ADF,EGF	3.1
	443099	A1372836	Hs.9003	hypothetical protein FLI13868	TM	3.1 ·
-	427022	AW245839	Hs.173255	small nuclear ribonucleoprotei	mm,SS,mm,SH3,ras,20G-Fe	3.1
5	452711	AW967047	Hs.293224	ESTs, Weakly similar to T00375	SS	3.1
	407236	W79485	Hs.173980	nuclear matrix protein NMP200	WD40,SS,TM,PTR2,7tm_1	3.1
	452537	AW247390	Hs.77735	hypothetical protein FLJ11618	SS,SNF2_N,helicase_C	3.1
	452139	AA099969	Hs.16331	Homo sapiens cDNA: FLJ21482 fi	SS	3.1
10	447629	AF034790	Hs.19105	translocase of inner mitochond	Tim17,SS,TM,pkinase,OTU	3.1
10	401097			C12000858*:gi[7363437 ref[NP_0	SS,TM,7tm_1,SS	3.1
	452736	C01164	Hs.4232	Homo sapiens PAC clone RP1-130	SS,SS,TM,TBC,Surp,ubiquit	3.1
	435507	Al143579	Hs.26510	vacuolar protein sorling 33B (	SS,Sec1,Sec1	3.1
	424934	U75370	Hs.153880	polymerase (RNA) mitochondrial	PPR,SS,TM,cNMP_binding,RN	3.1
	413245	BE244334	Hs.75249	ADP-ribosylation factor-like 6	SS,TM,kazal,Ribosomal_S8,	3.1
15	409858	NM_006586	Hs.56828	trinucleotide repeat containin	SS,SS,TM,B56	3.1
	424582	AF026849	Hs.150922	BCS1 (yeast homolog)-like	AAA,SS,PI-PLC-X,PH,PI-PLC	3.1
	431677	AK000496	Hs.306989	hypothetical protein FLJ20489	SS	3.1
	417947	AA323563	Hs.325309	hypothetical protein FLJ14598	SS,TM,PTPA	3.1
	409283	NM_004860	Hs.52788	fragile X mental retardation,	KH-domain,SS,TM,HMG_box	3.1
20	412813	AF086947	Hs.74617	dynactin 1 (p150, Glued (Droso	CAP_GLY,SS	3.1
	456535	AA305079	Hs.1342	cytochrome c oxidase subunit V	COX5B,SS,p450,actin	3.1
	432482	L19267	Hs.275924	dystrophia myotonica-containin	WD40,SS,pkinase,pkinase	3.1
	437256	AL137404	Hs.97871	Homo sapiens, clone IMAGE:3845	TM,SS	3.1
	440191	AI990417		tubulin, beta 5	SS, formiminotr, prenyltran	3.0
25	407972	AA827639	Hs.18587	- KIAA1588 protein	SS,TM	3.0
	420890	AA434058	Hs.100071	6-phosphopluconolactonase	Glucosamine_iso,SS	3.0
	440060	AI696387	Hs.126451	ESTs, Weakly similar to A46302	SS	3.0
	452222	AW806287	Hs.21432	SEX gene	SS,TM,Sema,TIG,PSI,GDI	3.0
	401772			NM_014520:Homo sapiens MYB bin	SS	3.0
30	453754	AW972580	Hs.172753	ESTs	SS,TM,ras,Ribosomal_S19,T	3.0
	423865	H05202	Hs.133968	FGF receptor activating protei	SS,TM	3.0
	450962	BE535647	Hs.25723	Sjogren's syndrome/scleroderma	SS,TM	3.0
	441954	AI744935	Hs.8047	Fanconi anemia, complementatio	TPR,SS,TM,AAA,cdc48_N,Ban	3.0
	412787	D87452	Hs.74579	KIAA0263 gene product	zf-CCCH,SS,TM,NTP_transfe	3.0
35	422034	AC006486	Hs.333069	Ets2 repressor factor	Ets,SS,pkinase,PAF-AH_lb	3.0
55	450788	Al738410	113.00000	ESTs	SS,TM	3.0
	452511	BE408178	Hs.285165	Homo sapiens cDNA FLJ20845 fis	SS, thiored, P5CR	3.0
	414380	BE391815	Hs.75981	ubiquitin specific protease 14	UCH-2,UCH-1,ubiquitin,SS	3.0
	407597	AA043925	Hs.339352	Homo sapiens brother of CDO (B	SS,TM,SS,TM	3.0
40	434955	BE276128	Hs.284286	mitochondrial ribosomal protei	SS	3.0
70	435632	AF220049	Hs.43549	uncharacterized hematopoietic	SS,UQ_con	3.0
	432465	D56165	Hs.275163	non-metastatic cells 2, protei	NDK,SS,NDK	3.0
	430526	AF181862	Hs.242407	G protein-coupled receptor, fa	7tm_3,homeobox,SS,TM	3.0
			115.242407		pkinase	3.0
45	453412	AJ003290	U- 46486	gb:AJ003290 Selected chromosom		3.0
73	446456	BE613933	Hs.15106	chromosome 14 open reading fra	UPF0143,SS	3.0
	433180	AB038651	Hs.31854	K562 cell-derived leucine-zipp	TM,Acetyltransf,TM,Acetyl	3.0
•	447322	BE617649	Hs.77690	RAB5B, member RAS oncogene fam	SS,oxidored_molyb,heme_1,	3.0
	422268	N25485	Hs.330310	maternal G10 transcript	G10,SS,WD40	3.0
50	419578	AF064853	Hs.91299	guanine nucleolide binding pro	WD40,SS,EPO_TPO	3.0
50	446929	AA076132	Hs.9460	Homo sapiens mRNA; cDNA DKFZp5	SS,TM,WD40	3.0
	TABLE 218					
			d identifier sumbor			
		er: Gene duste:	d identifier number			
55		Genbank acce				
55	Accession	Genualik acce	SSION HUMBERS			
	Oken	CAT Number	Annoneine			
	Pkey			ISECON A ASSECTE ANDSCOS A AZOLONE ALCONNEL A	AIC122CD AIAI27CC/7 DE2212C2 AI2/0010 AIC	0E031 A1000078 A1350617
	408215	10478_1		135629 AA338538 A1193603 AA781096 A1680061 A		
60		•		446461 Al355345 Al343638 Al343640 Al275091 M	110140 A11202133 A11230002 AA303130 A130	34313 AVV212000 N20320
00	400020	140001 4	AA626639 AW974648 AA652153 /	A A C A D C T A A A A A A A A A A A A A A A A A A		
	409938	116091_1 1253746_1		AW856717 AW861116 AW856706 AW856788 AW	DECTTA AMDECTOT AMDECTOR AMDECTOR AM	AIRECTON AMARECTTO
	411674	1200/40_1		AW856776 AW856635 AW856767	030114 AV1030101 AV103010U AV103010Z AV	1030/09 AW030/12
	440000	4047044 4			DDC DEACGYAY DEACGYAA DEGAGEA4	
65	413052	1347214_1		E062771 BE062636 BE062813 BE062699 BE0628		F44 T0440C AI7CECED
UJ	413837	139363_1		AW163385 Al929359 BE279279 AA132590 AW15		
				.1659582 Al969924 Al929284 Al340993 Al349083 A	4VVZ993ZZ AVV00403U AVVZ99313 AA 13Z3Z9 /	AI340991 AI912030
		*******	Al341293 Al650609 AA			
	413891	139759_1		925430 Al806151 AW003726 T15590 AA649945 A		
70				W778973 AI287859 AI983931 AW515101 AW1500	23 Algorado Algolii (garagou 10 Ala /U92) <i>F</i>	AW169748 AI991000
70	*****	4440000 4	AW513748 AI04058		070 DC010000 DC015000 DC010000 DC0111	42 DE044452 DE040500
	414023	1410860_1		BE247016 BE241984 BE241534 BE246091 BE2456	6/9 BE243620 BE245998 BE242329 BE2414	17 BE241457 BE242522
			BE241989 BE241464	_		
	416535	1599332_1				
75	417998	171375_1	AW967420 AA210915		10000 1 1 1000 100 000 000 1 11110 15- · · · · · ·	
75	418984	181094_1		330666 AA328941 W63573 AA758023 AA976306 h		
				19866 T49327 AA233722 AA631138 AA910314 AI3	7/9416 AI129321 AAB61574 AA635649 AI339	443 AW009533 AA677036
		40	AA948287 AA62		M . 10000=1	
	419069	181650_3		A913939 AI632681 AI813277 AI373652 AW13480	72 A1863574 AW305364 A1858557 A1670746 A	UU15036 AI935384 AI935317
00		40000		AI765223 AA884146 AA973341 AA234062		
80	419250	183289_2		H11254 AW403510 Al032786 AA767046 Al37611		
				959578 AA815039 AW292253 R05714 AA815462 A	AA235654 AA461274 W24933 AA300091 H00	515
	420160	191054_1		A255989 A1698206 A1468558	ED 4 4 000000 1111110111 11011000 1111	A 410 10 100 11000000
	421572	204022_1		J376907 AJ811618 AW138145 AW139465 AA4216	DB AAZ93069 AW118141 AI214980 AW66350	Z A1343486 A1553789
			AA650416 AI498947	•		
				245		

	423696	23112_1	Z92546 AA330586 Al570568 AW341487 Al827050 AW298668 Al792189 Al015693 Al733599 Al572251 Al672488 AW193262 Al244716 Al864375
			AI206100 AA912444 AI269365 AI640254 AW772466 AI867336 AA627604 H16914 AA358477 AA338009
	425080	246559_1	AI393498 R42314 AI088818 AI696468 AI418641 AA573152 F08817 AI910796 AW338984 R39024 AA729145 BE245956 AI093722 AA541730
_			F09835 Al242755 AA350447 AA865667 T93903 AW081029 AA493711 AA650030 N35995 N21491 T57002 Z25379 Al908851
5	427239	27647_1	BE270447 AW409921 BE207288 BE207170 D56355 BE263223 BE408171 BE262243 BE392439 BE292738 BE261776 BE314300 BE267719
			BE268715 BE513876 BE295291 BE297056 AA210923 BE407519 H51344 BE622905 AW248281 AW250313 T19021 AA355115 AA316879
			BE269633 BE621936 AA290724
	427391	27815_1	W50575 AK001212 AA155752 AA878366 AA090872 AB033013 AW249107 AA031890 AA112820 AW366388 N55156 AA326756 AW952294
10			AA180820 C03570 C03538 W60676 AW248674 AA034989 AA044781 AA074274 H26212 AI800572 AI127583 AI951785 AA856557 AI571746
10	*****	000000 4	H23835 Al589543 Al215670 AW879141 AA421182 Al734104 Al733923 AA430600
	428092 429545	286920_1	AWO19141 AA21102 A1734104 A1733923 AAA30000 AI824164 A1676005 AW129612 A1825903 AA773987 A1823645 A1823860 AA456229 A1824295 AA454622 A1264049 A1090237 A1669787 A1804012
	429343	305902_1	AI306153 W96164 AI298273 AW884073 AW883986
	430168	313927_1	AUSB8343 AA468507 AI47823 AW513008 AI762122 AI554512 AA862642 AA468976
15	433519	368801 2	BEZ63901 AA556086 A1190276 A094806 A1B31250 A1572668 AVVZ04552 A1560600 A1922941 R49621
13	438707	46360 1	188239 BE618914 AW385394 AW385398 AW385401 AI922683 AA907337 AA160504 AA928142 AA601969 AA010594 BE618528 AA160591
	440191	48804_3	A1990417 A1304400 A193071 A1742483 AW003408 AW131586 A1400201 A1556740 A1309186 AW665173 AW204722 A1215122 A1200785
	410151	10001_0	BE467373 A1147599 A1215120 A1076110 A1803429 A1262491 A1808243 A1281007 AW135212 AW205103 A1754349 A1004801 A1051273 AW768918
			AW103289 Al4
20	443402	5681_1	U77846 AA479373 AA346348 AA348194 M26867 AA728901 AA715367 AA377787 R64236 Al752721 R77311 AA339685 BE074254 AW938712
			AW068444 AA330624 AA347098 AA327507 AW391973 AA495763 AA479278 AW605018 T19644 AI204484 AW834745 AW081309 AW090002
			A1095659 A1131556 A156
	44459 <b>0</b>	6116_1	AA457456 AA907921 Al567715 AA579472 T64216 AA373128 F35533 AA722113 T64403 AA653738 F28806 AA595689 AA047537 AA022499
0.5			AW440532 F35782 AI554180 AI183767 AI806052 AA160379 AA481678 AI185031 AI148988 AI174482 AA868833 AI674395 AA481440 AI914985
25			AI698771 AA44
	445625	64558_1	BE246743 AA436942 AW024744 AW242177 AA975476 AW385185 R07536 R73462 AV654529 T57442 AJ399986 R50073 R48743 AJ769689
			AIB63005 AA317806 AI678000 AW189963 AI986207 AW471273 R73463 AI335104 AI590161 AI469257 AI954604 H21954 T25141 AA856793 R50074 AI708253 AI2
	448606	77159.1	BE613362 AA447862 H72036 AA393664 Al681334 AW139128 AA932579 Al302241 Al936800 AW960628 Al492148 C06192 AA336107 AA808008
30	410000	11100_1	AW615212 BE297403 BE298978 A1187207 AA928695 AI620631 AA938128 AI346527 AI040261 AA808401 AW130326 AI440313 AA868693
50			A1553329 A133246
	448677	775217 1	AIS50759 AI857497 AW151454
	450788	846840_1	Al738410 AW016905 Al971725
	452160	901991_1	BE378541 Al863051
35	453412	966264_1	AJ003290 AJ003288 AW276947
	455857	1376021_1	T70192 BE147696
	455928	1383899_1	BE170313 BE158339 BE158290
	457022	274445_1	AW377258 BE067468 BE067511 BE067515 BE067467 BE067514 AA397442
40	TABLE 21C		
70			responding to an Eos probeset
			lesponding to all cost process.  The Control of the
	. voi. coduc		The Fugit Indiaes at the control at Control (Control Control C

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
Strand: Indicates DNA strand from which exons were predicted

45 Nt\_position: Indicates nucleotide positions of predicted exons

Mt position

168236-168795

36116-36276 147706-148062 125325-125831 95473-95585,98900-99180

25818-26380

Pkov

	rkey	L/G1	Sualu	INC DOSIDORI
	400460	8389428	Plus	35559-36295
	400563	9844011	Plus	81941-82434
50	400747	7329330	Minus	71249-71441
	400846	9188605	Plus	39310-39474
	401097	9965518	Minus	60356-61096
	401128	8699792	Plus	37349-37885
	401655	9099093	Plus	79556-80132
55	401727	8134856	Plus	54342-54482
	401751	9828651	Plus	139165-139322
	401772	9966243	Plus	183917-184042
	402365	9454515	Minus	70928-71185
	402463	9796896	Minus	8818-8952
60	402665	8077033	Minus	11824-12090,14290-14544
	402793	6136940	Minus	69012-69165
	402916	7406502	Minus	361-474,541-687
	403028	7670577	Minus	114150-114272
	403325	8440025	Minus	109763-109926
65	404256	9367203	Plus	146931-147796

Minus

Minus

Plus

Plus

Plus Plus

7229907

6094661

2155224

8468968

9124019

8576099

Table 22A lists about 811 genes up-regulated in ovarian cancer compared to normal adult tissues that are tikely to encode extraceflutar or cell-surface proteins. These were selected as for Table 20A, except that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 4.0, the "average" ovarian cancer level was set to the 96th percentile value amongst various ovarian cancer specimens, the "average" normal adult tissue level was set to the 75th percentile value amongst various normalignant tissues, the "average" ovarian cancer value was greater than or equal to 80 units, and the predicted protein contained a structural domain that is indicative of enzymatic function or of transducing an intracellular signal, or of being modulatable by small molecules (e.g., pkinase, peptidase, phosphatase, or ion\_transporter). Predicted protein

TABLE 22A:

405189

405325

405356

405496 406101 406307

70

Pkey: Unique Eos probeset identifier number

ExAcon: Exemplar Accession number, Genbank accession number

UnigenelD: Unigene number Unigens Title: Unigene gene title Protein Dom.: Predicted protein domain R1: Ratio of tumor to normal body tissue

5	R1: Ratio of	tumor to norma	a body tissue			
5	Pkey	ExAcon	UniGene ID	Unigene Title	Protein Dom.	R1
	407223	H96850		gb:yw03b12.s1 Soares melanocyt	, , , , , , , , , , , , , , , , , , , ,	58.9
	430281	A1878842	Hs.237924	CGI-69 protein	mito_carr	46.7
10	410418		Hs.63325	transmembrane protease, serine	ldl_recept_a,trypsin	41.0
10	431773		Hs.268557	pleckstrin homology-like domai	PH	37.1 35.3
	438424 418969		Hs.25895 Hs.28907	hypothetical protein FLJ14996 hypothetical protein FLJ20258	SH3	35.2
	453028		Hs.31442	RecQ protein-like 4	DEAD,helicase_C	28.2
	407722		Hs.38041	pyridoxal (pyridoxine, vitamin	pfkB	28.2
15	451721	NM_006946		spectrin, beta, non-erythrocyt	spectrin,PH,CH	<b>27.9</b>
	416819		Hs.80205	pim-2 oncogene	pkinase	27.9
	430397		Hs.105607	bicarbonate transporter relate	HCO3_cotransp	27.7
	450334		Hs.24879 Hs.89499	phosphafidic acid phosphatase	PAP2 lipoxygenase,PLAT	26.7 25.3
20	418945 424420		Hs.146688	arachidonate 5-lipoxygenase prostaglandin E synthase	MAPEG	25.1
	412674		Hs.74451	calpain 4, small subunit (30K)	efhand	24.4
	430023		Hs.227729	FK506-binding protein 2 (13kD)	FKBP .	24.3
	444672		Hs.11669	laminin, alpha 5	laminin_EGF.laminin_G,EGF	24.0
25	413726		Hs.75510	annexin A11	annexin	23.1
25	438951 429099		Hs.6453 Hs.196177	inositol 1,3,4-triphosphate 5/ phosphorylase kinase, gamma 2	oxidored_nitro pkinase	23.0 23.0
•	431765		Hs.268541	novel SH2-containing protein 1	SH2	22.4
	422645		Hs.118890	glycogen synthase kinase 3 alp	pkinase	22.4
	413436		Hs.68061	sphingosine kinase 1	DAGKC	22.3
30	422639		Hs.173724	creatine kinase, brain	ATP-gua_Ptrans,ATP-gua_Pt	21.5
	429869	A1907018	Hs.15977	Target CAT	0100-11	21.3
	418891	NM_002419	Hs.89449 Hs.89631	mitogen-activated protein kina	SH3,pkinase,pyridoxal_deC RYDR_ITPR,RyR,SPRY,ion_tr	21.1 21.0
	419138 432866		Hs.279609	ryanodine receptor 1 (skeletal mitochondrial carrier homolog	mito_carr	20.9
35	452875		Hs.30928	DNA segment on chromosome 19 (	Euk_porin	20.8
	426997		Hs.173125	peptidylprolyl isomerase F (cy	pro_isomerase	20.8
	402916			ENSP00000202587*:Bicarbonate t	HCO3_cotransp	20.8
	425760	D17629	Hs.159479	galactosamine (N-acetyl)-6-sul	Sulfatase	20.7
40	400419	AF084545 NM_002496	Un 00442	Target Target CAT	EGF,ig,lectin_c,sushi,XII fer4	20.0 19.5
70	419444 459133		Hs.29656	cyclin-dependent kinase inhibi	ank	19.2
	447595		Hs.18953	phosphodiesterase 9A	PDEase	19.2
	422708		Hs.119324	kinesin-like 4	kinesin,homeobox	19.0
45	414837	U24266	Hs.77448	aldehyde dehydrogenase 4 famil	aldedh	18.8
45	429712		Hs.211914	ENSP00000233627*:NADH-ubiquino	oxidored_q6	18.5
	425848 451643	BE242709 M64437	Hs.159637 Hs.234799	valyl-IRNA synthetase 2 breakpoint cluster region	GST_C,GST_N,Tropomyosin RhoGEF,RhoGAP,PH,C2	18.4 18.1
	451643 447859		Hs.19851	peroxisornal biogenesis factor	NIOGEF, NIOGAF, FII, CZ	17.5
-:	426457		Hs.169965	chimerin (chimaerin) 1	DAG_PE-bind,RhoGAP	17.3
50	421612		Hs.106196	8D6 antigen	ldl_recept_a	17.1
	421363	NM_001381		docking protein 1, 62kD (downs	PH,IRS	16.9
	442739	NM_007274		cytosolic acyl coenzyme A thio	Acyl-CoA_hydro	16.8 16.8
	420568 421445	F09247 AA913059	Hs.247735 Hs.104433	protocadherin alpha 10 Homo sapiens, clone IMAGE:4054	cadherin asp	16.8
55	425424	NM_004954		ELKL motif kinase	pkinase,KA1,UBA	16.7
	446329	NM_013272		solute carrier family 21 (orga	kazal,OATP_N,OATP_C	16.5
	406620	M81105	Hs.146550	myosin, heavy polypeptide 9, n	myosin_head,Myosin_tail,I	16.4
	429109	AL008637	Hs.196352	neutrophii cytosolic factor 4	PX,SH3,OPR	16.3
6 <u>0</u>	429183	AB014604 N26362	Hs.197955	KIAA0704 protein	PH,Oxysterol_BP	16.2 16.2
00	444664 427640	N20302 AF058293	Hs.11615 Hs.180015	map kinase phosphatase-like pr D-dopachrome tautomerase	DSPc,Rhodanese MIF,Jate_protein_L2	16.2
	425123	AW205274	Hs.154695	phosphomannomutase 2	PMM	16.0
	416006	AA324251	Hs.78950	branched chain keto acid dehyd	E1_dehydrog	15.8
~=	412942	AL120344	Hs.75074	mitogen-activated protein kina	pkinase	15.8
65	423366	ZB0345	Hs.127610	acyl-Coenzyme A dehydrogenase,	Acyl-CoA_dh,Acyl-CoA_dh_M	15.7
	426391	AW161050	Hs.169611	second mitochondria-derived ac	p450	15.7 15.5
	424568 420029	AF005418 BE258876	Hs.150595 Hs.94446	cytochrome P450, subfamily XXV polyamine-modulated factor 1	aldo_ket_red	15.5
	433573	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G	7tm_2,EGF,cadherin,lamini	15.4
70	407619	AL050341	Hs.37165	collagen, type IX, alpha 2	Collagen	15.3
	427326	A1287878		gb:qv23f06.x1 NCI_CGAP_Lym6 Ho	7tm_1 1	15.2
	442620	C00138	Hs.8535	Homo sapiens mRNA for KIAA1668		15.1
	458130	AA115811	Hs.6838	ras homolog gene family, membe hypothetical protein MGC11314	ras,arf	15.0 15.0
75	449936 409230	AA938293 AA852431	Hs.60088 Hs.51299	NM_021074:Homo sapiens NADH de	complex1_24kD	14.7
	423801	NM_015071		GTPase regulator associated wi	RhoGAP,SH3,PH	14.0
	419639	AK001502	Hs.91753	hypothetical protein		13.6
	419298	AA853479	Hs.89890	pyruvate carboxylase	CPSase_L_chain,PYC_OADA,H	13.6
80	426108	AA622037	Hs.166468	programmed cell death 5	DUF122	13.5
οV	448133	AA723157 T18979	Hs.73769	folate receptor 1 (adult) Snf2-related CBP activator pro	Folate_rec helicase_C,AT_hook	13.5 13.5
	418736 436543	NM_002212	Hs.87908 Hs 5215	Integrin beta 4 binding protei	elF6	13.3
	431515		Hs.258583	endothelial differentiation, I	7tm_1	13.3
	429469	M64590	Hs.27 .	glycine dehydrogenase (decarbo	GDC-P	13.2
				0.4	7	

PCT/US02/19297

						40.0
	431462		Hs.256311	granin-like neuroendocrine pep		13.2
	444855	BE409261	Hs.12084	Tu translation elongation fact	GTP_EFTU,GTP_EFTU_D3,GTP_	13.2
	423464	NM_016240	Hs.128856	CSR1 protein	Collagen	13.1
_	450787	AB006190	Hs.25475	aquaporin 7	MIP	13.0
5	428539	AW410063	Hs.184877	solute carrier family 25 (mito	mito_carr	13.0
	436014	AF281134	Hs.283741	exosome component Rrp46	RNase_PH,RNase_PH_C	12.9
	416866	AA297356	Hs.80324	serine/threonine protein phosp	Metallophos	12.9
	433867	AK000596	Hs.3618	hippocalcin-like 1	efhand	12.9
	411408	U76666	Hs.69949	calcium channel, voltage-depen	ion_trans	12.8
10	432329	NM_002962		S100 calcium-binding protein A	S_100,efhand	12.7
10	447887	AA114050	Hs.19949	caspase 8, apoptosis-related c	ICE_p20,DED,ICE_p10	12.7
	427448	BE246449	Hs.2157	Wiskott-Aldrich syndrome (ecze	WH1,PBD,WH2	12.7
	428820	AA436187	Hs.172631	integrin, alpha M (complement	FG-GAP	12.7
	446603	NM_014835		oxysterol-binding protein-rela	Oxysterol_8P	12.6
15	422633	X56832	Hs.118804	enolase 3, (beta, muscle)	endase	12.6
IJ	446839	BE091926	Hs.16244	mitolic spindle coiled-coil re	Troponin	12.6
		U46922	Hs.77252	fragile histidine triad gene	HIT	12.5
	414757 428593	AW207440	Hs.185973	degenerative spermatocyte (hom	141	12.5
				N-acetylneuraminic acid phosph	Antifreeze, NeuB	12.5
20	432370	AA308334	Hs.274424		Aumeeze,Aeub	12.4
20	401542	V40000	11- 402400	C15001413*:gi]10645199[ref]NP_	6n2 in	12.3
	428782	X12830	Hs.193400	interleukin 6 receptor	fn3,ig	12.3
	425999	AW513051	Hs.332981	ESTs, Weakly similar to 138022	FAD_binding_2	12.2
	. 422301	AI752163	Hs.114599	collagen, type VIII, alpha 1	C1q,Collagen	
25	410720	AF035154	Hs.65756	regulator of G-protein signal	RGS,G-gamma,DEP	12.2
25	407143	C14076	Hs.332329	EST		12.1
	421321	NM_005309		glutamic-pyruvate transaminase	aminotran_1_2	12.1
	425251	Z22521	Hs.155342	protein kinase C, delta	pkinase,DAG_PE-bind,pkina	12.0
	431354	BE046956	Hs.251673	DNA (cytosine-5-)-methyltransf	PWWP,PHD	12.0
~ ~	420421	AF281133	Hs.343589	exosome component Rrp41	RNase_PH,RNase_PH_C	12.0
30	416714	AF283770	Hs.79630	CO79A antigen (immunoglobulin-	ig,ITAM,Zn_clus	120
	427336	NM_005658	Hs.2134	TNF receptor-associated factor	MATH .	12.0
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	Hydrolase	11.9
	436319	H90727	Hs.5123	inorganic pyrophosphatase	Pyrophosphatase	11.9
	400748			NM_022122:Homo sapiens matrix	• • •	11.9
35	428948	BE514362		FK506-binding protein 3 (25kD)	FKBP,PIP5K	11.8
	401215	-201100-		C12000457*:gi[7512178[pir][T30	trypsin	11.7
	401281			DKFZP586N2124 protein		11.7
	427397	A1929685	Hs.177656	calmodulin 1 (phosphorylase ki	efhand,RmaAD	11.7
	453496	AA442103	Hs.33084	solute carrier family 2 (facil	sugar_tr	11.7
40	409608	AF231023	Hs.55173	cadherin, EGF LAG seven-pass G	7tm_2,cadherin,GPS,lamini	11.7
70	424415	NM_001975		enolase 2, (gamma, neuronal)	enolase	11.7
	447495	AW401864	Hs.18720	programmed cell death 8 (apopt	pyr_redox	11.6
	426928	AF037062	Hs.172914	retinol dehydrogenase 5 (11-ci	adh_short	11.6
		AF03/002	ns. 172914		pkinase,LIM,PDZ	11.5
45	405371	DOCCC4	11- 407007	NM_005569*:Homo sapiens LIM do		11.4
43	416282	R86664	Hs.167257	brain link protein-1	Xfink .	11.4
	452295	BE379936	Hs.28866	programmed cell death 10	PH	11.4
	430390	AB023186	Hs.241161	KIAA0969 protein	PH	11.2
	430594	AK000790	Hs.246885	hypothetical protein FLJ20783	rn	11.2
50	443814	BE281240	Hs.9857	carbonyl reductase		
50	440242	AW295871		glucose transporter protein 10	0110 DI 1 DI - OCC	11.1
	447365	BE383676	Hs.334	Rho guanine nucleotide exchang	SH3,PH,RhoGEF	11.1
	400843			NM_003105*:Homo sapiens sortil	ldl_recept_a,fn3,ldl_rece	11.1
	422418	AK001383	Hs.116385	hypothetical protein FLJ10521	RhoGEF	11.0
~ ~	400232			NM_001895*:Homo sapiens casein	pkinase	10.9
55	426828	NM_000020		activin A receptor type II-lik	pkinase,Activin_recp	10.9
	431157	AI823969	Hs.132678	ESTs	MAPEG	10.8
	422616	BE300330	Hs.118725	. selenophosphate synthetase 2	AIRS,AIRS_C	10.8
	406779	AA412048	Hs.279574	CGI-39 protein; cell death-reg		10.8
<i>c</i>	400389	AL135841		olfactory receptor, family 2,	7tm_1	10.8
60	402207			Target Exon	A2M_N,A2M	10.8
	435615	Y15065	Hs.4975	potassium voltage-gated channe	ion_trans,KCNQ1_channel	10.8
	452434	D30934	Hs.29549	C-type lectin-like receptor-1	lectin_c	10.7
	402053			C11001722*:gi 11436283 ref[XP_		10.7
	418641	BE243136	Hs.86947	a disintegrin and metalloprote	disintegrin, Reprolysin, Pe	10.6
65	431512	BE270734	Hs.2795	tactate dehydrogenase A	ldh,ldh_C	10.6
	403213			NM_019595:Homo sapiens interse	SH3,efhand,C2,PH,RhoGEF	10.6
	412158	BE241740	Hs.785	integrin, alpha 2b (platelet g	FG-GAP,integrin_A	10.6
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (m	Peplidase_M10,hemopexin	10.6
	403949		•	C10000813*:gij5453992[ref[NP_0		10.6
70	457670	AF119666	Hs.23449	insulin receptor tyrosine kina	SH3	10.5
. •	418416	U11700	Hs.84999	ATPase, Cu transporting, beta	E1-E2_ATPase,HMA,Hydrolas	10.4
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding	BRCT	10.4
	422765	AW409701	Hs.1578	baculoviral IAP repeat-contain	BIRTK	10.4
	453023	AW028733	Hs.31439	serine protease inhibitor. Kun	Kunitz_BPTI	10.4
75	425694	U51333	Hs.159237	hexokinase 3 (white cell)	hexokinase,hexokinase2	10.4
, 5	423094	AB037108	Hs.6418	seven transmembrane domain orp		10.3
		VD021 100	110.0410	Target Exon	Carn_acyltransf	10.3
	40247B	AL031685	Hs.12785	KIAA0939 protein	Na_H_Exchanger,ABC2_membr	10.3
	444202			chemokine (C-C motil) receptor	7tm_1	10.3
80	425597	U28694	Hs.158324		UQ_con	10.2
οU	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E		10.2
	415200 .	AL040328	Hs.78202	SWI/SNF related, matrix associ	SNF2_N,helicase_C,bromodo	10.2
	414874	D26351	Hs.77515	Inositol 1,4,5-triphosphate re	RYDR_ITPR.ion_trans,MIR	
	423524	AF055989	Hs.129738	potassium voltage-gated channe	ion_trans,K_tetra,thaumat	10.2
	457558	AF083955	Hs.279852 .	G protein-coupled receptor	7tm_1,giobin	10.2

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						40.4
	445629	Al245701	Hs.193326	fibroblast growth factor recep		10.1
	434314	BE392921	Hs.3797	RAB26, member RAS oncogene fam	ras,ari	10.1
	402497			C1001261*:gi[2695979]emb[CAA70		10.1
_	449853	AF006823	Hs.24040	potassium channel, subfamily K	ion_trans	10.0
5	427672	AA356615	Hs.336916	death-associated protein 6		10.0
	412048	AW866863	Hs.73090	nuclear factor of kappa light	RHD,TIG,ank,death	10.0
	410079	U94362	Hs.58589	glycogenin 2	Glyco_transf_8	10.0
	420319	AW406289	Hs.96593	hypothetical protein	ras,arf	10.0
	420332	NM_001756		serine (or cystelne) proteinas	serpin	9.9
10	405474			NM_001093*:Homo sapiens acetyl	CPSase_L_chain,biotin_tip	9.9
	401507			C15000B10*:gi 11131272 sp P793		9.9
	431434	BE267696	Hs.254105	enolase 1, (alpha)	enolase	9.9
	447232		Hs.327	interteukin 10 receptor, alpha		9.8
	432343	NM_002960		S100 calcium-binding protein A	S 100	9.8
15	408931	AA251995	Hs.334648	poly(A) polymerase alpha	NTP_transf_2	9.8
IJ	421542	AA411607	Hs.118964	ESTs, Weakly similar to KIAA11	**** _aae	9.8
	421342		Hs.239307	tyrosyl-IRNA synthetase	DUF101	9.8
	430323	U40714		guardine nucleotide binding pro	G-alpha,arf	9.7
		AC005262	Hs.73797	embryonic ectodem development	WD40	9.7
20	. 424649	BE242035	Hs.151461		ldi_recept_a,fn3,ldi_rece	9.7
20	400772		11 400000	NM_003105*:Homo sapiens sortil		9.7
	450493	M93718	Hs.166373	nitric oxide synthase 3 (endot	flavodoxin,FAD_binding,NO	9.7
	401510			NM_017434:Homo sapiens dual ox	efhand,Ferric_reduct	9.7
	404596			Target Exon	-12	
25	451367	AA923729	Hs.26322	cell cycle related kinase	pkinase	9.7
25	417810	D28419	Hs.82609	hydroxymelhylbilane synthase	Porphobil_deam	9.6
	432855	AF017988	Hs.279565	secreted frizzled-related prot	Fz,NTR	9.6
	424263	M77640	Hs.1757	L1 cell adhesion molecule (hyd	fn3,ig,IRK	9.6
	430398	AF105202	Hs.241376	potassium voltage-gated channe	ion_trans,KCNQ1_channel	9.6
	424339	BE257148		endoglycan	MCM	9.6
30	429257	AW163799	Hs.198365	2,3-bisphosphoglycerate mutase	PGAM .	9.6
	407065	Y10141		gb:H.sapiens DAT1 gene, partia	SNF	9.6
	433938	AF161536	Hs.284292	ubiquinol-cytochrome c reducta		9.6
	409649	AA159216	Hs.55505	hypothetical protein FLJ20442	Y_phosphatase,DSPc	9.6
	404968			C4001170:gi[6863176[gb]AAF3040		9.5
35	400833			C11000890;gij3746443jgbjAAC639	7tm_1	9.5
	410191	Al609645		NM_021075*:Homo sapiens NADH d	-	9.5
	444633	AF111713	Hs.286218	junctional adhesion molecule 1	ig	9.4
	427747	AW411425	Hs.180655	serine/threonine kinase 12	pkinase	9.4
	415169	W42913	Hs.78089	ATPase, vacuolar, 14 kD	ATP-synt_F	9.4
40	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis	CARD	9.4
	422328	X60459	Hs.1513	interferon (alpha, beta and om		9.4
	445143	U29171	Hs.75852	casein kinase 1, delta	pkinase	9.4
	450883	NM_001348		death-associated protein kinas	pkinase	9.4
	414625	AA335738	Hs.76686	glutathione peroxidase 1	GSHPx	9.3
45		1010001100	115.70000	Target Exon	PH	9.3
72	401935	A141947490	Un 0/459		PALP,CBS	9.3
	418329	AW247430	Hs.84152	cystathionine-beta-synthase		· 9.3
	425242	D13635	Hs.155287	KIAA0010 gene product	HECT,IQ	9.2
	400404	AF161221	U- 00/0	katlikrein 14	trypsin	9.2
50	442332	Al693251	Hs.8248	Target CAT	fer2,molybdopterin,bac_dn	9.2
20	431534	AL137531	Hs.258890	Homo sapiens mRNA; cDNA DKFZp4		9.1
	402823			C1002456*:gi[9930918[emb]CAC05	CD14 CD20	
	404527			peptide YY, 2 (seminalplasmin)	GDA1_CD39	9.1
	439963	AW247529	Hs.6793	platelet-activating factor ace	PAF-AH_lb,Lipase_GDSL	9.1
e e	412970	AB026436	Hs.177534	dual specificity phosphatase 1	Rhodanese, DSPc	9.1
55	443553	AL040535	Hs.9573	ATP-binding cassette, sub-famil	ABC_tran	9.1
	400933			NM_004347:Homo sapiens caspase	ICE_p20,ICE_p10,CARD	9.0
	403268			NM_002210*:Homo sapiens integr	FG-GAP	9.0
	446673	NM_016361		LPAP for lysophosphatidic acid	acid_phosphat	9.0
<b>C</b> O	422531	AW967280	Hs.293894	ESTs, Weakly similar to HERC2	pkinase	9.0
60	421658	X84048	Hs.301760	frequenin (Drosophila) homolog	efhand	9.0
	401885			Target Exon	kinesin	9.0 .
	402651		•	NM_000721*:Homo saplens calciu	ion_trans	9.0
	457432	NM_005136	Hs.268538	potassium voltage-gated channe	ISK_Channel	9.0
	433146	AB033002	Hs.21413	solute carrier family 12, (pot		9.0
65	420090	AA220238	Hs.94986	ribonuclease P (38kD)	Ribosomal_L7Ae	9.0
	425281	AA444390	Hs.155482	hydroxyacyl glutathione hydrot	lactamase_B	9.0
	410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	SNF2_N,helicase_C	9.0
	407986	U32659	Hs.41724	interleukin 17 (cytotoxic T-ly		9.0
	431131	N84730	Hs.250616	isocitrate dehydrogenase 3 (NA	isodh .	9.0
70	422802	NM_004278		phosphatidylinositol glycan, c	DUF158	9.0
. •	447958	AW796524	Hs.68644	Homo sapiens microsomal signal		9.0
	438080	AA777381	Hs.291530	ESTs, Weakly similar to ALUC_H		9.0
	418843	AJ251016	Hs.89230	potassium intermediate/small c	CaMBD,SK_channel	9.0
	419244	Al436567	Hs.89761	ATP synthase, H transporting,	ATP-synt_DE	8.9
75	404676			Target Exon	• =	8.9
	428744	BE267033	Hs.192853	ubiquilin-conjugating enzyme E	UQ_con	8.9
	421474	U76362	Hs.104637	solute carrier family 1 (gluta	SDF	8.9
	421474	M89957	Hs.89575	CD79B antigen (immunoglobulin-	ig,ITAM	8.9
		AF207069	Hs.153357	procollagen-lysine, 2-oxogluta	20G-Fell_Oxy,Glycos_trans	8.9
80	424825			glucose-6-phosphatase, catalyt	PAP2	8.9
JU	444628	U01120	Hs.242	ENSP00000211797*:Helicase SKI2	Rasgap,PH	8.9
	404199	VI 010010	Un 404040		lectin_c,CUB,Kelch,PSI,EG	8.9
	428826	AL048842	Hs.194019	attractin		8.8
	410681	AW246890	Hs.65425	calbindin 1, (28kD)	efhand	
	415056	AB004662	Hs.77867 .	adenosine A1 receptor	7tm_1	8.8
				A 4	10	

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	400471			Target Exon		8.8
	400471 406591			NM_003888*:Homo saplens retina	atdedh	8.8
	425427	AI652662	Hs.157205	branched chain aminotransferas	aminotran_4	8.8
	410839	NM_006849		protein disutfide Isomerase	thiored,Rho_GDI,gntR	8.7
5	430037	BE409649	Hs.227789	mitogen-activated protein kina	pkinase	8.7
	450848	AI677994	Hs.428	fms-related tyrosine kinase 3	flt3_fig	8.7
	414534	BE257293	Hs.76366	BCL2-antagonist of cell death		8.7
	401454			NM_014226*:Homo sapiens renal	pkinase	8.7 · 8.7
10	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (mus	PGAM	8.7
10	433333	AI016521	Hs.71816	v-ald murine thymoma viral onc KIAA1337 protein	homeobox,pkinase,PH,pkina Patched	8.7
	430432 406128	AB037758	Hs.241419	NM_002920°:Homo sapiens regula	Oest_recep,zf-C4,hormone_	8.7
	419493	AF001212	Hs.90744	proteasome (prosome, macropain	PCI	8.7
	439569	AW602166	Hs.222399	CEGP1 protein	CUB,EGF	8.6
15	401134			C12001198:gij3183183[sp[Q92142	biopterin_H	8.6
	442286	W31847	Hs.50335	cytochrome P450 monooxygenase		8.6
	428376	AF119665	Hs.184011	pyrophosphatase (inorganic)	Pyrophosphatase	8.6
	433494	AB029396		bela-1,3-glucuronyltransferase	Glyco_tranf_43	8.6
20	427001	NM_006482		dual-specificity tyrosine-(Y)-	pkinase	8.6 8.6
20	437278	AA748017	Hs.290145	ESTs	cNMP_binding	8.6
	414463	T69078	Hs.76177	alpha-1-microglobulin/bikunin glycoprotein, synaptic 2	lipocalin,Kunitz_BPTI Steroid_dh	8.6
	421871 447827	AK001416 U73727	Hs.306122 Hs.19718	protein tyrosine phosphatase,	Y_phosphatase,fn3,ig,MAM	8.6
	403379	Giaizi	112.13110	Target Exon	DNA_pol_A	8.6
25	446872	X97058	Hs.16362	pyrimidinergic receptor P2Y, G	7tm_1	8.6
	432857	NM_016103		GTP-binding protein Sara	arf,ras	8.5
	420970	AA305079	Hs.1342	cytochrome c oxidase subunit V	COX5B .	8.5
	427221	L15409	Hs.174007	von Hippel-Lindau syndrome	VHL	8.5
	402209			Target Exon	A2M_N,A2M	8.5
30	400518			C10002057*:gi[3211705[gb]AAC21		8.5
	425606	U52112	Hs.158331	renin-binding protein	0055	8.5
	437965	AA843222	Hs.193534	ESTs, Moderately similar to AL	RasGEF .	8.5 8.5
	433392	AF038535	Hs.127588	synaptolagmin VII	C2	8.5
35	402191	A1701202	Ue 270720	NM_021733*:Homo sapiens testis	rae	8.5
33	458963 431857	Al701393 W19144	Hs.278728 Hs.271742	Rad and Gem-related 2 (rat hom ADP-ribosyltransferase (NAD; p	ras PARP,PARP_reg	8.5
	457579	AB030816	Hs.36761	HRAS-like suppressor	1744 J. 144 7.08	8.5
	409656	NM_005133		RCE1, prenyl protein protease	Abi	8.5
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, s		8.4
40	432499	BE276633		RAB6B, member RAS oncogene fam	ras,art	8.4
	400565			Target Exon		8.4
	401960			Target Exon	Branch	8.3
	432545	X52486	Hs.3041	uracil-DNA glycosylase 2	cyclin	8.3
15	445303	AW362198	Hs.12503	Interleukin 15 receptor, alpha	sushi	8.3
45	404528			peptide YY, 2 (seminatplasmin)	GDA1_CD39	· 8.3 8.3
	428542	D79989	Un 200007	KIAA0167 gene product	ank,PH,ArfGap,ras	8.3
	406868 405473	AA505445	Hs.300697	immunoglobulin heavy constant NM_001093°:Homo sapiens acetyl	CPSase_L_chain,biotin_lip	8.3
	408601	U47928	Hs.86122	protein A	7tm_1	8.3
50	415008	NM_002777		proteinase 3 (serine proteinas	trypsin	8.3
50	430258	AU076644	Hs.236963	protein phosphatase 2A, regula	-26-	8.3
	436483	AJ272063	Hs.283010	vanilloid receptor subtype 1	ank,ion_trans	8.3
	459302	NM_002314	Hs.36566	LIM domain kinase 1		8.3
·	437644	AA748575	Hs.136748	lectin-like NK cell receptor	lectin_c	8.3
55	421707		Hs.107054	lectomedin-2	Latrophilin,OLF,7tm_2,Gal	8.2
	414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/m	COesterase	8.2
	453898	AW003512	Hs.232770	arachidonate lipoxygenase 3	Callana.	8.2 8.2
	424053	AF057036	Hs.138520	collagen-like tail subunit (si	Collagen	8.2
60	457398	BE258532	Hs.251871	CTP synthase	GATase SH2,PH	8.1
UU	421504 406495	AW402997	Hs.105052	adaptor protein with pleckstri Terget Exon	SRCR	8.1
	453610	AW368882	Hs.33818	RecQ protein-like 5	DEAD,helicase_C	8.1
	424880		Hs.153614	retinitis pigmentosa GTPase re	RCC1	8.1
	423847	U16997	Hs.133314	RAR-related orphan receptor C	hormone_rec,zf-C4	8.1
65	409829	M33552	Hs.56729	lymphocyte-specific protein 1	Caldesmon	8.1
	401180			eukaryotic translation elongat	ion_trans,IQ	8.1
	452072	BE258857	Hs.27744	RAB3A, member RAS oncogene fam	ras,arf	8.1
	426484	AA379658	Hs.272759	KIAA1457 protein	IP_trans	8.1
70	402453			C1002496:gi 7363439 ref NP_039	7tm_1	8.1
70	457310	W28363	Hs.239752	nuclear receptor subfamily 2,	globin,cNMP_binding,pkina	8.1 8.1
	422069	AJ010063	Hs.343603	tilin-cap (telethonin)	NA CONTRACTOR OF THE PROPERTY	8.0
	400275	AW732284	Hs.3828	NM_006513*:Homo saptens seryl- mevalonate (diphospho) decarbo	GHMP_kinases	8.0
	434357 430299	W28673	Hs.106747	serine carboxypeptidase 1 prec		8.0
75	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	FKBP,TPR	8.0
	402393	A. 11 1713	. 10.010	ENSP00000085284*:CDNA FLJ20404	RhoGEF,PH	8.0
	429252	NM 004658	3 Hs.198312	RAS protein activator like 1 (	C2,PH,RasGAP,BTK	8.0
	456181	L36463	Hs.1030	ras inhibitor	RA,SH2,VPS9	7.9
0.5	431493	Al791493	Hs.129873	ESTs, novel cytochrome P450	p450	7.9
80	451558	NM_001089	9 Hs.26630	ATP-binding cassette, sub-fami	ABC_tran,SRP54	7.8
	415758	BE270465	Hs.78793	protein kinase C, zeta	pkinase,DAG_PE-bind,pkina	7.8
	419270		2 Hs.89839	EphA1	EPH_lbd,pkinase,SAM,fn3	7.8
	422837	U25441	Hs.121478	dopamine receptor D3	7tm_1 pkinase	7.8 7.8
	401118		•	Target Exon	hunge	1.0

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	426440	BE382756	Hs.169902	solute carrier family 2 (facil	sugar_tr	7.8
	418635	L11329	Hs.1183	dual specificity phosphatase 2	DSPc,Rhodanese,Y_phosphat	7.8
	432747 403672	NM_014404	Hs.278907	calcium channel, voitage-depen	PMP22_Claudin	7.8 7.8
5	437806	AJ424921	Hs.122487	C4001244:gij539933[pir] A61275 ESTs, Weakly similar to A54854	tubulin ResCAR	7.7
,	456890	U48213	Hs.155402	D site of albumin promoter (al	RasGAP DAGKc,bZIP	7.7
	424107	AB014606	Hs.139648	kinesin family member 1C	kinesin,FHA	7.7
	452695	AW780199	Hs.30327	mitogen-activated protein kina	in the state of th	7.7
4.0	433262	AI571225	Hs.284171	KIAA1535 protein	cNMP_binding,ion_trans	7.7
10	424198	AB029010	Hs.143026	KIAA1087 protein	Na_Ca_Ex,Calx-beta	7.6
	406496			Target Exon	SRCR	7.6
	425423	NM_005897	Hs.157180	intracistemal A particle-prom	BTB,Kelch	7.6
	402211 408710	Y10256	Ha 47007	KIAA0430 gene product mitogen-activated protein kina	ion_trans,K_tetra	7.6 7.5
15	457615	W56321	Hs.47007 Hs.111460	calcium/calmodulin-dependent p	pkinase,SAM_decarbox pkinase	7.5
1,5	402760	1133321	15.111400	NM_021797*:Homo sapiens eosino	Glyco_hydro_18,CBM_14	7.5
	425428	AL110261	Hs.157211	DKFZP586B0621 protein	C1q, Collagen	7.4
	423579	NM_004121		gamma-glutamyltransferase-like	G_glu_transpept	7.4
20	413104	L42374	Hs.75199	protein phosphatase 2, regulat	B56	7.4
20	419660	BE280337	Hs.194693	solute carrier family 7 (catio	aa_permeases	7.4
	424774	BE244179	Hs.153022	TATA box binding protein (TBP)	Ca bringle in	7.4
	402632 444159	AF116846	Hs.10431	Target Exon dead ringer (Drosophila)-like	Fz,kringle,ig ARID,SNF	7.4 7.4
	405714	A-110040	115.10401	ENSP00000221137:Olfactory rece	7tm_1	7.3
25	442732	AA257161	Hs.8658	hypothetical protein DKFZp434E	EGF,laminin_EGF,Xlink,S_m	7.3
	421758	BE397336	Hs.1422	Gardner-Rasheed feline sarcoma	SH2,SH3,pkinase	7.3
	415995	NM_004573		phospholipase C, beta 2	PLPLC-X,PLPLC-Y,C2	7.3
	405137			Target Exon		7.3
20	402460			C1001261*:gi 2695979 emb CAA70		7.3
30	431398	BE616547	Hs.2785	keratin 17	filament	7.3
	429592 429225	AB029041 BE250337	Hs.209646 Hs.198273	KIAA1118 protein Target CAT	Troponin	7.3 7.2
	423015	U18548	Hs.123034	G protein-coupled receptor 12		7.2
	454373	NM_005133		RCE1, prenyl protein protease	Abi	7.2
35	440188	AK001812	Hs.7036	N-Acetylglucosamine kinase	ROK	7.2
	432920	U37689	Hs.3128	polymerase (RNA) II (DNA direc	4	7.2
	446143	BE245342	Hs.306079	sec61 homolog	secY	7.2
	422201	NM_001505		G protein-coupled receptor 30	7tm_1	7.2
40	440869 435099	NM_014297 AC004770	Hs.4756	protein expressed in thyroid flap structure-specific endonu	lactamase_B XPG_N,XPG_J,5_3_exonuclea	7.1 7.1
40	437161	AA054477	Hs.25391	ESTs	AFG_N,AFG_I,D_0_exonuclea	7.1
	429683	AF148213	Hs.211604	a disintegrin-like and metallo	tsp_1,Reprolysin,Pep_M12B	7.1
	426268	AF083420	Hs.168913	serine/threonine kinase 24 (St	pkinase	7.1
4.5	445087	AW893449	Hs.12303	suppressor of Ty (S.cerevisiae	S1,SH2,Ribosomal_L23,pkin	7.1
45	416377	AA179930	Hs.293867	caspase recruitment domain pro		7.1
	421748	NM_014718		KIAA0726 gene product	cadherin	7.1
	426691	NM_006201		PCTAIRE protein kinase 1	pkinase	7.0
	428599 411898	AB033078 BE409714	Hs.186613 Hs.44856	sphingosine-1-phosphate lyase hypothetical protein FLJ12116	pyridoxal_deC	7.0 7.0
50	427010	AW138332	115,44050	muscle RAS oncogene homolog	ras	7.0
	457305	BE268048	Hs.236494	RAB10, member RAS oncogene fam	ras,arf	7.0
	431630	NM_002204		integrin, alpha 3 (antigen CD4	integrin_A,FG-GAP,Rhabd_g	7.0
	457764	AW028284	Hs.4815	nudix (nucleoside diphosphate	NUDIX	6.9
55	435575	AF213457	Hs.44234	triggering receptor expressed	lg .	6.9
55	456488	AW015098	Hs.301946	ESTs, Weakly similar to T30867	cha cha	6.9
	428761 430396	AF236119 D49742	Hs.193076	GR82-related adaptor protein 2 hyaturonan-binding protein 2	SH2,SH3	6.9 6.9
	422066	AW249275	Hs.241363 Hs.343521	malate dehydrogenase 2, NAD (m	trypsin,kringle,EGF ldh,ldh_C,adh_short,Semia	6.9
	445937	AI452943	Hs.321231	UDP-GatbetaGlcNAc beta 1,4- g	Galactosyl_T_2	6.9
60	457499	AA953015	Hs.274370	hypothetical protein FLJ20260	PH PH	6.8
	400845			NM_003105*:Homo sapiens sortil	ldl_recept_a,fn3,ldl_rece	6.8
	416931	D45371	Hs.80485	adipose most abundant gene tra	C1q,Collagen	6.8
	414915	NM_002462		myxovirus (influenza) resistan	dynamin_2,dynamin,GED	6.8
65	432990 458128	AL036071 W32474	Hs.279899	humor necrosis factor receptor	TNFR_c6 ras,ari,ldh	6.8 6.8
05	429542	AF038660	Hs.301746 Hs.206713	RAP2A, member of RAS oncogene UDP-Gal:betaGlcNAc beta 1,4- g	Galactosyl_T_2.ig	6.8
	401488	A 050000	113.2001 (0	Target Exon	Glyco_hydro_1	6.7
	456243	Al345001	Hs.82380	menage a trois 1 (CAK assembly	zf-C3HC4	6.7
~^	424321	W74048	Hs.1765	lymphocyte-specific protein ty	SH2,SH3,pkinase	6.7
70	405187			NM_014272:Homo sapiens a disin	Reprolysin,tsp_1,Pep_M128	6.7
	413055	AV655701	Hs.75183	cytochrome P450, subfamily IIE	p450	6.7
	448496	BE379077	Hs.130849	ESTs, Weakly similar to 138022	NADHdh_2	6.7
	419667 417103	AU077005 Z33905	Hs.92208 Hs.81218	a disintegrin and metalloprote hypothetical protein MGC3597	disintegrin,Reprotysin,Pe TPR.zf-C3HC4,PHD	6.7 6.7
75	407687	AK002011	Hs.37558	hypothetical protein FLJ11149	FAD_Synth	6.7
	456469	NM_005109		oxidative-stress responsive 1	zf-C2H2,pkinase	6.7
	449546	W86248	Hs.58819	ESTs	hexokinase	6.6
	428926	NM_001702		brain-specific angiogenesis in	7tm_2,tsp_1,GPS,HRM	6.6
00	404953			C1002000*:gi[12735712 ref[XP_0		6.6
80	449401	AL135401	Hs.23557	serologically defined colon ca	pro_isomerase	6.6
	429962	M69113	Hs.226795	glutathione S-transferase pl	GST_C,GST_N	6.6
	421547 430035	AA489908 NM_003463	Hs.1390 Hs.227777	proteasome (prosome, macropain protein tyrosine phosphalase t	Clathrin_lg_ch,proteasome Y_phosphatase,DSPc	6.6 6.6
	406867	AA157857	Hs.182265	keratin 19	filament,bZIP	6.6
				25		

	404946			Target Exon	3Beta_HSD	6.5
	435213	AA092510	Hs.5985	non-kinase Cdc42 effector prot		6.5 .
	411201	T74588	Hs.8509	ESTs. Weakly similar to C3HU c	A2M_N,A2M	6.5
5	419344	U94905	Hs.277445	diacytglycerol kinase, zeta (1	ank,DAGKa,DAGKc,DAG_PE-bi	6.5
5	426194 424681	T50872 AA054400	Hs.2001 Hs.151706	thromboxane A synthase 1 (plat KIAA0134 gene product	p450 helicase_C,PRK	6.5 6.5
	417903	NM_002342		lymphotoxin beta receptor (TNF	TNFR_c6	6.5
	408905	AV655783	Hs.661	Target CAT		6.5
	438646	A1973076	Hs.231958	matrix metalloproteinase 28		6.5
10	431530	X61615	Hs.2798	leukemia inhibitory factor rec	fn3	6.5
	428883	AA435959	Hs.258802	ATPase, (Na)/K transporting, b	Na_K-ATPase	6.5
	404757			Target Exon · interleukin 11	to make	6.4 6.4
	406370 443611	NM_014397	Hs 9625	NIMA (never in mitosis gene a)	bypsin pkinase	6.4
15	424008	R02740	Hs.137555	putative chemokine receptor, G	7tm_1	6.4
	444912		Hs.12124	putative prostate cancer susce	lactamase_B	6.4
	454460	X66945	Hs.748	fibroblast growth factor recep	ig,pkinase	6.4
	432269	NM_002447		macrophage stimulating 1 recep	pkinase,Sema,PSI,TIG,A4_E	6.4
20	458718	AJ359476	Hs.157699	ESTs	• •	6.4
20	405282	41/004740	11- 47000	Target Exon	Cache	6.4
	447245 442297	AK001713 NM_006202	Hs.17860	hypothetical protein FLJ10851 phosphodiesterase 4A, cAMP-spe	E1_dehydrog PDEase	6.3 6.3
	400894	INIVI_UUOZUZ	N3.03301	C11000129:gi[9938014 ref]NP_06	7tm_1	6.3
	440446	NM_013385	Hs.7189	pleckstrin homology, Sec7 and	PH,Sec7	6.3
25	430886	L36149	Hs.248116	chemokine (C motif) XC recepto	7tm_1 ·	6.3
	451394	NM_003595	Hs.26350	tyrosylprotein sulfotransferas	Sulfotransfer	6.3
	436523	BE612990	Hs.5212	single-strand selective monofu		6.3
	422714	AB018335	Hs.119387	KIAA0792 gene product	DUF221	6.3
30	408924	AW295606	Hs.236131	homeodomain-interacting protei	ECH.Peptidase_U7	6.3 6.3
50	414551 413254	AI815639 U40272	Hs.76394 Hs.75253	enoyl Coenzyme A hydratase, sh isocitrate dehydrogenase 3 (NA	isodh	6.3
	415010	NM_004203		membrane-associated tyrosine-	pkinase	6.3
	449761	AB009698	Hs.23965	solute carrier family 22 (orga	sugar_tr	6.3
2.5	432221	M21191	Hs.273415	aldolase A, fructose-bisphosph	glycolytic_enzy,Adeno_E3_	6.3
35	414513	AW239400	Hs.76297	G protein-coupled receptor kin	pkinase,RGS,pkinase_C	6.2
	458516	BE010749	Hs.255097	ESTs		6.2
	417985	AA187545	Hs.83114	crystallin, zeta (quinone redu	adh_zinc	6.2 6.2
	447507 418322	H59696 AA284166	Hs.18747 Hs.84113	POP7 (processing of precursor, cyclin-dependent kinase inhibi	Y_phosphatase,DSPc	6.2
40	428443	BE618106	Hs.184326	CDC10 (cell division cycle 10,	GTP_CDC,M	6.2
	423229	AC003965	Hs.125532	protease, serine, 26	trypsin	6.2
	408903	BE244377	Hs.48876	famesyl-diphosphate famesylt	SQS_PSY,dsm,z-alpha	6.2
	426176	AB000462	Hs.167679	SH3-domain binding protein 2	PH,SH2	6.1
45	421395	D90084	Hs.1023	pyruvate dehydrogenase (lipoam	E1_dehydrog	6.1
43	430517 435906	S80071	Hs.241597	solute carrier family 6 (neuro	SNF	6.1 6.1
	402758	A1686379	Hs.110796	SAR1 protein C1001899*:gi 12722636 ref XP_0	arf,ras Glyco_hydro_18	6.1
	434202	BE382411	Hs.3764	guanylate kinase 1	Guanylate_kin,CoaE,Viral_	6.1
	402115	•		NM_021624:Homo sapiens histami	7tm_1	6.1
50	407601	AC002300	Hs.37129	sodium channel, nonvoltage-gat	ASC	6.1
	404679			Target Exon		6.0
	450739	AI732707	11 0000	ESTs, Weakly similar to ALU7_H	VIR	6.0
	439888 415742	AB040949	Hs.6733	pancreas-enriched phospholipas	C2,Pi-PLC-Y,Pi-PLC-X,RasG	6.0 6.0
55	453190	BE410243 AB002354	Hs.78769 Hs.32312	thimet oligopeptidase 1 KIAA0356 gene product	Peptidase_M3 PH,PHD,RUN	6.0
-	439975	AW328081	Hs.6817	inosine triphosphatase (nucleo	Ham1p_like	6.0
	412800	AW950852	Hs.74598	polymerase (DNA directed), del	homeobox	6.0
	432805	X94630	Hs.3107	CD97 antigen	7tm_2,GPS,EGF	6.0
60	418964	174640		gb:yc57c12.r1 Stratagene liver	A2M_N,A2M	6.0
oo	417483	BE549343	Hs.82208	acyl-Coenzyme A dehydrogenase,	Acyl-CoA_dh,Acyl-CoA_dh_M	6.0
	419755 457276	H18444 AF235097	Hs.134846 Hs.227583	BAI1-associated protein 3 Homo sapiens chromosome X map	C2	6.0 6.0
	423908	AJ006422	Hs.135183	centaurin-alpha	PH,ArfGap	6.0
	432118	N98718 ·		gb:yy65g02.r1 Soares_multiple_		5.9
65	427334	R44789	Hs.33191	Homo saplens, Similar to trans		5.9
	424959	NM_005781		activated p21cdc42Hs kinase	pkinase,SH3	5.9
	453082	H18835	Hs.31608	hypothetical protein FLJ20041	ion_trans	5.9
	421168 422287	AF182277 F16365	Hs.330780	cytochrome P450, subfamily IIB	p450 COX7a,Phage_G	5.9 5.9
70	401736	7 10303	Hs.114346	cytochrome c oxidase subunit V C16000492*:gij3127193jgbJAAD05	AMP-binding	5.9
, .	434755	AA648502		ESTs	Mars -Deliving	5.9
	414962	AF273304	Hs.235376	XPMC2 protein	Exonuclease	5.8
	407338	AA773213		gb:ab66f10.s1 Stratagene lung	ig	5.8
75	448426	BE018315	Hs.280776	tankyrase, TRF1-interacting an		5.8
75	409686	AK000002	Hs.55879	Homo sapiens mRNA; cDNA DKFZp4	ABC_tran	5.8
	450778 423612	U81375 NM_002067	Hs.25450	solute carrier family 29 (nucl	Nucleoside_tran G-alpha,arf	5.8 5.8
	423812 430845	AF024690	Hs.248056	guanine nucleotide binding pro G protein-coupled receptor 43	7tm_1	5.8
	424741	AF051941	Hs.343824	nucleoside diphosphate kinase	NDK	5.8
80	412958	BE391579	Hs.75087	Fas-activated serine/threonine		5.8
	415701	NM_003878	Hs.78619	gamma-glutarnyl hydrolase (conj	GATase	5.8
	423158	H97991	Hs.193313	Target CAT	MoaA_NifB_PqqE	5.8
	414788	X78342	Hs.77313	cyclin-dependent kinase (CDC2-	pkinase	5.8
	412915	AW087727	Hs.74823 .	NM_004541:Homo sapiens NADH de	_	5.7
				25	· )	

	400004	41.025054	11- 400004	and a		E 7
	420904	AL035964	Hs.100221	nuclear receptor subfamily 1.	hormone_rec,zf-C4	5.7
	415503	U35601	Hs.78473	N-deacetylase/N-sulfotransfera	Sulfotransfer	5.7
	433074	AL045019	Hs.323462	Homo sapiens cDNA FLJ11214 fis	DEAD,helicase_C,dsm,Vira	5.7
_	409124	AW292809	Hs.50727	N-acetylghucosaminidase, alpha		5.7
5	428270	BE501549	Hs.107040	ESTs		5.7
	435114	AA775483	Hs.288936	mitochondrial ribosomal protei	ODC_AZ	5.7
	425211	M18667	Hs.1867	progastricsIn (pepsinogen C)	asp	5.7
	453054	A1878908	Hs.31547	Target CAT	•	5.7
	420730	NM_002691	Hs.99890	polymerase (DNA directed), del	ICL	5.7
10	415117	AF120499	Hs.78016	polynucleotide kinase 3'-phosp	Viral_helicase1	5.7
	400985			Target Exon		5.7
	413163	Y00815	Hs.75216	protein tyrosine phosphatase,	fn3.ig,Y_phosphatase	5.7
	413858	NM_001610				5.7
				acid phosphatase 2, lysosomal	acid_phosphat	
15	457308	AI416988	Hs.238272	inositol 1,4,5-triphosphate re	ion_trans,RYDR_ITPR,MIR	5.7
15	400551			C10001991*:gi[6624920]emb]CAB6	SRCR	5.7
	433472	Al541246	Hs.3343	phosphoglycerate dehydrogenase	2-Hacid_DH,2-Hacid_DH_C,M	5.7
	409531	BE384319	Hs.54702	xylosylprotein beta1,4-galacto	Galactosyl_T_2	5.7
	449139	BE268315	Hs.23111	phenylalanine-IRNA synthetase-	neur	5.7
	450207	T87615	Hs.14716	ESTs		5.7
20	400266			NM_002858*:Homo sapiens ATP-bi	ABC_tran	5.6
	430713	AA351647	Hs.2642	eukaryotic translation elongat	GTP_EFTU,GTP_EFTU_D3,GTP_	5.6
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (	TPR	5.6
	405683	0		Target Exon		5.6
	449181	X96783	Hs.23179	synaptotagmin V	C2	5.6
25						5.6
23	414457	AW514320	Hs.76159	ATPase, H transporting, lysoso	ATP-synt_C	
	415193	AL048891	Hs.12185 ·	hypothetical protein MGC14333		5.6
	434883	AW381538	Hs.19807	hypothetical protein MGC12959		5.6
	433135	AA443873	Hs.110477	dolichyl-phosphate mannosyltra	•	5.6
	413049	NM_002151	Hs.823	hepsin (transmembrane protease	trypsia	5.6
30	420899	NM_001629	Hs.100194	arachidonate 5-lipoxygenase-ac	MAPEG	5.6
	423397	NM_001838		chemokine (C-C motif) receptor	7tm_1	5.5 -
	443759	BE390832	Hs.134729	FXYD domain-containing ion tra		5.5
	454112	NM_000885		Integrin, alpha 4 (antigen CD4	integrin_A,FG-GAP	5.5
	405594	1411_000000	113.40004	NM_021949:Homo sapiens ATPase,	E1-E2_ATPase,Hydrolase	5.5
35		BE019494	Hs.79217			5.5
J J	416322			pyrroline-5-carboxylate reduct	P5CR,Octopine_DH_N	
	446755	AW451473	Hs.16134	serine/threonine kinase 10	pkinase,TYA	5.5
	411030	BE387193	Hs.67898	7-60 protein		5.5
	431498	AK001777	Hs.258551	aspartyl aminopeptidase	Peptidase_M18	5.5
40	433012	NM_004045		ATX1 (antioxidant protein 1, y	HMA	5.5
40	414907	X90725	Hs.77597	polo (Drosophia)-like kinase	pkinase,POLO_box	5.5
	424572	M19650	Hs.92909	2',3'-cyclic nucleotide 3' pho		5.5
	406617			Target Exon	efhand, Ferric_reduct	5.5
	421883	X55079	Hs.1437	glucosidase, alpha; acid (Pomp	trefoil,Glyco_hydro_31	5.4
	419525	179257	Hs.1259	asialoglycoprotein receptor 2	lectin_c	5.4
45	448093	AW977382	Hs.15898	2,4-dienoyl CoA reductase 2, p	adh_short	5.4
.5	411574	BE242842	Hs.6780	protein tyrosine kinase 9-like	cofilin_ADF	5.4
		DEZ4ZU4Z	115.0700			
	406432	742000	11- 40 4000	CD1E antigen, e polypeptide	Sulfotransfer	5.4
	428921	Z43809	Hs.194638	polymerase (RNA) II (DNA direc		5.4
EΛ	430337	M36707	Hs.239600	calmodulin-like 3	efland	5.4
50	427162	AB011133	Hs.173864	KIAA0561 protein	pkinase,PDZ	5.4
	414216	D86970	Hs.75822	TGFB1-induced anti-apoptotic f	oxidored_q4,myosin_head,b	5.4
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase,	lipoxygenase,PLAT	5.4
	424373	AJ133798	Hs.146219	copine VII	C2	5.4
	449405	AA001350		gb:zh83h05.r1 Soares_fetal_liv	mito_carr .	5.4
55	409983	D50922	Hs.57729	Kelch-like ECH-associated prot	BTB,Kelch	5.4
	455818	AI733747	Hs.71174	interleukin 21 receptor		5.4
	424357	AW961058	Hs.44856	hypothetical protein FLJ12116		5.4
	423606	AB011094	Hs.129892	KIAA0522 protein	PH,bZIP,IQ,Sec7	5.3
	432311	BE083080	Hs.274323	similar to sialyltransferase 7	Glyco_transf_29	5.3
60						5.3
00	450080	AB037831	Hs.24372	ESTs, Weakly similar to dJ207H	DEAD,GSPII_E	
	423778	Y09267	Hs.132821	flavin containing monooxygenas	FMO-like,pyr_redox	5.3
	402338		-	Target Exon	p450	5.3
	412276	BE262621	Hs.73798	macrophage migration inhibitor	MIF	5.3
~	437967	BE277414	Hs.5947	mel transforming oncogene (der	ras,arf	5.3
65	424766	BE388855	Hs.152978	proteaseome (prosome, macropai	PA28_alpha,PA28_beta	5.3
	447766 '	NM_016011	Hs.19513	CGI-63 protein	adh_zinc	5.3
	453660	X98507	Hs.286226	myosin IC	myosin_head,IQ	5.2
	435327	BE301871	Hs.4867	mannosyl (alpha-1,3-)-glycopro	HLH,Myc_N_term,Myc-LZ	5.2
	432336	NM_002759		protein kinase, Interferon-ind	dsrm,pkinase	5.2
70	445139	AB037848	Hs.12365	synaptolagmin XIII	C2	5.2
, 0		AB012722			kinesin	5.2
	429214		Hs.198256	kinesin-like 3		
	432462	AK000013	Hs.274701	thymidine kinase 2, mitochondr	dNK	5.2
	424387	Al739312	Hs.284163	ANKHZN protein		5.2
75	405697			gb:Human homeobox-like mRNA		5.2
75	450321	Y16521	Hs.24812	CDP-diacylglycerol synthase (p	Cytidylyltrans,Adeno_VII	5.1
	412939	AW411491	Hs.75069	eukaryotic translation elongat	SHMT	5.1
	445109	AF039916	Hs.12330	ectonucleoside triphosphate di	GDA1_CD39	5.1
	419073	AW372170	Hs.183918	Homo sapiens cDNA FLJ12797 fis	ig,tsp_1,ZU5	5.1
	409958	NM_001523		hyaturonan synthase 1	Glycos_transf_2	5.1
80	442599	AF078037	Hs.324051	RelA-associated inhibitor	SH3,ank	5.1
-		BE386095	Hs.112272	histone deacetylase 8	Hist_deacetyl	5.1
	424305					
	427247	AW504221	Hs.174103	integrin, alpha L (antigen CD1	vwa.integrin_A.F.G.GAP	5.1
	429061	Y14039	Hs.195175	CASP8 and FADD-like apoptosis	DED,ICE_p20	5.1
	420849	X52221	Hs.99987 .	excision repair cross-compleme		5.1
				0.5	•	

	453337	072447	U- 20204	abrili2012 of Coome horset 2N	CCDI III	5.1
	418910	R73417 Z25821	Hs.25391 Hs.89466	gbtyj92g12.r1 Soares breast 2N Homo sapiens, Similar to dodec	GSPU_III ECH	5.1
	425771	8E561776	Hs.159494	Bruton agammaglobulinemia tyro	SH2,SH3,pkinase,PH,BTK	5.1
	405202	00011110	12,100.0	NM_021734* Homo saplens deoxyn	mito_carr	5.1
5	451452	BE560065	Hs.26433	dolichyl-phosphate (UDP-N-acet	Glycos_transf_4	5.0
	418231	AA326895	Hs.83848	triosephosphate isomerase 1	TIM	5.0
	425165	NM_014434	Hs.154899	Target CAT		5.0
	407876	NM_004519		potassium voltage-gated channe	ion_trans,KCNQ1_channel	5.0
10	417831	H16423	Hs.82685	CD47 antigen (Rh-related antig	ig out our stisses	5.0
10	404716			NM_007313*:Homo sapiens v-abl	SH2,SH3,pkinase	5.0 5.0
	405020 426236	NM_004798	Un 160212	Target Exon kinesin family member 3B	7tm_1 kinesin	5.0
	433178	AB038269	Hs.253706	cysteinyl leukotriene CysLT2 r	7tm_1	5.0
	422340	AW296219	Hs.115325	RAB7, member RAS oncogene fami	arf,ras	5.0
15	439414	NM_001183		ATPase, H transporting, lysoso		5.0
	425846	AA102174	Hs.159629	myosin IXB	myosin_head,DAG_PE-bind,I	5.0
	413599	AJ006239	Hs.75438	quinoid dihydropteridine reduc	adh_short	5.0
	424168	L29277	Hs.321677	signal transducer and activato	SH2,STAT,STAT_bind,STAT_p	5.0
20	436042	AF284422	Hs.119178	cation-chloride cotransporter-	aa_permeases	5.0
20	410775	AB014460	Hs.66196	nth (E.coli endonuclease III)-	HhH-GPD WD40	5.0 5.0
	428734 420340	BE303044 NM_000734	Hs.192023	eukaryotic translation initiat CD3Z antigen, zeta potypeptide	ITAM	4.9
	433075	NM_002959	115.51001	sortilin 1	BNR	4.9
	400300	X03363		HER2 receptor tyrosine kinase	pkinase	4.9
25	426811	BE259228	Hs.172609	nucleobindin 1	efhand	4.9
	401577			NM_000761:Homo sapiens cytochr	p450	4.9
	409637	AA323948	Hs.55407	Homo saplens mRNA; cDNA DKFZp4	Collagen	4.9
	426831	BE296216	Hs.172673	S-adenosylhomocysteine hydrola	AdoHcyase	4.9
30	430904	U65402	Hs.248124	G protein-coupled receptor 31	7tm_1	4.9
30	423552	AF107028	Hs.129783	sodium channel, voltage-gated,	ig,Adeno_E3_CR2	4.9
	421487 402183	AF027406	Hs.104865	serine/threonine kinase 23 NM_004491*:Homo sapiens glucoc	pkinase FF	4.9 4.9
	456748	AW137749	Hs.125902	ubiquitin specific protease 2	UCH-1,UCH-2	4.9
	424771	BE397151	Hs.153003	serine/threonine kinase 16	pkinase	4.9
35	406441			Target Exon	Aa_trans	4.9
-	437053	AU077018	Hs.3235	keratin 4	filament,bZIP,Tropomyosin	4.9
	443044	N28522	Hs.8935	quinolinate phosphoribosyltran	QRPTase,QRPTase_N	4.9
	431204	F28841	Hs.250760	cytochrome c oxidase subunit V	dUTPase,COX6A,ras,ATP-syn	4.9
40	456417	L36531	Hs.91296	integrin, alpha 8	integrin_A,FG-GAP	4.8
40	436735	L48489	11. 2004	mannosyl (beta-1,4-)-glycoprot	T-	4.8
	441455	AJ271671	Hs.7854	zinc/iron regulated transporte	Zip ·	4.8 4.8
	446948 451564	BE409053 AU076698	Hs.299629 Hs.132760	peroxisomal long-chain acyl-co hypothetical protein MGC15729	sugar_tr,Condensation	4.8
	403771		115.132700	NM_003061:Homo sapiens slit (D	EGF, laminin_G, LRR, LRRNT, L	4.8
45	403248			ESTs, Weakly similar to 178885	SLT	4.8
	410214	L29555	Hs.301698	sialyltransferase 4A (beta-gal	Glyco_transf_29	4.8
	407047	X65965		gb:H.sapiens SOD-2 gene for ma	sodfe	4.8
	422668	AF199364	Hs.119120	E3 ubiquitin ligase SMURF1	C2,WW,HECT	4.8
50	436057	AJ004832	Hs.5038	neuropathy target esterase	cNMP_binding	4.8
50	431262	NM_006672		solute carrier family 22 (orga	sugar_tr	4.8
	406625 428659	Y13647 U66579	Hs.119597 Hs.188859	stearoyl-CoA desaturase (delta G protein-coupled receptor 20	FA_desaturase	4.8 4.8
	432716	AI762964	Hs.205180	ESTs		4.8
	414460	L00727	Hs.898	dystrophia myotonica-protein k	pkinase	4.8
55	400287	S39329	Hs.181350	kallikrein 2, prostatic	trypsin	4.8
	428945	D42046	Hs.194665 ·	DNA2 (DNA replication helicase	UvrD-helicase,Viral_helic	4.7
	420028	AB014680	Hs.8786	carbohydrate (N-acetylglucosam	Sulfotransfer	4.7
	402912			Target Exon	pkinase	4.7
60	443329	BE262943	Hs.9234	hypothetical protein MGC1936	00	4.7
UV	426120 430609	AA325243 AA302921	Hs.166887 Hs.247362	copine I dimethylarginine dimethylamino	C2 .	4.7 4.7
	451320	AW118072	N3.24730Z	diacylglycerol kinase, zeta (1	zf-C2H2,BAR,SH3	4.7
	447131	NM_004585	Hs.17466	retinoic acid receptor respond		4.7
	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A	zona_pellucida	4.7
65	406458			C14000133*:gi[1082739[pir]]C44	proteasome	4.7
	427804	AL049654	Hs.180871	protein kinase C, alpha bindin	PDZ	4.7
	450748	AI733093	Hs.247686	ESTs	7tm_1	4.7
	422937	U03270	Hs.122511	centrin, EF-hand protein, 1	efhand	4.7
70	407978	AW385129	Hs.41717	phosphodiesterase 1A, calmodul	PDEase	4.7
70	428773 456444	BE256238 AA884517	Hs.193163	bridging integrator 1	SH3,BAR	4.7 4.7
	405574	AADUNII	Hs.31856	ESTs, Weakly similar to KIAA14 Target Exon	pkinase	4.7
	442414	BE408758	Hs.8297	ribonuclease 6 precursor	ribonudease_T2	4.7
	418289	AW403103	Hs.83951	Hermansky-Pudlak syndrome		4.6
75	421601	AI660190	Hs.106070	cyclin-dependent kinase inhibi	COI	4.6
	422795	AB033109	Hs.120866	KIAA1283 protein	kazal,A2M,A2M_N	4.6
	433019	A1208513	Hs.279915	translocase of inner mitochand	zf-Tim10_DDP	4.6
	431522	A1625859	Hs.258609	protein tyrosine phosphatase,	fn3,Y_phosphatase	4.6
QΛ	400846	Alamacane	the econon	sortilin-related receptor, L(D	ldi_recept_a,fn3,ldl_rece	4.6
80	456881	AW028302	Hs.155079	protein phosphatase 2, regulat	B56 pkinase,PH_RGS	4.6 4.6
	418172 408433	X61157 AW162931	Hs.83636 Hs.45002	adrenergic, beta, receptor kin ras-related C3 botulinum toxin	ras	4.6 4.6
	439921	AL110209	Hs.6770	LCAT-like lysophospholipase	LACT .	4.6
	427122	AW057736	Hs.323910 .	HER2 receptor tyrosine kinase	pkinase,Furin-like,Recep_	4.6
		_		25	, , , , , , , , , , , , , , , , , , , ,	

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	427945	AW137156	Hs.181202	hypothetical protein FLJ 10038	Collagen	4.6
	451777	U09210	Hs.459	solute carrier family 18 (vesi	sugar_tr	4.6
	429938	BE296804	Hs.226377	phosphate cytidylytransferase	Cytidyfyltransf,COX6C	4.6
					Cyddyryndaisi, CC/CC	
~	412974	R18978	Hs.75105	emopamil-binding protein (ster		4.6
5	414702	L22005	Hs.76932	cell division cycle 34	UQ_con	4.6
	425795	AJ000479	Hs.159543	endothelial differentiation, G	7tm_1	4.6
	422454	U49070	Hs.161352	protein (peptidyl-prolyl cis/t	Rotamase,WW	4.6
	408135	AA317248	Hs.42957	methyltransferase-like 1	Methyltransf_4	4.6
_	457388	AF035300	Hs.264157	cadherin-like 22	cadherin,Cadherin_C_term	4.6
10	421140	AA298741	Hs.102135	signal sequence receptor, delt	Herpes_UL3	4.6
10						4.6
	434834	AF156774	Hs.324020	1-acylglycerol-3-phosphate 0-a	Acyltransferase	
	413407	Al356293	Hs.75339	inositol polyphosphate phospha	SH2,SAM	4.6
	402463			NM_014624:Homo sapiens S100 ca	efhand,S_100	4.5
		10/70/10	No 03007	protein phosphatase 1, regulat		4.5
1.5	417891	W79410	Hs.82887		105 00 050	
15	421681	AA384922	Hs.195175	CASP8 and FADD-like apoptosis	ICE_p20,DED	4.5
	426516	BE262660	Hs.170197	glutamic-oxaloacetic transamin	aminotran_1_2	4.5
	418963	BE304571	Hs.89529	aldo-keto reductase family 1,	aldo_ket_red	4.5
						4.5
	423664	NM_004714		dual-specificity tyrosine-(Y)-	pkinase	
	427681	AB018263	Hs.180338	turnor necrosis factor receptor	TNFR_c6,death,PH,Xlink,Rh	4.5
20	432893	NM_016154	Hs 279771	Homo sapiens clone PP1596 unkn	ras,arf	4.5
					F5_F8_type_C,pkinase	4.5
	413815	AL046341	Hs.75562	discoidin domain receptor fami		
•	405546			NM_018833*:Homo sapiens transp	ABC_membrane,ABC_tran	4.5
	416297	AA157634	Hs.79172	solute carrier family 25 (mito	mito_carr	4.5
	421962	D82061	Hs.288354	FabG (beta-ketoacyl-[acyl-carr	adh_short	4.5
25			113.200007			
25	415341	R00602		gb:ye74c04.r1 Soares fetal liv	pkinase	4.5
	456668	W81526	Hs.118329	ESTs, Moderately similar to GA	Neur_chan_LBD,Neur_chan_m	4.5
	456652	AW327546	Hs.111024	solute carrier family 25 (mito	mito_carr	4.5
					- · · · · · · · · · · · · · · · · · · ·	4.5
	407863	AA317089	Hs.597	glutamic-oxatoacetic transamin	aminotran_1_2	
	435891	AW249394	Hs.5002	copper chaperone for superoxid	sodcu,HMA	4.5
30	453997	AW247615	Hs.37003	v-Ha-ras Harvey rat sarcoma vi	ras	4.5
50		N28989			-	4.5
	449029		Hs.22891	solute carrier family 7 (catio	aa_permeases	
	424829	NM_002507	Hs.1827	nerve growth factor receptor (	death,TNFR_c6	4.5
	429362	T25833	Hs.200478	ublquitin-conjugating enzyme E	UQ_con	4.5
	429133	N31854	Hs.197116	solute carrier family 7 (catio	aa_permeases	4.5
25						
35	426079	D31220	Hs.166168	peter pan (Drosophila) homolog	7tm_1	4:4
	414814	D14697	Hs.77393	famesyl diphosphate synthase	polyprenyl_synt	4.4
	433261	AB040967	Hs.112034	KIAA1534 protein	PH,Oxysterol_BP	4.4
		70010001	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,			4.4
	402915			ENSP00000202587*:Bicarbonate t	HCO3_cotransp	
	418267	BE389537	Hs.83919	glucosidase I	Glyco_hydro_63	4.4
40	430716	BE387257	Hs.247831	Homo sapiens, Similar to myosi	ethand	4.4
. •	420874	X66357	Hs.336478	cyclin-dependent kinase 3	pkinase	4.4
	439902	AF174499	Hs.6764	histone deacetylase 6	Hist_deacetyl,zf-UBP	4.4
	400223			Eos Control	Skp1	4.4
	450611	NM_004405	He #10	distal-less homeo box 2	homeobox	4.4
45						4.4
43	412965	L06419	Hs.75093	procollagen-lysine, 2-oxogluta	20G-Fell_Oxy	
	435564	AF210652	Hs.16614	5(3)-deoxyribonucleotidase (dN		4.4
	416121	X92762	Hs.79021	tafazzin (cardiomyopathy, dila	Acyltransferase	4.4
		AI951628			lon_trans	4.4
	423323		Hs.127007	potassium channel, subfamily K		
	448191	NM_005881	Hs.20644	branched chain alpha-ketoacid	HATPase_c	4.4
50	456217	BE253181	Hs.81687	non-metastatic cells 3, protei	NDK,Arteri_glycop	4.4
	436415	BE265254	Hs.343258	proliferation-associated 2G4,	Peptidase_M24	4.4
					· opuesse_inz ·	4.4
	429218	AA225065	Hs.198269	Target CAT		
	407433	AF209923		gb:Homo sapiens orphan G-prote	7tm_3	4.4
	425955	T96509	Hs.248549	ESTs, Moderately similar to S6		4.4
55				keratin 19	filamentbZiP	4.3
J J	407230	AA157857	Hs.182265			
	410197	NM_005518		3-hydroxy-3-methylglutaryl-Coe	HMG_CoA_synt	4.3
	416409	R61573	Hs.79300	ubiquitin-conjugating enzyme E	UQ_con	4.3
•	447957	NM_014821		KIAA0317 gene product	Filamin,HECT	4.3
					ICE_p20,CARD,ICE_p10	4.3
60	421771	NM_001224		caspase 2, apoptosis-related c		
60	448886	AL137291	Hs.22451	hypothetical protein FLJ10357	PH,RhoGEF	4.3
	414821	M63835	Hs.77424	Fc fragment of IgG, high affin	lg .	4.3
	431096	AA324358	Hs.249227	Homo sapiens DNA, cosmid clone		4.3
					in find	4.3
	429892	NM_003803		myomesin 1 (skelemin) (185kD)	ig,fn3	
	450126	BE018138	Hs.24447	sigma receptor (SR31747 bindin		4.3
65	413781	J05272	Hs.850	IMP (inosine monophosphate) de	IMPDH_C,IMPDH_N,CBS,NPD	4.3
-				NM_005546*:Homo sapiens IL2-in	SH2,SH3,pkinase,PH,BTK	4.3
	406530			cood of it total appeals it call		
		41/00000	UL 400000	handballad and E. E. 100077		
	428363	AK000284	Hs.183860	hypothetical protein FLJ20277	GNT-1	4.3
	428363 413954	AK000284 AL037111	Hs.183860 Hs.75641	hypothetical protein FLJ20277 galactose-1-phosphate uridylyl	GalP_UDP_transf,GalP_UDP_	4.3
	413954	AL037111	Hs.75641	galactose-1-phosphate uridylyl	GalP_UDP_transf,GalP_UDP_	
70	413954 432179	AL037111 X75208	Hs.75641 Hs.2913	galactose-1-phosphate uridylyl EphB3	GalP_UDP_transf,GalP_UDP_ EPH_lbd,fn3.pkinase,SAM	4.3 4.3
70	413954 432179 456529	AL037111 X75208 AF014643	Hs.75641 Hs.2913 Hs.100072	galactose-1-phosphate uridylyl EphB3 connextn46.6	GalP_UDP_transf,GalP_UDP_ EPH_Ibd,fn3,pkinase,SAM connexin	4.3 4.3 4.3
70	413954 432179 456529 448988	AL037111 X75208 AF014643 Y09763	Hs.75641 Hs.2913 Hs.100072 Hs.22785	galactose-1-phosphate uridylyl EphB3 connextn46.6 gamma-aminobutyric acid (GABA)	GalP_UDP_transf,GalP_UDP_ EPH_lbd,fn3,pkinase,SAM connexin Neur_chan_LBD,Neur_chan_m	4.3 4.3 4.3 4.3
70	413954 432179 456529	AL037111 X75208 AF014643	Hs.75641 Hs.2913 Hs.100072	galactose-1-phosphate uridylyl EphB3 connextn46.6	GalP_UDP_transf,GalP_UDP_ EPH_Ibd,fn3,pkinase,SAM connexin	4.3 4.3 4.3 4.3
70	413954 432179 456529 448988 426626	AL037111 X75208 AF014643 Y09763 AI124572	Hs.75641 Hs.2913 Hs.100072 Hs.22785 Hs.323879	galactose-1-phosphate uridylyl EphB3 connexin46.6 gamma-aminobutyric acid (GABA) inhibitor of kappa light polyp	GalP_UDP_transf,GalP_UDP_ EPH_Ibd_fn3,pkinase,SAM common Neur_chan_LBD,Neur_chan_m zf-C2H2	4.3 4.3 4.3 4.3
70	413954 432179 456529 448988 426626 432956	AL037111 X75208 AF014643 Y09763 A1124572 AL037895	Hs.75641 Hs.2913 Hs.100072 Hs.22785 Hs.323879 Hs.279861	galactose-1-phosphate uridylyl EphB3 connexid46.6 gamma-aminobutyric acid (GABA) inhibitor of kappa light polyp CGI-31 protein	GalP_UDP_transf,GalP_UDP_ EPH_Ibd,fn3,pkinase,SAM connexin Neur_chan_LBD,Neur_chan_m zf-C2H2 thiored	4.3 4.3 4.3 4.3 4.3
	413954 432179 456529 448988 426626 432956 428970	AL037111 X75208 AF014643 Y09763 A1124572 AL037895 BE276891	Hs.75641 Hs.2913 Hs.100072 Hs.22785 Hs.323879 Hs.279861 Hs.194691	galactose-1-phosphate uridylyl EphB3 connextn46.6 gamma-aminobutyric acid (GABA) inhibitor of kappa light polyp CGI-31 protein retinoic acid induced 3	GalP_UDP_transf,GalP_UDP_ EPH_Ibd,fn3,pkinase,SAM connexin Neur_chan_LBD,Neur_chan_m zf-C2H2 thiored 7tm_3	4.3 4.3 4.3 4.3 4.3 4.3
70 75	413954 432179 456529 448988 426626 432956	AL037111 X75208 AF014643 Y09763 AI124572 AL037895 BE276891 AA306610	Hs.75641 Hs.2913 Hs.100072 Hs.22785 Hs.323879 Hs.279861	galactose-1-phosphate uridylyl EphB3 connextn46.6 gamma-aminobutyric acid (GABA) inhibitor of kappa light polyp CGI-31 protein retinoic acid induced 3 tumor necrosis factor receptor	GalP_UDP_transf,GalP_UDP_ EPH_Ibd,fn3,pkinase,SAM connexin Neur_chan_LBD,Neur_chan_m zf-C2H2 thiored	4.3 4.3 4.3 4.3 4.3 4.3 4.3
	413954 432179 456529 448988 426626 432956 428970 428953	AL037111 X75208 AF014643 Y09763 AI124572 AL037895 BE276891 AA306610	Hs.75641 Hs.2913 Hs.100072 Hs.22785 Hs.323879 Hs.279861 Hs.194691 Hs.348183	galactose-1-phosphate uridylyl EphB3 connextn46.6 gamma-aminobutyric acid (GABA) inhibitor of kappa light polyp CGI-31 protein retinoic acid induced 3 tumor necrosis factor receptor	GalP_UDP_transf,GalP_UDP_ EPH_Ibd,fn3,pkinase,SAM connexin Neur_chan_LBD,Neur_chan_m zf-C2H2 thiored 7tm_3	4.3 4.3 4.3 4.3 4.3 4.3
	413954 432179 456529 448988 426626 432956 428970 428953 423922	AL037111 X75208 AF014643 Y09763 AI124572 AL037895 BE276891 AA306610 AK001663	Hs.75641 Hs.2913 Hs.100072 Hs.22785 Hs.323879 Hs.279861 Hs.194691 Hs.348183 Hs.135458	galactose-1-phosphate uridylyl EphB3 connexti46.6 gamma-aminobutyric acid (GABA) inhibitor of kappa light polyp CGI-31 protein retinoic acid induced 3 tumor necrosis factor receptor muscle-specific beta 1 integri	GalP_UDP_transf,GalP_UDP_ EPH_Ibd_fn3,pkinase,SAM connexin Neur_chan_LBD,Neur_chan_m zf-C2H2 thiored 7tm_3 TNFR_c6	4.3 4.3 4.3 4.3 4.3 4.3 4.2 4.2
	413954 432179 456529 448988 426626 432956 428970 428953 423922 426613	AL037111 X75208 AF014643 Y09763 A1124572 AL037895 BE276891 AA306610 AK001663 U96132	Hs.75641 Hs.2913 Hs.100072 Hs.22785 Hs.323879 Hs.279861 Hs.194691 Hs.348183 Hs.135458 Hs.171280	galactose-1-phosphate uridylyl EphB3 connexti46.6 gamma-aminobutyric acid (GABA) inhibitor of kappa light polyp CGI-31 protein retinoic acid induced 3 tumor necrosis factor receptor muscle-specific beta 1 integri hydroxyacyl-Coenzyme A dehydro	GalP_UDP_transf,GalP_UDP_ EPH_Ibd_fn3,pkinase,SAM connexin Neur_chan_LBD,Neur_chan_m zf-C2H2 thiored 7tm_3 TNFR_c6 adh_short	4.3 4.3 4.3 4.3 4.3 4.3 4.2 4.2
	413954 432179 456529 448988 426626 432956 428970 428953 423922 426613 426566	AL037111 X75208 AF014643 Y09763 A124572 AL037895 BE276891 AA308610 AK001663 U96132 AF131836	Hs.75641 Hs.2913 Hs.100072 Hs.22785 Hs.323879 Hs.279861 Hs.194691 Hs.348183 Hs.135458 Hs.171280 Hs.170453	galactose-1-phosphate uridylyl EphB3 connexin46.6 gamma-aminobutyric acid (GABA) inhibitor of kappa light polyp CGI-31 protein retinoic acid induced 3 tumor necrosis factor receptor muscle-specific beta 1 integri hydroxyacyl-Coenzyme A dehydro tropomodufin	GalP_UDP_transf,GalP_UDP_ EPH_Ibd_fn3,pkinase,SAM connexin Neur_chan_LBD,Neur_chan_m zf-C2H2 thiored 7tm_3 TNFR_c6	4.3 4.3 4.3 4.3 4.3 4.3 4.2 4.2 4.2
75	413954 432179 456529 448988 426626 432956 428970 428953 423922 426613	AL037111 X75208 AF014643 Y09763 A1124572 AL037895 BE276891 AA306610 AK001663 U96132	Hs.75641 Hs.2913 Hs.100072 Hs.22785 Hs.323879 Hs.279861 Hs.194691 Hs.348183 Hs.135458 Hs.171280	galactose-1-phosphate uridylyl EphB3 connexti46.6 gamma-aminobutyric acid (GABA) inhibitor of kappa light polyp CGI-31 protein retinoic acid induced 3 tumor necrosis factor receptor muscle-specific beta 1 integri hydroxyacyl-Coenzyme A dehydro	GalP_UDP_transf,GalP_UDP_ EPH_Ibd_fn3,pkinase,SAM connexin Neur_chan_LBD,Neur_chan_m zf-C2H2 thiored 7tm_3 TNFR_c6 adh_short	4.3 4.3 4.3 4.3 4.3 4.3 4.2 4.2
75	413954 432179 456529 448988 426626 432956 428970 428953 423922 426613 426566 425179	AL037111 X75208 AF014643 Y09763 A1124572 AL037895 BE276891 AA306610 AK001663 U96132 AF131836 AJ224442	Hs.75641 Hs.2913 Hs.100072 Hs.22785 Hs.323879 Hs.278861 Hs.194691 Hs.348183 Hs.135458 Hs.171280 Hs.170453 Hs.155020	galactose-1-phosphate uridylyl EphB3 connexin46.6 gamma-aminobutyric acid (GABA) inhibitor of kappa light polyp CGI-31 protein retinoic acid induced 3 tumor necrosis factor receptor muscle-specific beta 1 integri hydroxyacyl-Coenzyme A dehydro tropomodufin putative mathyltransferase	GalP_UDP_transf,GalP_UDP_ EPH_Ibd_fn3,pkinase,SAM connexin Neur_chan_LBD,Neur_chan_m zf-C2H2 thiored 7tm_3 TNFR_c6 adh_short	4.3 4.3 4.3 4.3 4.3 4.3 4.2 4.2 4.2 4.2
	413954 432179 456529 448988 426626 432956 428970 428953 423922 426613 426566 425179 412715	AL037111 X75208 AF014643 Y09763 Al124572 AL037895 BE276891 AA306610 AK001663 U96132 AF131836 AJ224442 NM_000947	Hs.75641 Hs.2913 Hs.100072 Hs.22785 Hs.323879 Hs.279861 Hs.194691 Hs.348183 Hs.135458 Hs.171280 Hs.170453	galactose-1-phosphate uridylyl EphB3 connextn46.6 gamma-aminobutyric acid (GABA) inhibitor of kappa light polyp CGI-31 protein retinoic acid induced 3 tumor necrosis factor receptor muscle-specific beta 1 integri hydroxyacyl-Coenzyme A dehydro tropomodufin putative mathyltransferase primase, polypeptide 2A (58kD)	GalP_UDP_transf,GalP_UDP_ EPH_Ibd_fn3,pkinase,SAM connexin Neur_chan_LBD,Neur_chan_m zf-C2H2 thiored 7tm_3 TNFR_c6 adh_short	4.3 4.3 4.3 4.3 4.3 4.2 4.2 4.2 4.2 4.2 4.2
75	413954 432179 456529 448988 426626 432956 428970 428953 423922 426613 426566 425179 412715 459298	AL037111 X75208 AF014643 Y09763 A1124572 AL037895 BE276891 AA306610 AK001663 U96132 AF131836 AJ224442	Hs.75641 Hs.2913 Hs.100072 Hs.22785 Hs.323879 Hs.278861 Hs.194691 Hs.348183 Hs.135458 Hs.171280 Hs.170453 Hs.155020	galactose-1-phosphate uridylyl EphB3 connexti46.6 gamma-aminobutyric acid (GABA) inhibitor of kappa light polyp CGI-31 protein retinoic acid induced 3 tumor necrosis factor receptor muscle-specific beta 1 integri hydroxyacyl-Coenzyme A dehydro tropomodufin putative methyltransferase primase, polypeptide 2A (58kD) gbym86d09.r1 Soares adult bra	GalP_UDP_transf,GalP_UDP_ EPH_Ibd_fn3,pkinase,SAM connexin Neur_chan_LBD,Neur_chan_m zf-C2H2 thiored 7tm_3 TNFR_c6 adh_short	4.3 4.3 4.3 4.3 4.3 4.2 4.2 4.2 4.2 4.2 4.2
75	413954 432179 456529 448988 426626 432956 428970 428953 423922 426613 426566 425179 412715 459298 404879	AL037111 X75208 AF014643 Y09763 Al124572 AL037895 BE276891 AA306610 AK001663 U96132 AF131836 AJ224442 NM_000947	Hs.75641 Hs.2913 Hs.100072 Hs.22785 Hs.323879 Hs.278861 Hs.194691 Hs.348183 Hs.135458 Hs.171280 Hs.170453 Hs.155020	galactose-1-phosphate uridylyl EphB3 connexin46.6 gamma-aminobutyric acid (GABA) inhibitor of kappa light polyp CGI-31 protein retinoic acid induced 3 tumor necrosis factor receptor muscle-specific beta 1 integri hydroxyacyl-Coenzyme A dehydro tropomodufin putative methyltransferase primase, polypeptide 2A (58kD) gbym860/09_1 Soares adult bra NM_030807:Homo sapiens glucose	GalP_UDP_transf,GalP_UDP_ EPH_Ibd,fn3,pkinase,SAM connexin Neur_chan_LBD,Neur_chan_m zf-C2H2 thiored 7tm_3 TNFR_c6 adh_short Tropomodulin,pkinase	4.3 4.3 4.3 4.3 4.2 4.2 4.2 4.2 4.2 4.2 4.2
75	413954 432179 456529 448988 426626 432956 428970 428953 423922 426613 426566 425179 412715 459298	AL037111 X75208 AF014643 Y09763 Al124572 AL037895 BE276891 AA306610 AK001663 U96132 AF131836 AJ224442 NM_000947	Hs.75641 Hs.2913 Hs.100072 Hs.22785 Hs.323879 Hs.278861 Hs.194691 Hs.348183 Hs.135458 Hs.171280 Hs.170453 Hs.155020	galactose-1-phosphate uridylyl EphB3 connexti46.6 gamma-aminobutyric acid (GABA) inhibitor of kappa light polyp CGI-31 protein retinoic acid induced 3 tumor necrosis factor receptor muscle-specific beta 1 integri hydroxyacyl-Coenzyme A dehydro tropomodufin putative methyltransferase primase, polypeptide 2A (58kD) gbym86d09.r1 Soares adult bra	GalP_UDP_transf,GalP_UDP_ EPH_Ibd_fn3,pkinase,SAM connexin Neur_chan_LBD,Neur_chan_m zf-C2H2 thiored 7tm_3 TNFR_c6 adh_short	4.3 4.3 4.3 4.3 4.3 4.2 4.2 4.2 4.2 4.2 4.2
75	413954 432179 456529 448988 426626 432956 428970 428953 423922 426613 426566 425179 412715 459298 404879	AL037111 X75208 AF014643 Y09763 Al124572 AL037895 BE276891 AA306610 AK001663 U96132 AF131836 AJ224442 NM_000947	Hs.75641 Hs.2913 Hs.100072 Hs.22785 Hs.323879 Hs.278861 Hs.194691 Hs.348183 Hs.135458 Hs.171280 Hs.170453 Hs.155020	galactose-1-phosphate uridylyl EphB3 connexin46.6 gamma-aminobutyric acid (GABA) inhibitor of kappa light polyp CGI-31 protein retinoic acid induced 3 tumor necrosis factor receptor muscle-specific beta 1 integri hydroxyacyl-Coenzyme A dehydro tropomodufin putative methyltransferase primase, polypeptide 2A (58kD) gbym860/09_1 Soares adult bra NM_030807:Homo sapiens glucose	GalP_UDP_transf,GalP_UDP_ EPH_Ibd,fn3,pkinase,SAM connexin Neur_chan_LBD,Neur_chan_m zf-C2H2 thiored 7tm_3 TNFR_c6 adh_short Tropomodulin,pkinase	4.3 4.3 4.3 4.3 4.2 4.2 4.2 4.2 4.2 4.2 4.2

	400563			Target Exon	Pep_M128_propep	4.2
	430237	AJ272144	Hs.236522	DKFZP434P106 protein	abhydrolase	4.2
	425175	AF020202	Hs.155001	UNC13 (C. elegans)-like	DAG_PE-bind,C2	4.2
_	409067	BE260459	Hs.50267	putative GTP-binding protein s	ras	4.2
5	419982	AA252544	Hs.55610	solute carrier family 30 (zinc		4.2
	428394	AU076472	Hs.184141	glutaryl-Coenzyme A dehydrogen	Acyl-CoA_dh,Acyl-CoA_dh_M	4.2
	437696 454034	Z83844	Hs.5790	hypothetical protein dJ37E16.5	Hydrolase	4.2
	410237	NM_000691 AI750589	Hs.61258	aldehyde dehydrogenase 3 famil argininosuccinate lyase	aldedh lyase_1	4.2 4.1
10	451478	NM_012331		methionine sulloxide reductase	PMSR	4.1
10	415410	AF037332	Hs.278569	sorting nexin 17	PX_fn3,pkinase,SAM,EPH_lb	4.1
	406538	72 007 002	110.210000	Target Exon	bypsin	4.1
	424349	AF141289	Hs.145550	solute carrier family 7 (callo	aa_permeases	4.1
	441164	AB023180	Hs.7724	KIAA0963 protein	helicase_C	4.1
15	421318	U63973	Hs.103501	rhodopsin kinase	pkinase,pkinase_C,RGS	4.1
	439340	AB032436	Hs.6535	brain-specific Na-dependent in	sugar_tr,BT1	4.1
	417447	N73703	Hs.293267	ESTs	Głyco_hydro_31	4.1
	409693	AA010233	Hs.55921	glutamyl-prolyl-IRNA synthetas	WHEP-TRS,GST_C,HGTP_antic	4.1
20	403655			NM_003071:Homo sapiens SWI/SNF	SNF2_N,helicase_C,zf-C3HC	4.1
20	411142	NM_014256		transmembrane protein 3	GafactosyLT	4.1
	437016	AU076916	Hs.5398	guanine monphosphate synthetas	- GMP_synt_C,GATase	4.1
	422699	BE410590	Hs.119257	ems1 sequence (mammary tumor a	SH3,HS1_rep	4.1
	427202 421380	BE272922	Hs.173936	interleukin 10 receptor, beta	Tissue_fac	4.1
25	434142	D31833 U47927	Hs.1372 Hs.3759	arginine vasopressin receptor ubiquifin specific protease 5	7tm_1 zfubp,uch-2,uba,uch-1	4.1 4.1
23	427407	BE268649	Hs.177766	ADP-ribosyltransferase (NAD; p	BRCT,PARP,zf-PARP,PARP_re	4.1
	413749	AI929320	Hs.75516	tyrosine kinase 2	pkinase	4.1
	411927	BE274009	Hs.772	glycogen synthase 1 (muscle)	Glycos_transf_1	4.1
	419726	U50330	Hs.1274	bone morphogenetic protein 1	EGF,CUB,Astacin	4.1
30	423814	AF105020	Hs.132989	putative protein O-mannosyttra	PMT,MIR	4.1
	451355	NM_004197		serine/threonine kinase 19		4.1
	422556	NM_006245		protein phosphatase 2, regulat	856	4.1
	428284	AA535762	Hs.183435	NM_004545:Homo sapiens NADH de		4.1
	431968	AF117222	Hs.272261	UDP-Gat:betaGlcNAc beta 1,3-ga	Galactosyl_T	4.0
35	443639	BE269042	Hs.9661	proteasome (prosome, macropain	proteasome	4.0
	410039	AF207989	Hs.58014	Homo sapiens, Similar to G pro	7tm_3	4.0
	431066	AF026273	Hs.249175	interleukin-1 receptor-associa	pkinase,death	4.0
	452715	Z21093	Hs.30352	ribosomal protein S6 kinase, 5	pkinase	4.0
40	403692			NM_007037*:Homo sapiens a disi	Reprolysin,tsp_1,Pep_M12B	4.0
40	442549	A1751601	Hs.8375	TNF receptor-associated factor	zf-C3HC4,MATH,zf-TRAF	4.0
	427239	BE270447	11 000000	ubiquitin carrier protein	UQ_con	4.0
	451125	AA015779	Hs.226923	ESTs	Y_phosphatase	4.0
	425081	X74794	Hs.154443	minichromosome maintenance def	MCM	4.0
45	402171 402665			Target Exon	C2	4.0 4.0
73	420148	U34227	Hs.95361	Target Exon myosin VIIA (Usher syndrome 1B	myosin_head,IQ,MyTH4,SH3,	4.0
	412187	U68487	Hs.73739	5-hydroxytryptamine (serotonin	7tm_1	4.0
	412656	AF006011	Hs.74375	dishevelled 1 (homologous to D	PDZ,DEP,DIX,Dishevelled	4.0
	425786	U35234	Hs.159534	protein tyrosine phosphatase,	fn3,ig,Y_phosphatase,DSPc	4.0
50	424288		Hs.278682	Phosphafidylglycerophosphate S		4.0
	452230	AW135360	Hs.224170	ESTs	pkinase	4.0
	408449	NM_004408	Hs.166161	dynamin 1	PH,GED,dynamin,dynamin_2	4.0
	423883	AF250238	Hs.134514	ATP-binding cassette, sub-fami	ABC_tran,photoRC,SRP54,Ca	4.0
	422676	D28481	Hs.1570	histamine receptor H1	7tm_1	. 4.0
55	458639	BE247683	Hs.14611	dual specificity phosphatase 1	DSPc	4.0
	400726			C13000717*:gi[129376[sp[P26196	DEAD,helicase_C	4.0
	405370			NM_005569*:Homo sapiens LIM do	pkinase,LIM,PDZ	4.0
	413654	AA331881	Hs.75454	peroxiredoxin 3	AhpC-TSA .	4.0
60	432917 448362	NM_014125 AA641767		PRO0327 protein	augas le	4.0
. 00	424512	X53002	Hs.21015 Hs.149846	hypothetical protein DKFZp564L integrin, beta 5	sugar_tr	4.0 4.0
•	727312	A0000Z	115.143040	mægnin, oeta o	integrin_B,EGF	4.0
	TABLE 22B:					
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		Genbank acces				
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			AA776726 AI04097			
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	415995	1564_1				23 AI933994 AW751282 AW374413 AA578823
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75	440004	4000000 4	Al422290 AA46503			
	418964	1809680_1	T74640 T74649	14 1 PO40497 NILL 045700 DE040070 007	1000FR DE0F000F PRO-1-70 F12-1-	Topogo processo processos se constituente
	424339	23827_1				T66208 BE255806 BE254484 AA324163 H07952
	427010	27436_1		2 Al204971 Al282924 AW192547 Al65276 460 AW138931 AW136963 NW 012219 A		5999 BE551105 AA450260 Al080368 AA324154
80	421010	21700_1		150 AW 138331 AW 13833 NM_012219 A 11 AL118847 W44458 AI765270 AA45312		
50	427239	27647_1				BE292738 BE261776 BE314300 BE267719
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	427326	277229_1	AI287878 AI804160			
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D79989 NM_014770 U81031 AA352392 AA984512 H38328 AL120358 AL134787 AL134589 AI637763 AI671506 AA526909 AI651627 AW243560
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AB029396 T04934 R21715 R19005 H11563 H14256 R46605 Z40857 BE218899 AI457785 BE55098B AI693847 AA961017 H40944 M78617
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           TABLE 22C:
           Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of
30
                  human chromosome 22° Dunham, et al. (1999) Nature 402:489-495
           Strand: Indicates DNA strand from which exons were predicted
           Nt_position: Indicates nucleotide positions of predicted exons
                                       Strand
                                                     Nt position
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PCT/US02/19297 WO 02/102235

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                      7630897
                                   Minus
          403248
                      7656833
                                   Minus
                                                167439-167606
                                               73832-73962
117348-117560
          403268
                      7230852
                                   Minus
          403379
                      9438244
                                   Minus
10
                                               65668-65859
          403655
                      8736093
                                  Plus
                                               96600-96881,96951-97280,97393-97594
          403672
                      7283286
                                  Minus
                                               93803-93938
          403692
                      7387384
                                  Minus
          403771
                      7770492
                                               112901-113045
                                  Plus
          403949
                      7711972
                                  Minus
                                               1731-1941
15
          404199
                      6010176
                                  Minus
                                               1669-2740
                                               127737-127796,128080-128210,129888-130054,132545-132869
          404527
                      8152087
                                  Plus
                      8152087
                                               135325-135486
          404528
                                  Plus
                                               104807-105043
          404596
                      9958262
                                  Minus
          404676
                                               56167-56342,58066-58189,58891-59048,60452-60628
                      9797204
                                  Minus
20
          404679
                      9797204
                                                125964-126092,126691-127011,127774-127893
                                               123145-123417
100933-101083.101580-101782
          404716
                      9838068
7706327
                                  Minus
          404757
404879
                                  Plus
                                               78346-78473,78693-78893
                      5103013
                                  Plus
          404946
                      7382189
                                   Plus
                                                134445-134750
25
          404953
                      7387324
                                   Plus
                                                16588-17031,
          404968
                      6899755
                                   Plus
                                               39287-39606
                                               106606-107309
          405020
                      7137674
                                  Plus
                                                158969-159423
          405137
                      8570507
                                   Plus
                      7229826
                                                117025-117170,118567-118736
          405187
                                   Plus
30
          405202
                      7230116
                                                40209-40429
                                   Plus
                      3810573
2078469
          405282
                                   Minus
                                                10482-10689
                                               38980-39111
          405370
                                   Minus
                                                47657-47766,48461-48596
                      2078469
          405371
                                   Minus
                                                153074-153343,154501-154598,156879-156999,158863-159051,159910-160053,161109-161229,163035-163131,165163-
                      8439781
                                   Plus
          405473
35
                                                165259, 165868-166003, 167375-167552, 169252-169364, 171127-171281
          405474
                      8439781
                                                172005-172175
                      1054740
3820491
6960456
                                               124010-124183
33200-33646
          405546
                                   Plus
          405574
                                   Minus
                                                161628-161734,162823-163014,164439-164652
          405594
                                   Plus
40
                      4508157
                                                21701-21844
          405683
                                   Minus
          405697
                      4309923
                                   Minus
                                                56765-57010,57696-58016
          405714
                      4156179
                                   Minus
                                                42789-43553
                                               50425-50876
          406128
                      9159110
                                   Plus
                      9256130
                                   Plus
                                                125320-125482
          406370
45
                      9256504
                                                3804-3930,4026-4120,4929-5109
          406432
                                   Plus
          406441
                      9280715
                                                26200-26458
                                   Plus
                                               145874-146911
174661-174978
          406458
                      9756020
                                   Plus
                      7711328
7711328
          406495
                                   Minus
          406496
                                                178947-179264,181779-182087
                                   Minus
50
          406530
                      7711474
                                   Minus
                                                11703-11860,14711-14829,14920-14984,16232-16448,16916-17087
          406538
                      7711478
                                   Plus
                                                35196-35367,38229-38476,40080-40216,43522-43840
          406591
                      8224230
                                   Minus
                                               2117-2257,2436-2540
                      8439858
                                                36430-36552
          406617
                                   Plus
55
```

Table 23A lists about 779 genes up-regulated in ovarian cancer compared to non-malignant adult ovaries. These were selected as for Table 20A, except that the ratio of "average" ovarian cancer to "average" normal ovaries was greater than or equal to 4.0, the "average" ovarian cancer level was set to the 93rd percentile value amongst various ovarian cancer specimens, the "average" normal adult tissue level was set to the 93rd percentile value amongst various non-malignant adult ovaries, the "average" ovarian cancer value was greater than or equal to 200 units.

TABLE 23A:

60

Pkey: Unique Eos probeset identifier number

Ex. Accn: Exemplar Accession number, Genbank accession number

UG ID: UniGene number

65

Title: UniGene gene title
Protein Dom.: Predicted protein domain R1: Ratio of tumor to normal ovaries

	Pkey	Ex. Acon	UG ID	Title	Protein Dorn.	R1
70	421298	NM_002666	Hs.103253	perilipin	perilipin,SS	37.8
	437897	AA770561	Hs.146170	hypothetical protein FLJ22969	SS,TM,zf-DHHC	29.2
	453028	AB006532	Hs.31442	RecQ protein-like 4	DEAD,helicase_C,Fork_head	27.6
	441021	AW578716	Hs.7644	H1 histone family, member 2		27.2
	422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS	SS,TM,pkinase,fn3,kg	26.5
75	454017	AW023617	Hs.347130	hypothetical protein FLJ22709	SS.TM,myosin_head,RA,DAG_	25.9
. •	438424	AI912498	Hs.25895	hypothetical protein FLJ14996	SS.TM	25.8
	435017	AA336522	Hs.12854	angiotensin II, type I recepto	1	25.0
	409518	BE384836	Hs.3454	KIAA1821 protein	SS	23.3
	410418	D31382	Hs.63325	transmembrane protease, serine	SS,TM,ldl_recept_a,trypsi	22.8
80	439924	AI985897	Hs.125293	ESTs	SS	22.7
••	446374	AA329256	Hs.24756	ESTs. Moderately similar to al		22.6
	431773	BE409442	Hs.268557	pleckstrin homology-like domai	PH.SS.LIM.Troponin	21.4
	420839	AI792682	Hs.282960	hypothetical protein MGC10870	SS,DS,UPF0139,Glyco_hydro	21.4
	413435	AF238083	Hs.68061	sphingosine kinase 1	DAGKc	21.2
	410400			apanagoum omoog i	w	

	424420	BE614743	Hs.146688	prostaglandin E synthase	MAPEG,SS,TM,MAPEG	20.7
	422645	L40027	Hs.118890	glycogen synthase kinase 3 alp	pkinase,SS,Ets	20.7
	436725	BE045223	Hs.136912	hypothetical protein MGC10796	ļ	20.4
	422098	H03117	Hs.111497	similar to mouse neuronal prot	TM	20.2
5	429556	AW139399	Hs.98988	ESTs	SS,pkinase,PMP22_Claudin	20.1
_	434068	AA977935	Hs.127274	ESTs	SS	20.0
	423767	H18283	Hs.132753	F-box only protein 2	F-box,SS,F-box,HORMA	19.9
	423652	AF052122	Hs.130712	Homo sapiens clone 23929 mRNA	ABC1,SS,PID,PID	19.8
	422179	AF091619	Hs.112667	dynein, axonemal, intermediate	WD40,SS	19.3
10	441356	BE384361	Hs.182885	ESTs, Wealty similar to JC5024	SS,TM,ank	18.5
10	418969	W33191	Hs.28907	hypothetical protein FLJ20258	SH3,SH3	17.2
	432631	H08379	Hs.165563	hypothetical protein DKFZp434N	TM,DnaJ,UBA,ArfGap,homeob	17.2
	439108	AW163034	Hs.6467	synaplogyrin 3	Synaptogyrin,SS,TM,PDZ,WD	17.2
	451643	M64437	Hs.234799	breakpoint cluster region	RhoGEF,RhoGAP,PH,C2	17.2
15	434518	H56995	Hs.37372	Homo sapiens DNA binding pepti	SS	16.9
15	413244		Hs.159265	kruppel-related zinc finger pr	SS,TM,BTB,Pep_M12B_propep	16.3
		AW955951 AW451623	Hs.109752	putative c-Myc-responsive	co,tato tot ch_atteb_proper	16.2
	456642 421612	AF161254	Hs.106196	8D6 antigen	ldl_recept_a,SS,TM	16.0
				prostate epithelium-specific E	Ets,SAM_PNT	15.7
20	456177	BE315042	Hs.19210	hypothetical protein MGC11308	EB,OANCI III	15.6
20	409261	U24266	Hs.77448	aldehyde dehydrogenase 4 famil	aldedh	15.6
	414837	024200	NS.//440	Target Exon	Band_41	15.4
	401278	A10044C2	Un 22450		SS S	15.4
	444804	A1084452	Hs.22158	hypothetical protein FLJ21988		15.1
25	406620	M81105	Hs.146550	myosin, heavy polypeptide 9, n	myosin_head,Myosin_tail,I	15.0
25	421495	A1583067	Hs.149152	ESTs, Weakly similar to RHOP M	22 22	15.0
	416893	AA455588	Hs.62406	hypothetical protein FLJ22573	SS,rm,SS	
	442620	C00138	Hs.8535	Homo sapiens mRNA for KIAA1668	SS,RNA_pol_K	14.9 14.6
	406901	M14624	11- 700rs	gb:Human 4-beta-galactosyltran	C4 debudees	
30	416006	AA324251	Hs.78950	branched chain keto acid dehyd	E1_dehydrog	14.6 14.4
30	455557	AW995839		gb:QV4-BN0044-110200-108-h07 B	Metallophos	
	416819	U77735	Hs.80205	pim-2 oncogene	pkinase,SS,TM,OTU,K_tetra	14.3
	444441	AW613841	Hs.301394	hypothetical protein MGC3101		14.0
	406918	M88357		gb:Homo sapiens DNA-binding pr	zf-C2H2,SS	14.0
25	407605	W03512	Hs.6479	hypothetical protein MGC13272	SS,Sema,pkinase,TIG,PSI,e	13.6
35	447304	Z98883	Hs.18079	phosphatidylinositol glycan, c	SS,Peptidase_C2	13.6
	402365			Target Exon	SS,SS,TM,ig	13.4
	407767	W15398	Hs.38628	hypothetical protein	SS,zf-CCCH	13.3
	432931	AF174487	Hs.293753	Bcl-2-related ovarian killer p		12.7
40	439233	AA831893	Hs.292767	hypothetical protein FLJ23109	zf-C3HC4,TM,Sulfate_trans	12.7
40	423801	NM_015071		GTPase regulator associated wi	RhoGAP,SH3,PH	12.6
	430397	AI924533	Hs.105607	bicarbonate transporter relate	HCO3_cotransp,SS,TM	12.6
	411570	BE144584	Hs.314341	ESTs		12.5
	400206		•	Eos Control	SS,SS,Glyco_tranf_43,COLF	12.3
4.5	457941	Al004525	Hs.14587	ESTs, Weakly similar to AF1518	SS,TM,SS,TM	12.2
45	412674	X04106	Hs.74451	calpain 4, small subunit (30K)	efhand,SS,CAP_GLY	12.0
	400460			C11002253*:gi 129091 sp P23267	SS,TM,SCAN,zf-C2H2,KRAB	12.0
	417595	AA424317	Hs.6259	KIAA1698 protein	SS,TM,Glyco_hydro_31,Glyc	11.6
	428758	AA433988	Hs.98502	CA125 antigen; mucin 16	SS	11.5
<b>~ ^</b>	424707	BE061914	Hs.10844	Homo sapiens cDNA FLJ14476 fis	SS,SS,TM,Sema	11.5
50	444359	A1697160	Hs.143594	ESTs, Weakly similar to HS4L_H		11.5
	435158 -	AW663317	Hs.65588	DAZ associated protein 1	rrm,SS,rrm	11.3
	407688	W25317	Hs.37616	Human D9 splice variant B mRNA		11.3
	450503	R35917	Hs.301338	hypothetical protein FLJ 12587	SS	11.2
	427448	BE246449	Hs.2157	Wiskott-Aldrich syndrome (ecze	WH1,PBD,WH2,SS	11.2
55	406230			Target Exon		11.2
	432143	AL040183	Hs.123484	Homo sapiens, clone IMAGE:4178	SS,TM,cys_rich_FGFR	11.2
	433573	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G	SS,TM,7tm_2,EGF,cadherin,	11.1
	413726 -	AJ278465	Hs.75510	annexin A11	annexin,SS,annexin	11.1
<b>C</b> D	431974	AW972689	Hs.200934	ESTs	bZIP	11.0
60	428167	AA770021	Hs.16332	ESTs	SS,ig,fn3	11.0
	450461	BE408081	Hs.46736	hypothetical protein FLJ23476	SS ·	10.9
	412738	N34731	Hs.74562	siah binding protein 1; FBP in	homeobox	10.9
	445434	BE391690	Hs.9265	hypothetical protein FLJ20917	SS,PWWP,Exonuclease,lipoc	10.9
	444008	BE544855	Hs.236572	ESTs, Weakly similar to SFR4_H	SS,SS,SAC3_GANP	10.7
65	444410	BE387360	Hs.33719	ESTs, Moderately similar to S6	SS	10.6
	444607	AW405635	Hs.293687	ESTs -	SS,PI-PLC-X,PH,PI-PLC-Y,C	10.6
	404333			C7001735*:gi]7768636[dbj]BAA95	vwd	10.5
	401210			C12000519:gi 7710046 ref NP_05		10.5
<b>~</b> ^	434743	Al363410		ribosomal protein S18	SS,TM	10.4
70	434030	AW162336	Hs.3709	low molecular mass ubiquinone-	SS	10.4
	450029	AW073380	Hs.267963	hypothetical protein FLJ10535	SS,Pyridox_oxidase,zf-C2H	10.4
	439632	AW410714	Hs.334437	hypothetical protein MGC4248	SS,TM,transmembrane4	10.3
	438185	Y19188	Hs.320461	ESTs	SS	10.2
75	432031	AF039196	Hs.272367	hairless protein (putative sin	jmjC	10.2
75	405371			NM_005569*:Homo sapiens LIM do	pkinase,LIM,PDZ	10.1
	456741	W37608	Hs.184492	ESTs	SS,pkinase	10.1
	458130	AA115811	Hs.6838	ras homolog gene family, membe	ras,arf	10.0
	456977	AK000252	Hs.169758	hypothetical protein FLJ20245		10.0
00	420029	BE258876	Hs.94446	polyamine-modulated factor 1	aldo_ket_red,SS,TM,gla	10.0
80	445625	BE246743		hypothetical protein FLJ22635	SS,TM	9.9
	423366	ZB0345	Hs.127610	acyl-Coenzyme A dehydrogenase,	Acyl-CoA_dh,Acyl-CoA_dh_M	9.8
	458216	AW024282	Hs.104938	hypothetical protein MGC15906		9.8
	451721		Hs.26915	spectrin, beta, non-erythrocyt	spectrin,PH,CH,SS,Peptida	9.7
	421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054	asp,SS,TM,ion_trans,K_tet	9.7
					259	
					Last 1	

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				The state of the state of	00 5111 5115	0.7
	431354	BE046956	Hs.251673	DNA (cytosine-5-)-methyltransf activating transcription facto	SS,PWWP,PHD bzip,ntp_transf_2,SS,TBC	9.7 9.7
	443780 448133	NM_012068 AA723157	Hs.73769	folate receptor 1 (adult)	Folate_rec,SS	9.7
	444202	AL031685	Hs.12785	KIAA0939 protein	SS,TM,Na_H_Exchanger,ABC2	9.7
5	427640	AF058293	Hs.180015	D-dopactirome tautomerase	MIF late_protein_L2,SS,GS	9.6
	419167	A1589535	Hs.94875	ESTs, Wealthy similar to A35363	SS	9.6
	424518	L29472	Hs.1802	major histocompatibility compl	TM,ig,MHC_II_beta,SS,TM,A	9.6
	427497 .	AW139476	Hs.31240	ESTs	cc	9.6 9.6
10	420423	AA827718	Hs.88218	ESTs, Moderately similar to JC	SS hexokinase2.hexokinase	9.6
10	414756 407893	AW451101 BE408359	Hs.159489 Hs.43621	Homo sapiens, Similar to hypot	SS,SS,arf,ras,fn3,ras	9.5
	408294	BE141732	113.40021	gb:QV0-HT0101-061099-032-e07 H	Ammonium_transp	9.5
	442232	AI357813	Hs.337460	ESTs, Wealdy similar to A47582	SS,TM,TGFb_propeptide,TGF	9.4
	416866	AA297356	Hs.80324	serine/threonine protein phosp	Metallophos, Metallophos	9.4
15	419823	AW271708	Hs.118918	ESTs, Wealthy similar to M2OM_H	SS,TM	9.4
	422625	AW504698	Hs.155976	culin 4B	SS,SS,Cuttin,Cuttin	9.3
	401264	1179700		C18000090*:gij6678656[ref]NP_0 qb:Human dynactin mRNA, partia	SS,laminin_Nterm,laminin_ SS,TM,HCO3_cotransp,CAP_G	9.3 9.2
	407507 400833	U73799		C11000890:gij3746443[gb]AAC639	SS,TM,7tm_1	9.2
20	422064	AW452589	Hs.335742	ESTs	TM	9.2
20	452434	D30934	Hs.29549	C-type lectin-like receptor-1	lectin_c,SS,TM	9.2
	421363	NM_001381	Hs.103854	docking protein 1, 62kD (downs	PH,IRS,TM,PH,IRS,trypsin,	9.1
	427397	AI929685	Hs.177656	calmodulin 1 (phosphorylase ki	efhand,RmaAD,SS,efhand	9.1
25	431462	AW583672	Hs.256311	granin-like neuroendocrine pep	SS PMA MATERIAL PM	9.0
25	434796	AA812046	Un 472774	ESTs	SS,myb_DNA-binding,myb_DN	9.0 9.0
	422639 447867	Al929377 Al525268	Hs.173724 Hs.164303	creatine kinase, brain ESTs	ATP-gua_Ptrans,ATP-gua_Pt TM	9.0
	442472	AW806859	115.101000	gb:MR0-ST0020-081199-004-c03 S	SS,TM,Inos-1-P_synth,Occl	B.9
	455588	Al129903	Hs.74669	vesicle-associated membrane pr	synaptobrevin,SS,TM	8.9
30	454319	AW247736	Hs.101617	ESTs, Weakly similar to T32527	SS	8.9
	429527	AA454184	Hs.289014	ESTs		8.9
	432603	AA554920	Hs.105794	UDP-glucose:glycoprotein gluco	SS,TM	8.9
	410338	W03445	Hs.38205	gb:za05g11.r1 Soares melanocyt	pkinase WD40	8.9 8.9
35	452833 407363	BE559681 AF035032	Hs.30736 Hs.181125	KIAA0124 protein gb:Homo sapiens clone MCA1L my	SS,ig,SS,G_gku_transpept	8.8
55	414413	BE294877	15.101123	gb:601174162F1 NIH_MGC_17 Homo	SS	8.8
	431765	AF124249	Hs.268541	novel SH2-containing protein 1	SH2,SS,TM	8.8
	421694	BE387430	Hs.106880	bystin-like		8.8
	453683	AL079854	Hs.118598	Homo sapiens mRNA for KIAA1878	SS	8.8
40	418736	T18979	Hs.87908	Snt2-related CBP activator pro	SS,helicase_C,AT_hook,SS,	8.7
	450958	AL137669	Hs.348012	Homo sapiens mRNA; cDNA DKFZp4		8.7 8.7
	419725	U66048 D60945	Hs.92683	Homo sapiens clone 161455 brea gb:HUM141D04B Clontech human f	SS,TM	8.7
	415126 406301	D00343		Target Exon	TM	8.6
45	418843	AJ251016	Hs.89230	potassium intermediate/small c	TM,CaMBD,SK_channel,TM	8.6
	433396	A1742071	Hs.133205	ESTs	SS,TM	8.6
	434333	AA186733	Hs.292154	stromal cell protein		8.6
	407065	Y10141		gb:H.sapiens DAT1 gene, partia	SNF,SS,TM	8.6
50	452851	AW173191	Hs.213117	ESTs	SS,Sema RhoGEF	8.6 8.6
50	422418 447859	AK001383 AK002194	Hs.116385 Hs.19851	hypothetical protein FLJ10521 peroxisomal biogenesis factor	NIOGEF	8.6
	420836	AW958453	Hs.204959	hypothetical protein FLJ 14886	SS.ras ·	8.6
	429099	BE439952	Hs.196177	phosphorylase kinase, gamma 2	pkinase,SS,SNF2_N,helicas	8.6
	419639	AK001502	Hs.91753	hypothetical protein	·	8.6
55	429712	AW245825	Hs.211914	ENSP00000233627*:NADH-ubiquino	oxidored_q6,SS,TM,rrm	8.5
	452554	AW452434	Hs.58006	ESTs, Weakly similar to ALU5_H	SS,PAS,HLH	8.5
	441076	N49809	Hs.11197 Hs.194301	Homo sapiens, clone IMAGE:3343	14	8.5 8.5
	428860 421901	U38291 AB014554	Hs.109299	microtubute-associated protein protein tyrosine phosphalase,	M SAM,SS,TM,rrm,PDZ	8.4
60	441363	AW450211	Hs.126825	ESTs, Weakly similar to A46302	SS,TM,HSP20,7tm_1	8.4
• •	443801	AW206942	Hs.253594	intron of: trichorhinophalang	GATA	8.4
	432862	AW004958	Hs.236720	amnionless protein	SS,MATH,zf-TRAF,zf-C3HC4	8.4
	431849	Al670823	Hs.85573	hypothetical protein MGC10911	SS,TM	8.4
65	423662	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc	SS SS	8.3 8.3
05	404365	1151222	Un 150227	Target Exon hexokinase 3 (white cell)	hexokinase,hexokinase2,he	8.3
	425694 423098	U51333 AA321980	Hs.159237 Hs.204682	ESTs	nexora asome sources	8.3
	434552	AA639618	Hs.325116	Homo saplens, clone MGC:2962,	SS	B.2
	418361	AW505368	Hs.12460	gb:UI-HF-BN0-atu-d-03-0-UI.r1		8.2
70	·427433	D82070	Hs.177972	chromosome 4 open reading fram	SS,pkinase	8.2
	420138	BE268854	Hs.177729	ESTs	SS	8.2
	426391	AW161050	Hs.169611	second milochondria-derived ac	SS	8.1 8.1
	457613 427502	AA598869 AI811865	Hs.173770 Hs.7133	ESTs Homo sapiens, clone IMAGE:3161	SS,TM,ABC_tran,Glyco_tran	8.1
75	427502 437215	AL117488	1 10.7 100	Human clone 23564 mRNA sequenc	SS	8.1
	423384	AL133632	Hs.127808	Homo sapiens mRNA; cDNA DKFZp4	<del></del>	8.1
	447151	AI022813	Hs.92679	Homo sapiens clone CDABP0014 m	SS,TM,LRR,aminotran_1_2	8.0
	431898	AK000020	Hs.272018	hypothetical protein FLJ20013		8.0
00	454291	AW384847	Hs.213534	ESTs, Weakly similar to MUC2_H	SS,XRCC1_N,BRCT,lactamase	8.0
80	430354	AA954810	Hs.239784	human homolog of Drosophila Sc	SS,TM,ig	0.8 0.8
	459302 422766		Hs.36566	LIM domain kinase 1	BIRTK,SS,TM	8.0
	422765 425944	AW409701 AK000664	Hs.1578 Hs.164256	baculoviral IAP repeal-contain hypothetical protein FLJ20657		7.9
	450873	BE464016	Hs.238956	ESTs -	SS,zI-C2H2,rm	7.9
					260	

	AEADAC	ANAMACAGE	U. 6006	ESTs		70
	454246 450635	AW245185 AW403954	Hs.6996 Hs.25237	mesenchymal stem cell protein	4HBT	7.9 7.9
	422305	AI928242	Hs.293438	ESTs, Highly similar to AF1984	SS	7.9
_	425760	D17629	Hs.159479	galactosamine (N-acetyl)-6-sul	Sulfatase, SS, TM	7.9
5	413534	BE146961	11- 04007	gb:QV4-HT0222-011199-019-b12 H	SS,TM	7.8
	446931 421726	Al348856 AK001237	Hs.21627 Hs.319088	gb:tb05a05.x2 NCI_CGAP_Lu26 Ho hypothetical protein FLJ10375	TM	7.8 7.8
	427461	AA531527	Hs.332040	hypothetical protein MGC13010	SS,TM,ACAT,LRR	7.8
	448993	AI471630		KIAA0144 gene product		7.8
10	443136	NM_001440		exostoses (multiple)-like 3	Exostosin, SS, TM	7.8
	427725	U66839	Hs.180533	mitogen-activated protein kina	pkinase	7.8
	400923 419757	AA773820	Hs.63970	Target Exon ESTs	SS,TM,DUF289 SS,TM	7.8 7.8
	458834	Al566883	Hs.196446	ESTs	50,1.11	7.8
15	427899	AA829286	Hs.332053	serum arnyloid A1	SS,SAA_proteins,SS,SAA_pr	7.7
	452399	BE513301	Hs.29344	hypothetical protein, clone 24	SS, perilipin	7.7
	436543	NM_002212	Hs.5215 Hs.301696	Integrin beta 4 binding protei	eiF6	7.7 7.7
	431811 414534	AB040972 BE257293	Hs.76366	hypothetical protein FLJ11560 BCL2-antagonist of cell death	SS,TM,Band_7,AAA,cdc48_N, SS,hormone_rec,zf-C4	7.7
20	455885	BE153524		gb:PM0-HT0339-241199-002-C03 H	SS_pkinase	7.7
	427721	AI582843	Hs.180455	RAD23 (S. cerevisiae) homolog	ubiquitin,UBA,integrin_B,	7.6
	430432	AB037758	Hs.241419	KIAA1337 protein	TM,Patched,TM	7.6
	427273 450334	AW139032	Hs.107376	hypothetical protein DKFZp434N	SS,SS,TM PAP2,SS	7.6 7.6
25	413564	AF035959 BE260120	Hs.24879	phosphatidic acid phosphatase gb:601146990F1 NIH_MGC_19 Homo	FAF255	7.6
	410397	AF217517	Hs.63042	DKFZp564J157 protein	SS,homeobox,UPF0160,DUF23	7.6
	439539	BE348395	Hs.121589	ESTs	SS,Fork_head	7.5
	400286			C16000922:gij7499103[pir][T209	TM,ABC_tran,ABC_membrane	7.5
30	416472	AA180756	Hs.340316	ESTs, Moderately similar to AL	zf-C2H2	7.5
50	418641 419492	BE243136 AA243547	Hs.86947 Hs.19447	a disintegrin and metalloprote PDZ-LIM protein mystique	disintegrin,Reprolysin,Pe LIM,SS,SH3,Sorb,Metalloph	7.5 7.5
	420970	AA305079	Hs.1342	cytochrome c oxidase subunit V	COX5B	7.5
	406495			Target Exon	SRCR,TM,Acetyltransf	7.5
25	448043	AJ458653	Hs.201881	ESTs	PHD	7.4
35	401724	1477040	Hs.1757	C16001374:gij6755086[ref]NP_03	TM,PLAT,SS	7.4
	424263 428092	M77640 . AW879141	กร.เกลเ	L1 cell adhesion molecule (hyd ESTs	fn3,ig,lRK,SS,TM,fn3,ig,R SS,TM	7.4 7.3
	453023	AW028733	Hs.31439	serine protease inhibitor, Kun	Kunitz_BPTI,SS,TM,ion_tra	7.3
40	400137			Eos Control		7.3
40	436127	W94824	Hs.11565	RIKEN cDNA 2010100012 gene	Corona_7,SS,TM	7.3
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	UPP_synthetase,HMG14_17	7.3
	432747 448859	NM_014404 BE272446	Hs.278907 Hs.265317	calcium channel, voltage-depen hypothetical protein MGC2562	PMP22_Claudin,SS,TM,PMP22 SS,TPR	7.3 7.3
	407619	AL050341	Hs.37165	collagen, type IX, alpha 2	SS,Collagen,SS,Collagen	7.3
45	429299	A1620463	Hs.347408	hypothetical protein MGC13102	SS,TM,gla	7.3
	401674	*******	11 4=0400	C16001417*:gi[7500345[pir]]T21	FAD-oxidase_C,FAD_binding	7.2
	412289 424198	AW935967 AB029010	Hs.170162 Hs.143026	KIAA1357 protein KIAA1087 protein	SS SS,TM,Na_Ca_Ex,Catx-beta,	7,2 7.2
	412173	T71071	115.145020	gb:yc50b05.r1 Stratagene liver	CPSase_L_chain	7.2
50	438113	AI457908	Hs.8882	ESTs	SS,TM,7tm_1	7.2
	429869	AI907018	Hs.15977	Target CAT	-m	7.2
	439963	AW247529	Hs.6793	platelet-activating factor ace ESTs	PAF-AH_lb,Lipase_GDSL,SS,	7.2
	425041 448340	Al377150 Al492910	Hs.150914 Hs.32362	ESTS	SS	7.2 7.1
55	406779	AA412048	Hs.279574	CGI-39 protein; cell death-reg	SS,SS	7.1
	431005	AA490544	Hs.127269	ESTs, Weakly similar to T02345	WD40	7.1
	421273	AJ245416	Hs.103106	U6 snRNA-associated Sm-like pr	Sm,SS,tRNA-synt_1,GST_C,G	7.1
	409649 430281	AA159216	Hs.55505	hypothetical protein FLJ20442	Y_phosphatase,DSPc,TM mito_carr,SS,TM	7.0 7.0
60	430201 444672	A1878842 Z95636	Hs.237924 Hs.11669	CGI-69 protein laminin, alpha 5	laminin EGF.laminin G.EGF	7.0 7.0
•	405928			Target Exon	SS,cystatin,Coprogen_oxid	7.0
	421321		Hs.103502	glutamic-pyruvate transaminase	aminotran_1_2,SS,TM,LRR	6.9
	439905	AW799755	Hs.110953	relinoic acid induced 1	HLH	6.9
65	451937 426675	AF119664 AW084791	Hs.27299 Hs.133122	transcriptional regulator prot hypothetical protein FLJ14524	SS,integrin_B,fn3,Catx-be SS,TM,aminotran_1_2	6.9 6.9
05	438627	AI087335	Hs.123473	ESTs	TM,Reticulon	6.9
	438951	U51336	Hs.6453	inositol 1,3,4-triphosphate 5/	SS,oxidored_nitro,SS	6.8
	421758	BE397336	Hs.1422	Gardner-Rasheed feline sarcoma	SH2,SH3,pkinase	6.8
70	423228	AL137491	Hs.125511	Homo sapiens mRNA; cDNA DKFZp4	SS,TM,sushi	6.8
70	405346 432746	AA564512	Hs.24301	Rag C protein polymerase (RNA) II (DNA direc	RCC1 SS,TM,EF1BD	6.8 6.8
	452798	AI918771	Hs.257170	ESTs	SS,TM,TNFR_c6	6.7
	426315	AA854219	Hs.348137	Homo sapiens, clone IMAGE:3542	SS,crystall	6.7
75	440317	BE561888		gb:601346093F1 NIH_MGC_8 Hamo		6.7
75	438857	A1627912	Hs.130783	Forssman synthetase	SS,RA,RasGEF,RasGEFN	6.7
	452072 433938	BE258857 AF161536	Hs.27744 Hs 284292	RAB3A, member RAS oncogene fam	ras,arf,SS,PDEase TM	6.7 6.7
	433938 423106	AF161536 N52572	Hs.284292 Hs.13702	ubiquinol-cytochrome c reducta ESTs, Moderately similar to AL	1 144	6.7 6.7
	453101	AW952776	Hs.94943	ESTs	TM	6.7
80	420307	AW502869	Hs.66219	ESTs	SS,TM	6.7
	415056	AB004662	Hs.77867	adenosine A1 receptor	7tm_1,SS,TM	6.7
	454262	AW612232	Hs.254835	ESTS	SS,TM,voltage_CLC,CBS	6.7 6.6
	409227 413908	AA806165 BE409966	Hs.130323 Hs.323813	Homo sapiens, clone IMAGE:3960 Homo sapiens, clone MGC:2867,	SS,zI-C2H2	6.6
						-14
					261	

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	457274	AW674193	Hs.227152	mannan-binding lectin serine p	SS,TM,SS,TM,Ctathrin_lg_c	6.6
	419157 431424	AA234540 AI222969	Hs.23871	ESTs ESTs	pkinase SS	6.6 6.6
	412464	T78141	Hs.22826	ESTs, Weakly similar to I55214	SS,cadherin,crystall	6.6
5	430168	AW968343		DKFZP434I1735 protein	SS,TM,efhand,efhand	6.6
	455035	AW851734	11-04040	gb:MR2-CT0222-011199-007-e10 C	00 TH 05 4 D L	6.6
	422682 453367	W05238 AW732847	Hs.94316 Hs.70573	ESTs, Weakly similar to T31613 PKCI-1-related HIT protein	SS,TM,DEAD,helicase_C,Lam SS,TM	6.6 6.6
	450593	AF129085	Hs.25197	STIP1 homology and U-Box conta	TPR,SS,TM,Rhomboid,lactam	6.6
10	420319	AW406289	Hs.96593	hypothetical protein .	ras,arf	6.6
	431131	NB4730	Hs.250616	isocitrate dehydrogenase 3 (NA	isodh,isodh	6.6
	431297 410082	AA651771 AA081594	Hs.3076 Hs.158311	ESTs Musashi (Drosophila) homolog 1	SS,HECT,phoslip	6.6 6.5
	441307	AW071696	Hs.209065	hypothetical protein FLJ14225	SS,TM	6.5
15	454582	AW816029		gb:MR3-ST0220-151299-027-b10 S	filament	6.5
	407299	AA460205	Hs.289770	ESTs, Weakly similar to 138022	7- 400 TH7- 4	6.5
	422837 407722	U25441 BE252241	Hs.121478 Hs.38041	dopamine receptor D3 pyridoxal (pyridoxine, vitamin	7tm_1,SS,TM,7tm_1 pfkB,SS .	6.5 6.4
	417810	D28419	Hs.82609	hydroxymethylbilane synthase	Porphobil_deam	6.4
20	445333	BE537641	Hs.44278	hypothetical protein FLJ12538	SS	6.4
	402197 419390	AI701162	Hs.90207	Target Exon	SS,TM,ATP1G1_PLM_MAT8,ig,	6.3 6.3
	447754	AW073310	Hs.163533	hypothetical protein MGC11138 intron of HER4	SS,TM,PMP22_Claudin,PMP22	6.3
05	444664	N26362	Hs.11615	map kinase phosphatase-like pr	DSPc,Rhodanese,SS,TM	6.3
25	421190	U95031	Hs.102482	mucin 5, subtype B, tracheobro	Cys_knot,vwc	6.3
	432872 430023	A1908984 AA158243	Hs.279623 Hs.227729	selenoprotein X, 1 FK506-binding protein 2 (13kD)	DUF25,SS,Ribosomal_L3,FDZ SS,FKBP,SS,PDGF,C2,Pi-PLC	6.3 6.3
	413343	BE392026	Hs.334346	hypothetical protein MGC13045	SS,DnaJ	6.2
20	417852	AJ250562	Hs.82749	transmembrane 4 superfamily me	transmembrane4,SS,TM	6.2
30	403128 413055	AVECE301	U. 75102	KIAA1033 protein	SS,TM,tubulin,EGF,F5_F8_t	6.2
	427812	AV655701 AA770424	Hs.75183 Hs.98162	cytochrome P450, subfamily IIE ESTs	p450 SS	6.2 6.2
	457761	AW401809	Hs.4779	KIAA1150 protein	SS,UM,SS	6.2
35	453099	H62087	Hs.31659	thyroid hormone receptor-assoc	SS	6.2
33	426048 407223	Al768853 H96850	Hs.134478	ESTs gb:yw03b12.s1 Soares melanocyt	TM SS,TM,SS,TM,DDOST_48kD	6.2 6.2
	445634	AI624849	Hs.344612	ESTs, Weakly similar to NEL1_H	vwd	6.2
	441197	BE244638	Hs.166	sterol regulatory element bind	HLH	6.1
40	421707 435750	NM_014921 AB029012	Hs.107054 Hs.4990	lectomedin-2 KIAA1089 protein	Latrophilin,OLF,7tm_2,Gal SS,TM	6.1 6.1
. •	432353	NM_016558		SCAN domain-containing 1	SCAN	6.1
	427326	AI287878		gb:qv23f06.x1 NCI_CGAP_Lym6 Ho	SS,TM,7tm_1,SS,TM	6.1
	447128 419444	AI271898 NM_002496	Hs 90443	cyclin K Target CAT	fer4,SS,TM,V_ATPase_sub_a	6.1 6.1
45	457978	AA776638	16.50710	gb:ae78g04.s1 Stratagene schiz	SS,PH,IQ,RasGEF,RasGEFN,R	6.1
?	410445	AA199830	11	gb:zq75h01.r1 Stratagene hNT n		6.1
	431857 407143	W19144 C14076	Hs.271742 Hs.332329	ADP-ribosyltransferase (NAD; p EST	PARP,PARP_reg,SS,TM,Pepti SS,TM	6.1 6.0
	408724	AI685842	Hs.294143	ESTs, Weakly similar to T22914	SS,pkinase,tubulin	6.0
50	436685	W28661	Hs.5288	Homo sapiens mRNA; cDNA DKFZp4	SS,TM,pkinase,Activin_rec	6.0
	441583 418802	Al791499 AB028989	Hs.205742 Hs.88500	ESTs, Weakly similar to ALUA_H milogen-activated protein kina	WD40,Pico_P2A,M,SS	6.0 6.0
	414927	T83587	Hs.186476	ESTs	SS,Sulfatase	6.0
<i></i>	434314	BE392921	Hs.3797	RAB26, member RAS oncogene fam	ras,arf,SS	6.0
55	414157	BE297801	Hs.103845	ESTs, Moderately similar to I5	SS	6.0
	424415 406487	NM_001975	ris. 140300	enolase 2, (gamma, neuronal) Target Exon	enolase, SS, Atrophin-1, Atr SS, TM	6.0 6.0
	447365	BE383676	Hs.334	Rho guanine nucleotide exchang	SH3,PH,RhoGEF	6.0
60	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20,	WD40,SS,TM,fn3,EGF,fn3,ig	6.0
UU	442297 426440	NM_006202 BE382756	Hs.169901 Hs.169902	phosphodiesterase 4A, cAMP-spe solute carrier family 2 (facil	PDEase sugar_tr,SS,TM,sugar_tr	5.9 5.9
	418256	AW845318	Hs.12271	f-box and leucine-rich repeat	SS,SS,TM,HSF_DNA-bind	5.9
	431543	AW969619	Hs.259768	adenylate cyclase 1 (brain)	TM	5.9
65	430344 428539	AA476827 AW410063	Hs.171012 Hs.184877	hypothetical protein FLJ22349 solute carrier family 25 (mito	HLH mito_carr,SS,TM,profilin,	5.9 5.9
05	403938	ATTIOOS	113.104077	Target Exon	Ephrin	5.9
	456950	AF111170	Hs.306165	Homo sapiens 14q32 Jagged2 gen	SS,TM,DSL	5.9
	451481	AA300228	Hs.295866 Hs.3828	hypothetical protein DKFZp434N	CUMP Manage OC THE	5.9
70	434357 443553	AW732284 AL040535	Hs.9573	mevalonate (diphospho) decarbo ATP-binding cassette, sub-fami	GHMP_kinases,SS,TM ABC_tran,SS	5.9 5.9
	433333	AI016521	Hs.71816	v-akt murine thyrnoma vtral onc	homeobox.pkinase,PH.pkina	5.9
	430600	AW950967	Hs.274348	HLA-B associated transcript-3	ubiquitin,SS,TM,G-patch,a	5.9
	409034 421542	Al684149 AA411607	Hs.172035 Hs.118964	hypothetical protein similar t ESTs, Weakly similar to KIAA11	SS SS,SS	5.9 5.9
75	431534	AL137531	Hs.258890	Homo sapiens mRNA; cDNA DKFZp4	SS,TM,ras	5.9
	409608	AF231023	Hs.55173	cadherin, EGF LAG seven-pass G	SS,TM,7tm_2,cadherin,GPS,	5.9
	423464 422379	NM_016240 AA932860	Hs.133864	CSR1 protein ESTs	Collagen, SS	5.9 5.8
00	443887	NM_004729	Hs.9933	Ac-like transposable element	zf-BED	5.8
80	450122	BE313765	Hs.343443	ESTs, Weakly similar to 138022	SS,TM,Y_phosphatase,LON,A	5.8
	404807 445303	AW362198	Hs.12503	Target Exon interleukin 15 receptor, alpha	UPF0027 SS,sushi,SS	5.8 5.8
	445631	AK001822		Homo sapiens cDNA FLJ 10960 fis		5.8
	412091	R06185		gb:ye94d03.r1 Soares fetal liv	SS,TM,IBR,IBR	5.8
					262	

Message   March   Ma							
COURT   COUR		446536	W74413	Hs.15251	hypothetical protein	SS	5.8
13944   EBESISD   Halfield   EDESISD   Halfield			BE395875	H5.279009	ENCONDECTOR TO THE PROPERTY OF		
5			00001000	Un 61622			
Comparison	5						
49133   U40943   Be.5855   Florent End   F	,		AVYJUJUGJ	HS.333141			
Add			1140343	He 29656			
10   41197   AWS32917   AWS3291			040040	113.23000			
10 411219 AW032917 420077 AW001476 Hs. 306122 cyllenous pages cDNA FLI 14216 fs. 140072 Hs. 13092 Hs. 1309			RE083422	Hs.56851			
### ### ### ### ### ### ### ### ### ##	10						
440672				Hs.306122		TM.Steroid_dh.SS	
467579							
15		416759	AK000978	Hs.79741			5.7
444655 4269281 ks.12984 fs.16505 bypothetical profesh 1220512 st.16107797 al. 18.10505 bypothetical profesh 1220512 st.1610787 al. 18.10505 bypothetical profesh 1220512 st.1610787 al. 18.10505 bypothetical profesh 1220512 st.1610787 bypothetical profesh 1220512 st.1610787 bypothetical profesh 1221478 bypothetical profesh 1221478 st.161078 bypothetical profesh 1221478 bypothetical profesh 12		446562	BE272686	Hs.15356	hypothetical protein FLJ20254	hormone,SS,pfkB	5.7
421543 AMAPISS HS. 158216 hypothetical protein FLUZ0512 TM (47141 HS.163215) hypothetical protein FLUZ0512 TM (47141 HS.263215) hs. 31097 hs. 3	15						
407757							
419125							
477141   May							
48805 AV65783 Hs.661 Terpet CAT 480787 AB06199 Ls.25476 482967 AB06199 Ls.278311 ploted B1 Seria, AB06199 Ls.278311 ploted B1 Seria, AB06199 Ls.278311 ploted B1 Seria, AB07876 Hs.18799 EST6 482761 AB07876 Hs.18799 EST6 482761 AB07876 Hs.127831 ploted B1 Seria, AB07876 AB07876 Hs.12783 ploted B1 Seria, AB07876 AB0	20						
450787	20					55,1M,GlyCOS_trailsi_4	
432496						ARD SO TM	
Add						1411 100, 1141	
25         42708 41742         A81017430 A17520         Hs. 118234 Hs. 126039         Hs. 126239 Hs. 278911 Hs. 126039         Hs. 126239 Hs. 278929 Hs. 278929 Hs. 126039         Hs. 126239 Hs. 126039         Hs. 126239 Hs. 126039 Hs. 126039 Hs. 126039 Hs. 126039         Hs. 126239 Hs. 126039 Hs. 126039						Sema PSI TIG SS TM TIG Se	
417412	25						
432761 A-152099 K-5.279911 interleukin 17C   SS   S.   43204 BE018302 H-5.2894   St.   434161 BE018302 H-5.2894   St.   434161 BE018302 H-5.2894   St.   434161 BE018302 H-5.2146   M.A./176 protein   Sc.   434161 BE018302 H-5.2146   M.A./176 protein   Sc.   434161 BE018302 H-5.2146   M.A./176 protein   Sc.   434161 MAY-9126 H-5.21045   M.A./176 protein   Sc.   434161 MAY-9126 H-5.2004   M.A./176 protein   Sc.   43720 MAY-9126 H-5.2004   M.A./176 protein   Sc.   43333 AFB6161 H-5.14610   M.A./176 protein   M.A./176 protein   Sc.   435271 MAY-9126 H-5.17918   M.A./176 protein   M							
454151						SS .	5.7
ASSIST   ASSISTED   ASSISTED   ASSIST					placental growth factor, vascu	PDGF,SS	5.7
417677   M., 0.01605   H. 8.2399   H. 9.1603   H. 9.1603   H. 9.1604   H. 9.		454151	AA047169	Hs.154088	hypothetical protein FLJ22756	SS,TM,Gtycos_transf_4	
451558 MM_001089 Hz_26530 APR-binding cassella, sub-famil hypothetical protein F-L13710 Aprox 471933 APR-binding cassella, sub-famil hypothetical protein F-L13710 Sp. 471934 APR-binding cassella, sub-famil hypothetical protein F-L13710 Sp. 471934 APR-binding protein F-L13710 Sp. 471934 APR-binding cassella, sub-famil hypothetical protein familiance for superior variety of sprotein familiance for superior variety of sup	30					SS,DIX,PDZ,DEP,Dishevelle	
49755 AV769126 Hs.170345 hs.140272 ESTs, Weakly similar to AUU_H Shinbon, histome 5.6 store 2.00 protein FL111808 spt. Dr. K72p-34M116_11 434 (synony C1600161-4-g71801278]emb)CAS1 5.6 store 5.6 store 2.00 protein FL111808 spt. Dr. K72p-34M116_11 434 (synony C1600161-4-g71801278]emb)CAS1 5.6 store 3.0 stor							
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43943	35						
459271	33					DZIP,35,AIIPC-13A	
401699 447877 U73727 Hs. 19718 profeln prospin phosphatase, profeln prospin phosphatase, profeln profe				(15.114011		SS PI3 PM kinasa PI3Ka	
40			AD-10304			00,110_111_001000;110100	
499125			U73727	Hs.19718		Y phosphatase.fn3.ig.MAM.	
450437	40						
415514							5.6
455 421678 AA19008 Hs.106730 422472 R59096 Hs.279329 rd.10chondrial carrier hornolog 414918 AI219307 Hs.72222 hypothetical protein FL113459 41496 Bet40573 Hs.2323636 hs. 106830 414757 U46922 Hs.77252 436014 AF281134 Hs.283414 Hs.28451 AI70210 Hs.14582 Hs.283414 Hs.28451 AI703414 Hs.244349 hs.244			F11301	Hs.138329		SS,TM	5.6
42972 R59096 Hs. 108730 chromosome 22 open reading fra milochondrial carrier homology 42972 (Asylos) BE410573 Hs. 223336 homo saplens, clone IMAGE:4063 HIT 5.6 miloc carr 5.6 milochondrial carrier homology 85, TM, EM, effand 5.6 miloc carr 5.6 milochondrial carrier homology 85, TM, effand 5.6 miloc carr 5.6 milochondrial carrier homology 85, TM, effand 5.6 miloc carr 5.6 milochondrial carrier homology 85, TM, effand 5.6 miloc carr 5.6 milochondrial carrier homology 85, TM, effand 5.6 miloc carr 5.5 miloc carr 5.6 miloc carr 5.6 miloc carr 5.6 miloc carr 5.5 miloc carr 5.6 miloc carr 5.5 miloc carr 5.6 miloc carr 5.5 miloc carr 5		437926	BE383605	Hs.300816	small GTP-binding protein	SS,TM,TPR	
42/472	4.5						
A14918   A1219207   Hs.72222   hypothetical protein FLJ13459   SS,TM_ehand   5.6	45						
143906   BE410573   Hs. 283636   Homo saplens, clone IMAGE:4063   SS,TM,Exo_endo_phos,BNR,A   5.6   Hs. 77752   Hs. 283741   Hs. 168890   Hs. 24349   Hs. 245874   Hs. 168890   Hs. 24349   Hs. 14552   Hs. 14552   Hs. 14552   ESTs   Wilson saplens clone 23771 mRNA   5.6   Homo saplens clone 23771							
\$\frac{41757}{45614}							
436014         AF2B1134         Hs.283741         exosome component Rrp46         RNase_PH_C,SS,TG         5.6           421896         AF035306         Hs.106890         Homo sapiens chore 23771 mRNA         5.5           445871         AVI035771         Hs.244349         Hs.145862         ESTs_Weakly similar to FOR4 M         SS,TM_efhand_efhand         5.5           55         429720         M79091         Hs.20378         KIAA1115 protein         SS,TM_phosphalase         5.5           4329720         M79091         Hs.232770         KIAA1115 protein         SS,TM_phosphalase         5.5           4329720         M79091         Hs.227770         KIAA1115 protein         SS,TM_phosphalase         5.5           4329720         M79091         Hs.227870         KIAA1115 protein         SS,TM_phosphalase         5.5           432333         BE248021         Hs.278767         ESTs         SS,TM_hillpoxygenase J         SS,TM_phosphalase         5.5           406244         Hs.278362         Hs.278362         Hs.278362         SSTs, Hillpoxygenase J         SS,TM_Na.sulph_symp         5.5           408215         BE614290         Hs.278362         Hs.278362         SS,TM_HILL,TRM_zHCCCH         5.5           422013         N92696         Hs.293354 <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>							
421696 APU35701 Hs.106890 Homo sapiens clone 23771 mRNA 5.5 408015 AW135771 Hs.244349 epidermal differentiation comp 4557 Hs.16877 Hs.244349 epidermal differentiation comp 5.5 445871 A/702901 Hs.145582 ESTs, Weakly similar to FOR4 M SS,TM, phosphalase 5.5 425098 AW295349 Hs.8038 ESTs SS,TM 5.5 429720 M79091 SS3898 AW003512 Hs.232770 arachidonate lipoxygenase 3 SS,TM, lipoxygenase, PLAT, 5.5 449225 R39108 Hs.1067 ESTs SS,TM SS,TM, sulph_symp 5.5 449225 BE614290 SSTS, Hghly similar to T46395 SS,TM, lipoxygenase, PLAT, 5.5 406244 SS, EBE614290 SS, STM, lipoxygenase, PLAT, 5.5 40624 SS, STM, lipoxygenase,	50						
408015   AW135771   Hs. 244349   epidermal differentiation comp   445871   A7702901   Hs. 145582   ESTs, Weakly similar to FOR4 M   SS,TM,ehand,efinand   5.5	-					14(20) 14(4(20) 11(0) 00)	
445871							
42598         AW295349         Hs.8038         ESTs         SS,TM         5.5           429720         M79091         Hs.232770         gb:EST01239 Subtracted Hippoca         arachidonate lipoxygenase 3         SS,TM,Ipoxygenase,PLAT,s         5.5           48225         R39108         Hs.5777         ESTs         SS,TM,Na_sulph_symp         5.5           43233         BEC38302         Hs.278352         ESTs, Highly similar to T46395         SS,TM,AAA,Ribosomal_L2         5.5           408215         BE614290         male-enhanced antigen         SS,TM,AAA,Ribosomal_L2         5.5           408244         Al803516         Hs.272891         Hs.293354         SS,Ethand,TGF-beta,TGFb_p         5.5           422013         N92696         Hs.1293616         Hs.129616         ESTs         SS,TM,ADUF60,trypsin,CUB,u         5.5           427859         AA416856         Hs.98170         ESTs         SS,TM,DUF60,trypsin,CUB,u         5.5           437654         BE337032         Hs.12765         Hs.18765         Hs.18765         SS,TM,DUF60,trypsin,CUB,u         5.5           447451         AVR46456         Hs.98170         Hs.18765         Hs.18765         SS,TM,SS,TM,Synaptobrev         5.4           419376         R43144         Hs.217765 <t< td=""><td></td><td>445871</td><td>Al702901</td><td>Hs.145582</td><td>ESTs, Weakly similar to FOR4 M</td><td>SS,TM,efhand,efhand</td><td>5.5</td></t<>		445871	Al702901	Hs.145582	ESTs, Weakly similar to FOR4 M	SS,TM,efhand,efhand	5.5
429720   M79091   453898   AW003512   Hs.232770   439225   R39108   Hs.6777   ESTs   ESTs   SS,TM,Na_sulph_symp   5.5		411813	NM_014931	Hs.72172	KIAA1115 protein	SS,TM,Y_phosphatase	5.5
453898 AW003512 Hs.232770 arachidonate lipoxygenase 3 SS,TM,lipoxygenase,PLAT,s S.5 449225 R39108 Hs.6777 ESTs SS,TM,Na_sulph_symp 5.5 SS,TM,SS,TM,Na_sulph_symp 5.5 SS,TM,Na_sulph_symp 5.5 SS,TM,Na_	55.	425098	AW295349	Hs.8038	ESTs	SS,TM	
Add							
A2233							
A32538   BE258332   Hs.278362   male-enhanced antigen   SS,TM,AAA,Ribosomal_L2   S.5						SS, IM, Na_sulpn_symp	
408215	60					CC TM AAA Gibocomol 1.2	
406244	UU			NS.210002			
A36041   A1803516   Hs.272891   hippocatcin-like protein 4   SS.efhand,TGF-beta,TGFb_p   5.5			DE014230			COLOUR HIGHWAY IN STREET COURT	
65         422013         N92696         Hs.293354         ESTs         SS,TM         5.5           427859         A4368080         Hs.129616         ESTs         SS         5.5           427859         A4416856         Hs.98170         ESTs         SS,TM,DUF60,trypsin,CUB,u         5.5           435540         BE397032         Hs.14468         hypothetical protein MGC14226         SS,TM,DUF60,trypsin,CUB,u         5.5           427747         AW411425         Hs.180655         serine/threonine kinase 12         pkinase,SS,TM,synaptobrev         5.4           431630         NM_002204         Hs.26829         Integrin, alpha 3 (antigen CD4         integrin_AFG-GAP,Rhabd_g         5.4           419576         R43144         Hs.21919         ESTs         TM         5.4           447374         AF263462         Hs.18376         KIAA1319 protein         SS,Myosin_tail,M         5.4           431275         T56571         Hs.10041         ESTs         SS,HLH         5.4           404343         BE299671         Hs.16219         wingless-type MmTV integration         SS,Myosin_tail,M         5.4           421779         Al879199         Hs.108219         wingless-type MmTV integration         SS,mt,SS         5.4           <			AI803516	Hs.272891		SS.efhand.TGF-beta.TGFb p	
65 427659 AA416856 Hs.98170 ESTs SS,TM,DUF60,trypsin,CUB,u 5.5 427859 AA416856 Hs.98170 ESTs SS,TM,DUF60,trypsin,CUB,u 5.5 435540 BE397032 Hs.14686 hypothetical protein MGC14226 SS,TM 47747 AW411425 Hs.180655 serine/Itreordine kinase 12 pkinase,SS,TM,synaptobrev 5.4 41456 Al458911 Hs.127765 ESTs 5.4 145976 R43144 Hs.21919 ESTs TM 415976 R43144 Hs.21919 ESTs TM 415976 R43144 Hs.21919 ESTs SS,Myosin_tail,M 5.4 421775 T56571 Hs.10041 ESTs SS,HUH 5.4 404343 C7002191*:gijS053028 gb AAD388 SS,BU,H 5.4 421779 Al879159 Hs.108219 wingless-type MMTV integration 2S,wnt,SS 5.4 418678 MM_001327 Hs.167379 cancer/testis antigen (NY-ESO SS,TM,zF-C2H2 5.4 418678 NM_001327 Hs.263310 uracil-DNA glycosytase 2 417193 Al922189 Hs.28839 ybrg0festical protein FLJZ2795 SS 432545 X52486 Hs.3041 uracil-DNA glycosytase 2 417193 AJ922189 Hs.28839 ybrg0festical protein FLJZ2795 SS,TM,BinLHH_signal,tubu 5.3 42296 NM_007275 Hs.8186 lung cancer candidate ST, and ca							
427859 AA416856 Hs.98170 ESTs SS,TM,DUF60,trypsin,CUB,u 5.5 A35540 BE397032 Hs.14468 hypothetical protein MGC14226 SS,TM 5.5 427747 AW411425 Hs.180555 serine/threonine kinase 12 pkinase,SS,TM,synaptobrev 5.4 A41856 AK58911 Hs.127765 ESTs 5.4 A41830 NM_002204 Hs.265829 integrin, alpha 3 (antitigen CD4 integrin, AFG-GAP,Rhabd_g 5.4 A47374 AF263462 Hs.18376 KJAA1319 protein SS,Myosin_tail,M 5.4 A43145 Hs.1041 ESTs SS,Myosin_tail,M 5.4 A43145 Hs.25310 Hs.10341 Hs.106319 wingless-type MMTV integration SS,Myosin_tail,M 5.4 A21779 AJ879159 Hs.108219 wingless-type MMTV integration SS,wnt,SS 5.4 A217811 Hs.26330 Hs.28330 Hs.28330 Hs.28330 Hs.28330 A42266 NM_007275 Hs.8186 hung cancer candidate ST, A33670 AJ278803 Hs.123428 ESTs SS,TM,Glyco_hydro_56,Glyc 5.3 A436670 AJ278803 Hs.123428 ESTs SS,TM,Glyco_hydro_56,Glyc 5.3 A278803 Hs.123428 ESTs SS,TM,Glyco_hydro_56,Glyc 5.3	65						
A35540   BE397032   Hs.14468   hypothetical protein MGC14226   SS,TM   S5.5						SS,TM,DUF60,trypsin,CUB,u	5.5
70         431630 431630 431630 415976 447374 AF263462 431275 AB79159		436540	BE397032	Hs.14468	hypothetical protein MGC14226		
70 431630 NM_002204 Hs.265829 Integrin, alpha 3 (antigen CD4 integrin_A.FG-GAP,Rhabd_g 5.4 415976 R43144 Hs.21919 ESTs TM 5.4 447374 AF263462 Hs.18376 KIAA1319 protein SS,Myosin_tail,M 5.4 431275 T56571 Hs.10041 ESTs SS,HLH 5.4 404343 C7002191*.gij5053028 gb AAD388 SS,ABC_tran 5.4 421779 AI879169 Hs.108219 wingless-type MMTV integration cancertestis antigen (NY-ESO SS,mt,SS 5.4 457310 W28363 Hs.239752 uracil-DNA glycosylase 2 hs.28390 Hs.3041 Hs.288390 Hypothetical protein FLJ22795 SS cyclin,SS,cyclin 5.3 499164 AA705639 gb:ag990e09:r1 Stratagene hNT n SS,TM,Glyco_hydro_56,Glyc 5.3 438670 AI275803 Hs.123428 ESTs			AW411425			pkinase,SS,TM,synaptobrev	
415976 R43144 Hs.21919 ESTs TM 5.4 47374 AF263462 Hs.18376 KIAA1319 protein SS,Myosin_tail,M 5.4 431275 T56571 Hs.10041 ESTs SS,HLH 5.4 404343	70						
A47374	70						
75 431275							
75 40343 C7002191*.gijS053028jgbJAAD388 SSABC_tran 5.4 431461 BE299571 Hs.256310 likely ortholog of mouse ZFP28							
A31461			1303/1	113.10041			
A1879159	75		BE299671	Hs.256310		,	
418678 NM_001327 Hs.167379 cancer/tes/is antigen (NY-ESO- SS,TM,zf-C2H2 5.4 457310 W28363 Hs.239752 nuclear receptor subfamily 2, 5.3 417193 A/922189 Hs.288390 hs.3041 your display a feet of the first						SS.wnt.SS	
80 437310 W23363 Hs.239752 nuclear receptor subfamily 2, hypothetical protein FLJ22795 SS 5.3 432454 X52486 Hs.3041 Homo septiens, clone IMAGE:3953 409164 AA705639 Hs.8185 Hs							
80 432545 X52486 Hs.3041 uracil-DNA glycosylase 2 cyclin,SS,cyclin 5.3 432545 X52486 Hs.3041 uracil-DNA glycosylase 2 cyclin,SS,cyclin 5.3 409164 AA705639 Homo sapiens, clone IMAGE:3953 442296 NM_007275 Hs.8186 lung cancer candidate SS,TM,FintUH_signal,tubu 5.3 438670 AI275803 Hs.123428 ESTs SS,TM,Glyco_hydro_56,Glyc 5.3						-	
80 432545 X52486 Hs.3041 uracil-DNA glycosytase 2 cyclin, SS,cyclin 5.3 456573 Al2798111 Homo sapitens, clone IMAGE:3953 409164 AA705639 gb:ag90e09:r1 Stratagene hNT n 438670 Al275803 Hs.123428 ESTs SS,TM,Glyco_hydro_56,Glyc 5.3 SS,TM,Glyco_hydro_56,Glyc 5.3	0.0					SS	5.3
456573         AlZ79811         Homo sapiens, clone IMAGE:3953         5.3           409164         AA705639         gb:ag90e09.r1 Stratagene hNT n         SS,TM,HinLHH_signal,tubu         5.3           442296         NM, 007275         Hs.8186         lung cancer candidate         SS,TM,Glyco_hydro_56,Glyc         5.3           438670         Al275803         Hs.123428         ESTs         5.3	80					cyclin,SS,cyclin	5.3
442296 NM_007275 Hs.8186 lung cancer candidate SS,TM,Glyco_hydro_56,Glyc 5.3 438670 Al275803 Hs.123428 ESTs 5.3		456573					
438670 ALZ75803 Hs.123428 ESTs 5.3							
						SS,1M,Glyco_hydro_56,Glyc	
		4380/0	A12/38U3	ns.123428	E318		5.3

PCT/US02/19297

	400257			ENSP00000000452:BAD protein (B	SS,harmone_rec,zf-C4	5.3
	449514	AW970440	Hs.23642	protein predicted by clone 235	SS,PX,arf,lipocalin,PHD,z	5.3
	427336	NM_005658		TNF receptor-associated factor	MATH, SS, MATH, AZM_N, AZM, NT	5.3
_	414551	AI815639	Hs.76394	enoyl Coenzyme A hydratase, sh	ECH.Peptidase_U7,SS,TM	5.3
5	447960	AW954377	Hs.26412	ring finger protein 26	SS,TM,Cbl_N,Cbl_N2,Cbl_N3	5.3
	430605	AJ245433	Hs.247323	G4 protein	SS,TM,G-patch,ubiquitin,a	5.3
	456849	AA622394	Hs.153177	ribosomal protein S28	SS,TM	5.2
	430513	AJ012008	Hs.241586	G6C protein	SS,TM,GST_C,abhydrolase CUT,homeobox,beta-lactama	5.2 5.2
10	424437 427815	BE244700 BE072019	Hs.147049 Hs.12851	cut (Drosophila)-like 1 (CCAAT phosphalidylserine synthase 2	SS,TM,7tm_1	5.2
10	417903	NM_002342		lymphotoxin beta receptor (TNF	TNFR_c6,SS	5.2
	420476	AW575863	Hs.136232	ESTs	SS,HLH	5.2
	409960	BE261944		hexokinase 1	SS,TM	5.2
	436325	AL390088	Hs.7393	hypothetical protein from EURO	SS,Synapsin_C.SS	5.2
15	444439	AI458883	Hs.143545	hypothetical protein MGC11303	SS,TM,PAF-AH_p_II	5.2
	412915	AW087727	Hs.74823	NM_004541:Homo sapiens NADH de		5.2
	418891	NM_002419		miliogen-activated protein kina	SH3,pkinase,pyridoxal_deC	5.2
	430323	U40714	Hs.239307	tyrosyl-IRNA synthetase	DUF101,SS,tRNA-synt_1b,tR	5.2
20	432396	AW295956	Hs.11900	hypothetical protein FLJ14972	SS	5.2 5.2
20	457843 429252	AW138211 NM_004658	Hs.128746	ESTs RAS protein activator like 1 (	C2,PH,RasGAP,BTK,SS,C2,PH	5.1
	429225	BE250337	Hs.198273	Target CAT	WD40	5.1
	412104	AW205197	Hs.240951	Homo saplens, Similar to RIKEN	SS,TM	5.1
	449750	H28586	Hs.32325	ESTs	SS,ras	5.1
25	442725	A1935786	Hs.131035	ESTs, Weakly, similar to CA24_H	SS,SS,TM,PX,PH,PLDc,arres	5.1
	430390	AB023186	Hs.241161	KIAA0969 protein	PH,SS,TM	5.1
	421658	X84048	Hs.301760	frequenin (Drosophila) homolog	efhand	5.1
	426928	AF037062	Hs.172914	relinol dehydrogenase 5 (11-ci	adh_short,SS,adh_short,TG	5.1
20	428924	AI016405	Hs.98959	ESTs, Weakly similar to JC5314	SS,TMJectin_c	5.1
30	458876	A1650896	Hs.195347	ESTs	En totala in	5.1 5.1
	402632	A18/411470	Hs.848	Target Exon	Fz,kringle,ig FKBP,TPR,SS	5.1
	413762 419451	AW411479 AL907117	Hs.90535	FK506-binding protein 4 (59kD) syntaxin binding protein 2	Sec1,SS,TM	5.1
	456155	R85182	Hs.7175	ESTs, Weakly similar to AF1568	SS ·	5.1
35	422396	W21872	Hs.7907	ESTs, Weakly similar to T19486		5.1
	413983	BE348384	Hs.279194	ESTs		5.0
	447598	A1799968	Hs.199630	ESTs	SS,TM	5.0
	425858	AA364923		gb:EST75602 Pineal gland II Ho	SS,TM,Peptidase_M10,fn2,h	5.0
40	440511	AF132959	Hs.7236	eNOS interacting protein	SS,TM,MAGE,Ribosomal_S17,	5.0
40	452661	AW449413	Hs.257152	ESTs		5.0
	412800	AW950852	Hs.74598	polymerase (DNA directed), del	homeobox,SS,efhand,hexoki	5.0
	446603	NM_014835	HS.15519	oxysterol-binding protein-rela	Oxysterol_BP,SS laminin_Nterm,laminin_Nte	5.0 5.0
	402884 448680	AW245890	Hs.21753	ENSP00000164597:PR00566. JM5 protein	WD40,SS,TM,KOW,HLH	5.0
45	431515	NM 012152		endothelial differentiation, I	7tm_1	5.0
7.5	427204	AA405404	Hs.215725	ESTs	SS,SS	5.0
	425169	AW292500	Hs.128514	ESTs	SS	5.0
	412940	BE295701	Hs.819	homeo box B7	homeobox,SS,homeobox,home	5.0
	440839	Al142078	Hs.135562	ESTs	SS	5.0
50	443814	BE281240	Hs.9857	carbonyl reductase		5.0
	434243	AA628062	Hs.200358	ESTs, Moderately similar to AL	SS,TM	5.0
	435605 .	AF151815	Hs.4973	hypothetical protein	SS,TM,SS,TM,ABC_tran,ABC_	5.0
	417116	Z43916	Hs.7634	hypothetical protein FLJ12287	SS,TM,filament,IF_tail	5.0 5.0
55	403055	DEC12004	Us 205720	C2002219*:gi]12737280 ref XP_0	kard CC TM is skings	4.9
55	420856 405594	BE513294	Hs.205736	NM_021949:Homo sapiens ATPase,	kazal,SS,TM,ig,pkinase E1-E2_ATPase,Hydrolase,SS	4.9
	405334			Target Exon	SS,TM,MIP	4.9
	419493	AF001212	Hs.90744	proteasome (prosome, macropain	PCI,SS,CDK5_activator	4.9
	413764	BE162704	,	gb:PM1-HT0454-301299-001-d08 H	SS	4.9
60	409169	F00991	Hs.50889	(clone PWHLC2-24) myosin light		4.9
	446933	AL137659	Hs.297214	HSPC141 protein	SS,TM,ank,EGF,notch,MATH,	4.9
	409139	AI681917	Hs.3321	ESTs, Highly similar to IRX1_H	SS,homeobox	4.9
	456672	AK002016	Hs.114727	Homo sapiens, clone MGC:16327,	SS,PK,PK_C,myosin_head,Rh	4.9
65	420842	A1083668	Hs.50601	hypothetical protein MGC10986	SS .	4.9 4.9
05	421909	NM_013375		TATA-binding protein-binding p	disintegrin, Reprolysin, Pe	4.9
	419667 443496	AU077005 AJ006973	Hs.92208 Hs.9482	a disintegrin and metalloprote target of myb1 (chicken) homot	VHS,GAT,TM,Heme_oxygenase	4.9
	400933	A3000373	113.3402	NM_004347:Homo sapiens caspase	ICE_p20,ICE_p10,CARD,SS,I	4.9
	456143	H11097	Hs.61960	hypothetical protein	SS,pkinase	4.9
70	427527	AI809057	Hs.153261	immunoglobulin heavy constant	SS,TM,ig	4.9
	414265	BE410411	Hs.75864	endoplasmic reticulum glycopro		4.9
	433933	AI754389		Homo saplens clone TCCCIA00164	SS,TM,SS,TM,SH2,Y_phospha	4.9
	452302	AF173867	Hs.28906	glucocorticoid modulatory elem	SAND SS	4.9
75	409938	AW97,4648		gb:EST386752 MAGE resequences,	SS,Adap_comp_sub,GYF	4.8
75	400845		11. 00 171 1	NM_003105*:Homo sapiens sortil	Idl_recept_a,fn3,ldl_rece	4.8
	425976	C75094	Hs.334514	NG22 protein	SS,TM,pkinase,SH2,SH3,BNR	4.8
	452969 413163	W92792	Hs.77575	hypothetical protein MGC3136 protein tyrosine phosphatase,	fn3,ig,Y_phosphatase,SS,T	4.8 4.8
	413163 434962	Y00815 AK001574	Hs.75216 Hs.4291	golgi perepheral membrane prot	Hotel - Thurstermers 1991	4.6 4.8
80	434962	AI751740	Hs.86172	paired related homeobox protei	homeobox	4.8
55	440869	NM_014297		protein expressed in thyroid	lactamase_B,SS,XRCC1_N,BR	4.8
	453446	BE299996		gb:600944574F1 NIH_MGC_17 Homo		4.8
	412159	AF286598	Hs.9271	KIAA1071 protein	bZIP	4.8
	438999	AW276811		gb:xp66c02.x1 NCI_CGAP_Ov39 Ho		4.8

	420233	AA256714	Hs.194864	hypothetical protein FLJ22578	SS	4.8
	414576	AK000405	Hs.76480	ubiquitin-like 4	ubiquitin, SS, TM, G6PD, G6PD	4.8
	433669	AL047879	Hs.80475	ESTs, Weakly similar to ALU2_H	SS,TM,RNA_pol_L,RasGAP,C2	4.8
	448984	AW751955	Hs.22753	hypothetical protein FLJ22318	SS SS	4.8
5	426912	AL043054	Hs.256657	ESTs, Weakly similar to A46302	SS	
•	418945	BE246762	Hs.89499			4.8
				arachidonate 5-lipoxygenase	Ipoxygenase,PLAT,SS	4.8
	440333	A1378424	Hs.288761	hypothetical protein FLJ21749	SS,TM,IP_trans,pkinase,pk	4.8
	425615	AF023614	Hs.158341	transmembrane activator and CA	TM	4.8
10	458040	BE280562	Hs.287711	hypothetical protein FLJ22692		4.8
10	458367	AA088470	Hs.83135	Homo sapiens, Similar to RIKEN	SS,tRNA-synt_2d	4.8
	433294	AA582082	Hs.199410	ESTs		4.8
	437671	AA536047	Hs.9850	hypothetical protein MGC1842		4.8
	425338	H16716	Hs.182648	Homo sapiens cDNA FLJ14444 fis		4.8
	447946	Al566164	Hs.165827	ESTs	SS.PTN_MK.7tm_1.DAGKc.DAG	4.7
15	447205	BE617015	Hs.11006	ESTs, Moderately similar to T1		
13	416880	H99640			SS,TM,LRRCT,Sema	4.7
			Hs.53687	EST		4.7
	440150	AW975738	Hs.7001	Homo sapiens, clone IMAGE:3940	SS,TM,SS,TM,Peptidase_M22	4.7
	426268	AF083420	Hs.168913	serine/threonine kinase 24 (St	pkinase,pkinase	4.7
20	429253	Y11739	Hs.198313	winged-helix nude	Fork_head,SS,TM,glycotyti	4.7
20	450261	AA788727	Hs.34068	ESTs, Weakly similar to A43932	SS	4.7
	439246	A1498072		membrane-associated tyrosine-	SS,SS,TM	4.7
	419120	BE271922		ESTs, Weakly similar to zinc f	SS,TM,DENN,Cytidylyltrans	4.7
	416487	AW190458	Hs.79347	KIAA0211 gene product	SS,zI-C2H2	4.7
	413837	AW163525		titin-cap (telethonin)	SS,Methyltransf_3	4.7
25	419887	AW292562	Hs.187628	ESTs	TM	4.7
	410277	R88621	Hs.26249	ESTs, Weakly similar to T2D3_H	SS,TM,SS	4.7
	415169					
		W42913	Hs.78089	ATPase, vacuolar, 14 kD	ATP-synt_F,\$\$,TM,CH,Filam	4.7
	410892	AW809762	Hs.222056	Homo saplens cDNA FLJ11572 fis	007140071470711	4.7
20	407754	AA527348	Hs.288967	Homo sapiens cDNA FLJ14105 fis	SS,TM,SS,TM,TSPN,tsp_3,SE	4.7
30	409877	AW502498	Hs.15220	zinc finger protein 106		4.7
	431629	AU077025	Hs.265827	interferon, alpha-inducible pr	pkinase,SH2,SH3	4.7
	438800	AB037108	Hs.6418	seven transmembrane domain orp	SS,TM	4.7
	420823	R96881	Hs.63609	Hpall tiny fragments locus 9C	TM	4.7
	418900	8E207357	Hs.3454	KIAA1821 protein	SS	4.7
35	402400	0220.001		Target Exon	SS,TM,RNase_HII,bZIP,DUF2	4.7
	419625	U91616	Hs.91640	nuclear factor of kappa light		4.7
	433319	AA583232	113.31040	ESTs	ank,SS,TM	
			U- 452027		SS None Burn	4.7
	424959	NM_005781		activated p21cdc42Hs kinase	pkinase,SH3	4.7
40	432750	NM_014440		interleukin 1, epsilon	IL1	. 4.7
40	425954	AK000633	Hs.164476	hypothetical protein FLJ20626	SCAN,zf-C2H2,KRAB,SS,KRAB	4.7
	447245	AK001713	Hs.17860	hypothetical protein FLJ10851	E1_dehydrog	4.7
	427101	R87591	Hs.172884	ESTs	SS,TM	4.6
	447544	AA401573	Hs.288284	hypothetical protein FLJ22378	SS,TM	4.6
	400266			NM_002858*:Homo sapiens ATP-bi	ABC_tran	4.6
45	412841	Al751157	Hs.101395	hypothetical protein MGC11352	SS,TM	4.6
	422066	AW249275	Hs.343521	malate dehydrogenase 2, NAD (m	ldh,ldh_C,adh_short,Semia	4.6
	414874	D26351	Hs.77515			
	418373	AW750770		inositol 1,4,5-triphosphate re	TM,RYDR_ITPR,ion_trans,MI	4.6
			Hs.84344	CGI-135 protein	SS,TM,PMP22_Claudin,2OG-F	4.6
50	424487	T08754	Hs.6259	KIAA1698 protein	SS,SS,TM,Glyco_hydro_31,G	4.6
50	426571	AA381642		gb:EST94816 Activated T-cells		4.6
	433941	AA620612		ESTs	SS,TM,TNFR_c6	4.6
	421717	AF230924	Hs.107187	divalent cation tolerant prote		4.6
	450883	NM_001348	Hs.25619	death-associated protein kinas	pkinase,GTP_EFTU,EFG_C,GT	4.6
~ ~	427361	AW732480	Hs.7678	cellular retinoic acid-binding	SS,TM,aminotran_1_2,LRR	4.6
55	420421	AF281133	Hs.343589	exosome component Rrp41	RNase_PH,RNase_PH_C	4.6
	414513	AW239400	Hs.76297	G protein-coupled receptor kin	pkinase,RGS,pkinase_C,SS,	4.6
	431498	AK001777	Hs.258551	aspartyl aminopeptidase	SS,Peptidase_M18,SS,TM,Y_	4.6
	432593	AW301003	Hs.51483	ESTs, Weakly similar to hypoth	SS,TM,adh_short	4.6
	404661			C9000306*:gi 12737280 ref XP_0	Oo, mgaan_anon	4.6
60	412790	NM_014767	He 74593		kazal thumplohulie 1 of	4.0
J J				KIAA0275 gene product	kazal,thyroglobulin_1,zf-	4.6
	456243	AI345001	Hs.82380	menage a trois 1 (CAK assembly	zf-C3HC4	4.6
	426222	BE391706	Hs.168073	DKFZP727M231 protein	GSH_synthase	4.6
	439594	AI245026	Hs.111099	hypothetical protein MGC10974	CLP_protease	4.6
CF	409114	AA070021		gb:zm67h03.r1 Stratagene neuro		4.6
65	429049	AW452125	Hs.119273	KIAA0296 gene product	SS,TM,trypsin	4:6
	424271	Al991887	Hs.305882	5-oxoprolinase (ATP-hydrolysin		4.6
	418741	H83265	Hs.8881	ESTs, Weakly similar to S41044	SS,TM,pkinase,Activin_rec	4.6
	450493	M93718	Hs.166373	nitric oxide synthase 3 (endot	flavodoxin,FAD_binding,NO	4.6
	433074	AL045019	Hs.323462	Homo sapiens cDNA FLJ11214 fis	DEAD,helicase_C,dsrm,Vira	4.6
70	444893	AW249312	Hs.12109	WD40 protein Clao1	WD40	4.6
	420508	AJ270993	Hs.98428	homeo box B6	homeobox.SS.homeobox.home	4.6
	409591	AA532963	Hs.9100	Homo sapiens cDNA FLJ13100 fis	SS,TM,UM,homeobox	4.6
	456181	L36463				
			Hs.1030	ras Inhibitor	RA,SH2,VPS9,SS,TM,Nucleos	4.6
75	439270	BE268278	Hs.28393	hypothelical protein MGC2592	SS,TM,HCO3_cotransp	4.6
13	440104 -	AA132838	Hs.239894	hypothetical protein MGC2803	SS,DS	4.5
	423279	AW959861	Hs.290943	ESTs	SS	4.5
	445087	AW893449	Hs.12303	suppressor of Ty (S.cerevisiae	S1,SH2,Ribosomal_L23,pkin	4.5
	· 404036			Target Exon	SS,TM,cadherin,cadherin	4.5
00	431832	AW276866	Hs.192715	ESTs	Ets,SAM_PNT	4.5
80	433886	AA613596	Hs.28412	ESTs	SS	4.5
	426735	T78716	Hs.120446	ESTs	Oxysterol_BP,PH	4.5
	417825	AW838994	Hs.6363	heparan sulfate 6-O-sulfotrans	SS,TM	4.5
	455600	BE061053	. 13.0000	gb:QV0-BT0041-271099-037-d09 B	C4	
	423858		Un 122/02			4.5
	464000	AL137326	Hs.133483	Homo sapiens mRNA; cDNA DKFZp4	SS,TM	4.5
					265	

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	421680	AL031186	Hs.289106	Human DNA sequence from clone	SS,SS,rrm,zf-RanBP,rrm,GA	4.5
	408157	AA047685	Hs.62946	ESTs	pkinase	4.5
	434303	AW204058	11. 4 10004	transforming growth factor bet ESTs	SS,TM,SSF,FG-GAP,vwa,inte	4.5
5	440745 419344	AW303627 U94905	Hs.143301	diacylglycerol kinase, zeta (1	ank,DAGKa,DAGKc,DAG_PE-bi	4.5 4.5
9	447208	BE315291	Hs.277445 Hs.237971	hypothetical protein MGC5627	BULDAGINADAGINAD_F C-W	4.5
	436163	R84938	113.237371	gb:yt65f04_r1 Soares retina N2		4.5
	456856	AK001528	Hs.347285	Homo sapiens, Similar to DiGeo		4.5
••	410817	AI262789	Hs.93659	protein disulfide isomerase re	SS,thiored	4.5
10	434558	AW264102	Hs.39168	ESTs	SS,TM,LRRCT,LRR	4.5
	440548	AL117408	Hs.7274	DKFZP434P1750 protein		4.5
	450200	AW975625	Hs.173088	ESTs	zf-UBP,zf-C3HC4	4.5
	432434	AL161977	Hs.2994	PCTAIRE protein kinase 3	SS,pkinase	4.5
15	440042	A1073387	Hs.133898 Hs.278429	ESTs	SS	4.5
13	454328 458196	AW372097 AI802408	FIS.270429	hepatocellular carcinoma-assoc ubiquitin A-52 residue ribosom	SS,TM,fn3,FKBP,TPR	4.5 4.5
	433472	AI541246	Hs.3343	phosphoglycerate dehydrogenase	2-Hacid_DH,2-Hacid_DH_C,M	4.5
	408928	AW295827	Hs.255479	hypothetical protein MGC5566	A_deaminase,A_deaminase	4.5
	448093	AW977382	Hs.15898	2,4-dienoyl CoA reductase 2, p	adh_short,NDK	4.5
20	426272	AW450671	Hs.189284	ESTs		4.5
	453610	AW368882	Hs.33818	RecQ protein-like 5	SS,DEAD,helicase_C,SS,DEA	4.5
	441327	AK001706	Hs.7778	hypothetical protein FLJ10751	SS,TM,7tm_1	4.5
	424681	AA054400	Hs.151706	KIAA0134 gene product	helicase_C,PRK,SS,TM,7tm_	4.5
25	443443	AJ344042	Hs.9347	regulator of G-protein signal	TM,Na_Pi_cotrans	4.5
25	426677 412482	AW949856 A1499930	Hs.97165	ESTs	SS SS	4.5
	425236	AW067800	Hs.334885 Hs.155223	mitochondrial GTP binding prot stanniocalcin 2	Stanniocalcin,SS	4.4 4.4
	423229	AC003965	Hs.125532	protease, serine, 26	trypsin,SS	4.4
	412338	AA151527	Hs.69485	hypothelical protein FLJ12436	SS,TM,TIG,Sema,PSI	4.4
30	419395	BE268326	Hs.90280	5-aminoimidazole-4-carboxamide	AICARFT_IMPCHas,MGS,AICAR	4.4
	442462	AF031405		gb:AF031405 Soares fetal liver		4.4
	439975	AW328081	Hs.6817	inosine triphosphatase (nucleo	Ham1p_fike,SS	4.4
	423876	BE502835	Hs.15463	Homo sapiens, clone IMAGE:2959	SS,efhand	4.4
25	423220	BE394920	Hs.125262	aladin	WD40,TM,Activin_recp,pkin	4.4
35	411574	BE242842	Hs.6780	protein tyrosine kinase 9-like	coffin_ADF,SS,TM	4.4
	448947	BE615408	Hs.337228	ESTs, Weakly similar to AXHU a	SS,TM,ig,pkinase	4.4
	407755 414849	AI151353 AW372721	Hs.29742 Hs.291623	Homo sapiens serine palmitoyl ESTs, Weakly similar to unname	SS,TM,aminotran_1_2	4.4 4.4
	458171	AI420016	Hs.192090	ESTs	TM,pkinase SS,TM	4.4
40	424443	AI751281	Hs.284161	hypothetical protein from EURO	SS,TM,SS,TM	4.4
	427002	AA524093	Hs.23158	ESTs	SS,zf-C2H2	4.4
	404344			C7002191*:gij5053028jgbjAAD388	SS,ABC_tran	4.4
	427458	BE208364	Hs.29283	ESTs, Weakly similar to LKHU p	SS,F5_F8_type_C,EGF,TGT	4.4
10	419764	BE262524	Hs.93183	vasodilator-stimulated phospho	WH1	4.4
45	446872	X97058	Hs.16362	pyrimidinergic receptor P2Y, G	7tm_1,SS,TM	4.4
	435615	Y15065	Hs.4975	potassium voltage-gated channe	ion_trans,KCNQ1_channel	4.4
	403945	200020		Target Exon		4.3
	435593 421899	R88872	Hs.4964 Hs.109281	DKFZP586J1624 protein	Herpes_HEPA,SS	4.3
50	425245	AJ011895 AI751768	Hs.155314	Nef-associated factor 1 KIAA0095 gene product	Virus_HS,bZIP,G-gamma,Myo SS,TM	4.3 4.3
50	423348	AA324687	16.155514	gb:EST27558 Cerebellum II Homo	SS,TM	4.3
	452105	AA022838	Hs.6570	ESTs, Weakly similar to S10889	SS,TM,TBC,rrm	4.3
	431934	AB031481	Hs.272214	STG protein	SS	4.3
	429499	AA453809	Hs.99350	ESTs		4.3
55	453485	BE620712	Hs.33026	hypothetical protein PP2447	SS,TM	4.3
	459393	BE409283	Hs.193264	hypothetical protein MGC3234		4.3
	405364			ENSP00000239138*:Guanine nucle		4.3
	428345	AI242431	Hs.118282	PAP-1 binding protein	SS,TM	4.3
60	435327	BE301871	Hs.4867	mannosyl (alpha-1,3-)-glycopro	SS,HLH,Myc_N_term,Myc-LZ,	4.3
00	413053	D50922	Hs.65377 Hs.57729	Kelch-like ECH-associated prot	TM,SS,TM,EF_TS,UBA,transm BTB,Kelch,SS,TM	4.3 4.3
	409936	AK001691	Hs.57655	hypothetical protein FLJ10829	SS,TM	4.3 4.3
	421592	AF009801	Hs.105941	bagpipe homeobox (Drosophila)	homeobox,SS	4.3
	424251	AA677466	Hs.143696	coactivator-associated arginin	SS,SNF2_N,helicase_C,brom	4.3
65	414788	X78342	Hs.77313	cyclin-dependent kinase (CDC2-	pkinase	4.3
	432805	X94630	Hs.3107	CD97 antigen	SS,TM,7tm_2,GPS,EGF,SS,TM	4.3
	424927	AW973666	Hs.153850	hypothetical prolein C321D2.4	SS,TM	4.3
	456863	T16837	Hs.4241	ESTs	fusion_gly,homeobox,TM	4.3
70	417823	R88869	Hs.102447	TSC-22-like	PWWP	4.3
70	406621	X57809	Hs.181125	immunoglobulin lambda locus	SS SS AFD SS	4.3
	431493	AI791493	Hs.129873	ESTs, novel cytochrome P450	SS,p450,SS	4.3
	412958 431658	BE391579 BE409917	Hs.75087 Hs.266935	Fas-activated serine/threonine tRNA selenocysteine associated	SS,pkinase rm,SS,RCC1	4.3 4.3
	419579	W49529	Hs.296200	hypothetical protein AF053356_	MSP_domain,SS,TM,CUB,NTR,	4.3 4.3
75	410076	T05387	Hs.7991	ESTs	SS	4.2
	406773	AA812424	Hs.76067	heat shock 27kD protein 1	HSP20,SS	4.2
	424709	AL137589	Hs.152149	hypothetical protein DKFZp434K		4.2
	418419	X55039	Hs.85004	centromere protein B (80kD)	CENP-B,HTH_5	4.2
00	447377	X77343	Hs.334334	transcription factor AP-2 alph	TF_AP-2,TF_AP-2	4.2
80	416931	D45371	Hs.80485	adipose most abundant gene tra	C1q,Collagen,SS	4.2
	411674	AW861123		gb:RC3-CT0297-120200-014-a05 C	SS	4.2
	419073	AW372170	Hs.183918	Homo sapiens cDNA FLJ12797 fis	SS,ig,tsp_1,ZU5,SS,TM,Nuc	4.2
	405867	AA157857	Hs.182265	keratin 19	filament,bZIP,SS,filament	4.2
	432183	AW151952	Hs.46679	hypothetical protein FLJ20739	SS	4.2
					200	

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	418910	Z25821	Hs.89466	Homo sapiens, Similar to dodec	ECH,SS,TM,aminotran_3,ABC	4.2
	437300 426615	AL040504 AA400578	Hs.25063 Hs.6473	PRO0461 protein gb:zu70a11.r1 Soares_testis_NH	SS,TM,pkinase,cyclin,F-bo	4.2 4.2
	421453	AA234652	Hs.104555	neuropeptide FF-amide peptide	SS,bZIP,zf-C2H2,bZIP,zf-C	4.2
5	409616	AA076248		gb:zm18c10.r1 Stratagene pancr		4.2
	444744	BE394732	Hs.147562	ESTs	SS	4.2
	412575	AA113177	12- 000740	gb:zm29e05.s1 Stratagene panor	TM,ER_lumen_recept	4.2 4.2
	429542 435995	AF038660 BE260415	Hs.206713 Hs.348198	UDP-Gat:betaGlcNAc beta 1,4- g hypothetical protein FLJ20262	Galactosyl_T_2,ig,SS,TM,A	4.2
10	451585	AK001171	Hs.326422	hypothetical protein MGC4549	SS,Metallophos	4.2
	456153	AW972270	Hs.144054	ESTs	SS,TM	4.2
	455340	AW901435		gb:RC0-NN1012-270300-031-a10 N		4.2
	457268	AW272279		ESTs, Moderately similar to AL	Ot t 00	4.2
15	432311 409656	BE083080 NM_005133	Hs.274323	similar to sialytransferase 7 RCE1, prenyl protein protease	Glyco_transf_29 Abi,SS,CPSase_L_chain,HMG	4.2 4.2
13	424919	BE314461	Hs.153768	U3 snoRNP-associated 55-kDa pr	WD40,SS,KH-domain	4.2
	416528	H65052	Hs.337621	ESTs		4.2
	415137	AI634834	Hs.72451	Homo sapiens PAC done RP5-108		4.2
20	417334	AA337572	Hs.157240	hypothetical protein MGC4737	SS,TM,ion_trans	4.2
20	451920 413049	AA224483 NM_002151	Hs.27239	DKFZP586K0524 protein hepsin (transmembrane protease	SS,TM,SS,TM trypsin,SS,TM,ATP1G1_PLM_	4.2 4.2
	458988	AW410431		CGI-119 protein	0)psii(00;1114A11 101_1 211_	4.2
	406964	M21305	1,0,2000.0	FGENES predicted novel secrete		4.2
05	451595	AW965569	Hs.20996	ESTs	SS,WD40	4.2
25	449728	AI820751	Hs.107635	ESTs -4	SS ·	4.1
	453245 432238	T99801 AL133057	Hs.339751 Hs.274135	ESTs Homo sapiens mRNA; cDNA DKFZp4	TM,ABC_tran WD40,LRR	4.1 4.1
	430037	BE409649	Hs.227789	mitogen-activated protein kina	pkinase	4.1
	442196	AI902646	Hs.31844	hypothetical protein FLJ12586	SS,SCAN	4.1
30	425251	Z22521	Hs.155342	protein kinase C, delta	pkinase,DAG_PE-bind,pkina	4.1
	415014	AW954064	Hs.24951	ESTs	CO of COLICA CERTA of P. hou	4.1
	440088 418837	BE559877 U48263	Hs.183232 Hs.89040	hypothetical protein FLJ22638 prepronociceptin	SS,zf-C3HC4,SPRY,zf-B_box Opiods_neuropep,SS	4.1 4.1
	410239	AI568350	Hs.61273	hypothetical protein MGC2650	SS,ART,TM	4.1
35 ·	446975	BE246446	Hs.16695	ubiquitin-activating enzyme E1	ThiF,UBACT	4.1
	453968	AA847843	Hs.62711	High mobility group (nonhiston	SS,HMG_box	4.1
	448241	AW811064	Us 7054	gb:MR2-ST0131-211099-008-c06 S	SS Zip,SS,TM,Cytidylyltransf	4.1 4.1
	441455 450848	AJ271671 AJ677994	Hs.7854 Hs.428	zinc/iron regulated transporte fms-related tyrosine kinase 3	flt3_lig,SS,Ribosomal_L13	4.1
40	429218	AA225065	Hs.198269	Targel CAT	SS,Nop	4.1
	425437	AK000482	Hs.181780	hypothetical protein FLJ20241		4.1
	406613	*********	11. 05/0/0	Target Exon	SS,pkinase,LRR,LRRCT,Ribo	4.1
	431239 436057	AL039971 AJ004832	Hs.251216 Hs.5038	hypothetical protein DKFZp434A neuropathy target esterase	ank,WH2 cNMP_binding,SS,TM,cNMP_b	4.1 4.1
45	415193	AL048891	Hs.12185	hypothetical protein MGC14333	SS,TM,aminotran_1_2,LRR	4.1
	424619	BE387282	Hs.207443	hypothetical protein MGC10848		4.1
	432968	BE614192	Hs.279869	melanoma-associated antigen re	SS,TM,RGS,DIX	4.1 4.1
	428156 414084	BE269388 AW168771	Hs.182698 Hs.71574	mitochondrial ribosomal protei hypothetical protein FLJ14926	SS SS,P5CR,EF1BD	4.1
50	424964	AW161271	Hs.153961	ARP1 (actin-related protein 1,	actin,SS	4.1
	431410	AW299534	Hs.105739	ESTs		4.1
	435968	AW161481		integral membrane protein 3	тм .	4.1
	432351 426120	Al270313 AA325243	Hs.127762 Hs.166887	hypothetical protein MGC12982 copine I	C2,SS,aminotran_5	· 4.1 4.1
55	416877	BE386266	Hs.85658	hypothetical protein FLJ23436	02,00,2111110021_0	4.1
	425970	AK001500	Hs.165186	hypothetical protein FLJ13852	SS,P5CR,Epimerase,zf-C2H2	4.1
	434848	BE256304	Hs.32148	AD-015 protein	SS,TM,SS,TM,LRR,P,Peptida	4.1
	458715	AK000973	Hs.16725	hypothetical protein FLJ10111	IBR,zf-C3HC4,SS,TM,IRF,CK	4.1
60	435851 425538	AA700946 BE270918	Hs.164026	ESTs Homo sapiens, clone IMAGE:3534	SS,SNF2_N,helicase_C,brom	4.1 4.1
50	425556 444416	AW288085	Hs.11156	hypothetical protein	zf-C3HC4,SpoA,PHD,TM,syna	4.0
	426831	BE296216	Hs.172673	S-adenosylhomocysteine hydrola	AdoHcyase,SS	4.0
	444596	BE560662	Hs.11417	Rab acceptor 1 (prenylated)	SS,TM,lig_chan,ANF_recept	4.0
65	439685	AW956781	Hs.293937	ESTs, Weakly similar to FXD2_H	SS,PWWP,TSC22	4.0 4.0
05	447402 450184	H54520 W31096	Hs.18490 Hs.237617	hypothetical protein FLJ20452 Homo sapiens, clone IMAGE:3447	SS,TM SS	4.0
	426068	AF029778	Hs.166154	jagged 2	DSL,EGF,vwc,granulin,SS,T	4.0
	459255	Al493244	Hs.239500	hypothetical protein MGC13114	SS	4.0
70	403182	0004 (022	11- 04550	Target Exon	SS	4.0
70	432078 459167	BE314877 BE504370	Hs.24553	hypothetical protein FLJ 12541 ESTs, Weakly similar to CA13_H	SS,TM SS	4.0 4.0
	452747	8E153855	Hs.61460	lo superfamily receptor LNIR	SS,TM,ig,HLH	4.0
	444633	AF111713	Hs.286218	junctional adhesion molecule 1	ig,SS,TM,HLH	4.0
75	434171	BE247688	Hs.347349	KIAA0948 protein	DIDOLD ULLAND AL Annual Land	4.0
75	422155	AW249152 Al571225	Hs.284171	sirtuin (silent mating type in KIAA1535 protein	SIR2,HLH,Myc_N_term,Myc-L SS,TM,cNMP_binding,ion_tr	4.0 4.0
	433262 442599	AF078037	Hs.324051	RelA-associated inhibitor	SH3,ank,SS,TM,HHHLig	4.0
	452500	AW373011	Hs.54558	hypothetical protein FLJ22222		4.0
00	437563	AJ217204	Hs.144968	ESTs	00	4.0
80	432234	AA531128 AAAA3873	Hs.115803	ESTs deficited phosphate mannocultra	SS	4.0 4.0
	433135 447495	AA443873 AW401864	Hs.110477 Hs.18720	dolichyl-phosphate mannosyltra programmed cell death 8 (apopt	pyr_redox,SS,Ets	4.0
	452857	BE072814	Hs.258519	ESTs, Moderately similar to S6	SS	4.0
	427834	AA506101	Hs.285813	hypothetical protein FLJ11807	SS,TM	4.0
					267	

	418963 437340	BE304571 AL353935	Hs.89529 Hs.135917	aldo-keto reductase family 1, hypothetical protein DKFZp761D	aldo_ket_red TBC,bZIP,WD40,WD40	4.0 4.0
	455928	BE170313		gb:QV4_HT0536-040500-193-g02 H	SS	4.0
5	400607 424825	AF207069	Hs.153357	Target Exon procollagen-lysine, 2-oxogluta	SS,homeobox 20G-Fell_Oxy,Glycos_trans	4.0 4.0
•	438143	BE500981	Hs.269652	ESTs	2001 011_075,03500_0880	4.0
	433173	Z35093	Hs.3196	surfeil 1	SURF1,SS,TM,SURF1,SURF4	4.0
	412550	R52452	Hs.26370	gb:yg80g07.r1 Soares infant br		4.0
10	TABLE 23B:					
		e Eos probes: : Gene cluste		mber		
•		Genbank acce		5		
15	Pkey	CAT Numbe				•
15	408215	10478_1		A307674 N35629 AA338538 AI193603 AA	.781096 AI680061 AI613258 AW276647 BI	E221263 Al348910 Al985031 Al090078 Al359617
		_		J160210 AJ446461 AJ355345 AJ343638 AJ	343640 Al275091 M78746 AW262795 AW2	250002 AA503756 AI934519 AW272086 N26520
	408294	1050553_1	AA626639 BE141732 U	175823 BE141331 AW178416 AW178430 I	BE141343 BE141298 BE141702 BE14128	5
20	409114	110088_1			AAD82183 AA115915 AA085147 AA1259	05 AA063336 AA079206
	409164 409616	110421_1 114348_1		A064707 AL036920 A1651598 A120958 AA122152 AA076249		
	409938	116091_1		A652153 AA649671 AA078582		
25.	409960	116270_1				BE314003 AA908246 AW960808 AA385346
25.				uzu43 aa 135037 aau 18870 aas 17395 a 1932839 aio56920	A318793 AA318783 AA319160 BEUUU960.	AW370250 AW370244 T85930 AA759250
	410445	120374_2	AA199830 A	1143895 AW961629 AA322482		
	411219 411674	1236055_1 1253746_1		\W832913 AW832906 AW832788 AW832 \W861126 AW856717 AW861116 AW866		856780 AW856782 AW856789 AW856772
30	411074	1200140_1		W856786 AW856776 AW856835 AW856		030700 AV030702 AV030709 AV030772
	412091	1276564_1		891805 AW901892 AW901895		
	412173 412575	1280870_1 130769_1		902279 AW897608 JW894515 AA113847		
~~	413534	1375357_1		E146780 BE146788 BE146967 BE146774	BE146963 BE146907	
35	413564	1376722_1	BE260120 B			
	413764 413837	1387163_1 139363_1		E162705 BE162732 BE162702 BE162694 AW163255 AW163385 AI929359 BE27927		7252 Al692198 AW003514 T24436 Al765658
			AW157459 A	41810740 A1659582 A1969924 A1929284 A1	340993 Al349083 AW299522 AW664650 A	
40	414413.	1443696_1	Al341293 Al BE294877 B	650609 AA279 E294759		
10	415126	1523506_1		346 D81568 D80539		
	419120	182026_1				V504757 N51688 Al400700 AA578548 AA714130 16817 AA593859 AW952245 AW341739 AA805093
			AA779455 A		943 MA409943 MV44/4620 MA/6/ 103 MA32	CEUCUBAA EE 11 PEWA CESSEEWA EE 86 11 80.
45	422155	21235_1				37 BE258447 BE253088 AA297721 H68948
				J/U3/2 H14246 ALU/936/ K24361 AW40: 126063 AA26	3997 AA297034 AA297092 F11858 AJ3725	97 AA297787 Z42780 AA297072 T81280 T83544
	423348	227276_1	AA324687 A	A325155 AW962038		
50	425858 426571	257265_1 269283_1		.W963483 BE182774 C21461 A381664 AW963560 AW949848 AA38172	ROALREAA RO	
30	427326	277229_1		804160 AA400787		
	428092 429720	286920_1		AA421182 AI734104 AI733923 AA430600		
	429720	308153_1 313927_1		773950 AA586573 AA457225 \A468507 AI478223 AW513008 AI762122	Al554512 AA862642 AA468976	
55	431424	333110_1		A806560 AA504839 AA805261		
	433319 433933	363095_1 377703_1	AA583232 A		1863355 AW131720 A1674922 A1949042 A1	990050 A1623178 AWA69497 AA620354
•	433941	377883_1		A994983 AA994990	100000 111 1011 20 1101 4022 11040042 11	330000 AI020170 AI11403437 AW20004
60	434303	383224_1 3925_1		41424379 A1669663 AA629077 AW613033		IE A A 24 E 407 A 1622020 A A 202422 \$142702
oo	434743	3929_1				16 AA215407 A1633829 AA292122 N42783 951 AW966080 M78807 N31947 AA521151
			AA278866 A	A044784 AA700		
	434796 435851	393400_1 411522_1		W974514 AA764999 AA649302 A702712 AA947620		
65	·436163	41515_6		47151 AA310309 AW063200 Al569528 Al	307823 N49975	
	437215	43473_1	AL117488 A			
	438999 439246	467686_1 47021_3		AA829050 AA829190 W251083 AA985226 AA852987 AI392809	AA206609 AW190187 AA555262 AF08605	7 F35814 AW516382 AA377885 N50847 F27148
70	440045	_	AA731186 A	A417728 AI003145	•	
70	440317 442462	49187_1 543232_1	AF031405 F	BE560615 BE562102		
	442472	543371_1		AW806852 AF049582		
	445625	64558_1				T57442 Al399986 R50073 R48743 Al769689 469257 Al954604 H21954 T25141 AA856793
75			R50074 AI7		1947 (273 K73403 AJ333104 AJ390101 AF	103237 A1934004 HZ1934 123141 AAB30793
	445631	6457_1				2527 Al343924 Al380749 AA93B153 T66966
			AI655000 AI H19058 R11		BE501355 AI637925 AW779200 AI524755	AW593995 Al336927 Al336928 Al357036 R60592
00	447128	70934_1			58001 Al553937 AA149853 H00719 Al7652	259 AW973696 F25787 F35749 Al568815
80	440244	750404 /		AA554539 C00201 AA961610 AW059537	R77127	
	448241 448993	756181_1 79225_1		AW811160 Al478413 E540637 BE265481 AW407710 BE51388:	2 BE546739 AA053597 BE140503 BE2185	14 AW956702 Al656234 Al636283 Al567265
			AW340858	BE207794 AA053085 R69173 AA292343 A		AA399460 Al760441 AA346416 BE047245
			AA730380 /	4A3,94063 AA454		

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BE299996 BE297115 BE270415 BE295214 BE296526
AWB16029 AWB13292 AWB16156 AWB13333 AWB16159 AWB13302 AWB13344 AWB13172
AWB51734 AWB51676 AWB51693 AWB51713 AWB51722 AWB51616 AWB51731 AWB51618 AWB51648 AWB52215
            453446
                           967533_1
                           1228976_1
1249762_1
            454682
            455035
                           1283604_1
                                          AW901435 BE094527
            455340
  5
            455557
                           1325974_1
                                          AW995839 AW995907
                                          BE061053 BE008959 BE008957 BE091618
BE153524 BE153576 BE153583
BE170313 BE158339 BE158290
                           1335877_1
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            455885
                           1380385_1
            455928
                           1383899_1
                                          AIZ79811 AI301071 AI214696 AI279813 AA588460 AA287256 BE171665
                           201205_1
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10
                           310453_1
                                          AW272279 AA461542 AA460615
            457268
                                          AA776638 BE439540
                           448900_1
            457978
                                          AI802408 AA907424 A1279233 AI302762 N33153 BE045678 AI863332 AW173558 AI302328 Z20793 D25594 BE326823
BE504370 AI243453 AI809556 AI702878 AI702163 AI300626 AW072219 AI369492 AI349587 AW779061 W78149 AA055693 AA974162 AI394380
AI830098 AW054857 AI870008 AW207658 AW665508 AW300595 AI192992 AW628019 AI274365 AA906922 N92547 AW054727 AW206667
                           503719_1
            458196
            459167
                           92053_1
                                          AW136707 AW13761
15
                                          AL045934 AL039532 H55531
            459271
                           969257_1
            TABLE 23C:
            Project. Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
20
            Strand: Indicates DNA strand from which exons were predicted
            Nt_position: Indicates nucleotide positions of predicted exons
25
                                                         Nt_position
            Pkey
400460
                                          Strand
                                                         35559-36295
                           8389428
                                          Pius
            400607
                                          Plus
                                                         3112-4159
                           9887666
                                                          187599-188138
            400833
                           8705148
                                          Minus
                                                         34428-34612
94518-94659
            400845
                           9188605
                                          Plus
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            400923
                           7637836
                                          Minus
                                                          105330-105503
                                          Minus
            400933
                           7651935
            401210
                                                          166969-167133,169760-169877,171563-171733
                           7712287
                                          Plus
            401264
                           9797154
                                          Plus
                                                          130810-130927,133367-133504
            401278
                           9799936
                                          Plus
                                                         98428-98573
35
                                                         9877-11997
            401609
                           7705041
                                          Minus
                                                          138786-138927,139157-139298,139440-139599,139960-140159
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401724
                           7689903
                                          Phis
                           7656694
                                          Plus
                                                          150063-150241
                                                          199466-199585
            402197
                                          Plus
                           8576113
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                           9454515
                                          Minus
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                                                         19813-20084,20163-20263
80123-80322
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                           9929688
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            402400
                           9945145
                                          Minus
                                          Plus
Plus
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            402632
                                                         47980-48191
361-474,541-687
            402884
                           9926562
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                           7406502
                                          Minus
45
            403055
                           8748904
                                          Minus
                                                          109532-110225
                                                          122884-123018,123134-123283,123372-123695,123779-123940,124059-124256
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                           7331426
                                          Plus
                                                          102163-102345.102545-102725
            403182
                           9838273
                                          Plus
                                                          48636-48822
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                                          Plus
            403945
                            7711869
                                           Minus
                                                          32141-32263
50
                                                         65247-67529,112537-114863
137948-138024,138111-138300
122664-122931
            404036
                            8567760
                                           Minus
            404333
                           9802821
                                           Minus
            404343
                           9838093
                                           Plus
            404344
                            9838093
                                           Plus
                                                          127865-128384
                            9964977
                                                          50151-50319,50859-51098
            404355
                                           Plus
 55
             404661
                            9797073
                                           Plus
                                                          33374-33675,33769-34008
                                                          100933-101083,101580-101782
124246-124422
             404757
                            7706327
                                           Plus
            404807
405334
                            4165210
                                           Minus
                                                          139386-139856
                            3135285
                                           Plus
             405346
                            2981263
                                                          101982-102171
                                           Plus
                                                          48325-48491,49136-49252
47657-47766,48461-48596
161628-161734,162823-163014,164439-164652
 60
             405364
                            2281075
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             405371
                            2078469
                                           Minus
             405594
                            6960456
                                           Plus
                                                          2923-3209
             405928
                            7717155
                                           Minus
                                                          71716-72515
             406230
                            4760409
                                           Plus
 65
             406244
                            7417725
                                           Plus
                                                          39422-39595
             406301
                            8575868
                                           Plus
                                                          57291-57494
             406487
                            7711306
                                           Plus
                                                          82039-82902
             406495
                                                          174661-174978
                            7711328
                                           Minus
             406613
                            2957168
                                           Plus
                                                          5029-5147
 70
             Table 24A lists about 117 genes down-regulated in ovarian cancer compared to non-malignant adult ovaries. These were selected as for Table 23A, except that the numerator
```

was set to the 75th percentile amongst various on-malignant over yas specimens, the denominator was set to the 95th percentile value amongst various overlan cancers, the numerator was greater than or equal to 75 units, and the ratio was greater than or equal to 2.0 (i.e., 2-fold downregulation in tumor vs. normal ovaries).

75

Pkey: Unique Eos probeset identifier number

Ex. Accn: Exemplar Accession number, Genbank accession number UG ID: UniGene number

80 Title: UniGene gene title

Protein Dom.: Predicted protein domain

R1: Ratio of normal ovaries to tumor

	Okou	Eu Assa	IIC ID	Title	Protein Dom.	R1
	Pkey 428232	Ex. Acon BE272452	UG ID Hs.183109	Title monoamine oxidase A	Amino_oxidase,pyr_redox,F	16.9
	433563	AI732637	Hs.277901	ESTs	SS	10.8
_	444931	AV652066		general transcription factor I	SS,Glypican	8.7
5	451573	AW130351		ESTs	SS	8.3
	429570	BE242256	Hs.2441	KIAA0022 gene product	lectin_c,SS,TM SS	7.9 7.5
	453510 410295	A1699482 AA741357	Hs.42151	ESTs nidogen (enactin)	SS,EGF,Id]_recept_b,thyro	6.9
	438549	BE386801	Hs.21858	trinucleotide repeat containin	SS,serpin,SS,WD40,FYVE	6.5
10	407969	AA046217	Hs.105370	ESTs	SS,Pep_M128_propep,Reprol	6.2
	414541	BE293116	Hs.76392	aldehyde dehydrogenase 1 famil	aldedh	6.0
	448438	BE613081	Hs.24654	Homo sapiens cDNA FLJ11640 fis		5.7
	441422	R43777	Hs.21364	ESTs	SS,TM Amidinotransf	5.1 3.9
15	413391 428022	A1223328 Z39686	Hs.75335 Hs.27865	glycine amidinotransferase (L- ' ESTs	SS	3.6
13	423044	AA320829	Hs.97266	protocadherin 18	35	3.6
	416039	AA376989	Hs.78989	alcohol dehydrogenase 5 (class	adh_zinc,HCV_NS4a,TM,adh_	3.5
	452854	AA437061	Hs.14060	prokineticin 1 precursor	SS	3.4
20	436772	AW975688	11 70004	metallothionein 1E (functional	SS,TM,7tm_2,HRM	3.2
20	415162	AF035718 AA709186	Hs.78061 Hs.99070	transcription factor 21	HLH SS	3.2 3.1
	427794 433072	A1928037	Hs.158832	ESTs ESTs	SS	3.1
	418318	U47732	Hs.84072	transmembrane 4 superfamily me	transmembrane4	29
~~	410059	NM_007038		a disintegrin-like and metallo	Reprolysin,tsp_1,Pep_M12B	2.9
25	431933	Al187057	Hs.132554	ESTs	TM,SS,TM	2.9
	420303	AA258282	Hs.278436	KIAA1474 protein		2.8 2.8
	438780 427661	M64936 AA410292	Hs.104761	gb:Homo saplens refinoic acid- ESTs	SS,wnt	2.8
	437342	AW903297	Hs.236438	hypothetical protein DKFZp761K	Sec7,PH	2.8
30	453828	AW970960	Hs.293821	ESTs	SS,Pep_M12B_propep,Reprol	2.7
	418444	AI902899 .	Hs.85155	butyrate response factor 1 (EG	zf-CCCH,SS	2.7
	453767	AB011792	Hs.35094	extracellular matrix protein 2	vwc,LRR,SS,LRR	2.7
	413624	8E177019	Hs.75445	SPARC-like 1 (mast9, hevin)	kazal,SS,kazal	2.7 2.7
35	413305 414504	NM_000426 AW069181		Horno sapiens cDNA: FLJ23176 fi sterile-atpha motif and leucin	laminin_B,laminin_EGF,lam SS,pkinase,SAM	27
33	439897	NM_015310		KIAA0942 protein	Sec7,PH	2.7
	421639	NM_012082		Friend of GATA2	SS	27
	442498	U54617	Hs.8364	Homo sapiens pyruvate dehydrog	HATPase_c,HATPase_c	2.6
40	410494	M36564	Hs.64016 .	protein S (alpha)	EGF,laminin_G,gla	2.6
40	452958 449648	AA883929	Hs.40527	ESTs ESTs	SS SS	2.6 2.5
	435519	AW205607 Al218950	Hs.253499 Hs.125461	hypothetical protein FLJ11539	SS	2.5
	433690	Al373949	Hs.279610	hypothetical protein FLJ10493	SS	2.5
	424319	AW961026		ESTs, Wealty similar to ALU8_H		2.5
45	420174	A1824144	Hs.199749	ESTs		2.5
	421709	AA159394	Hs.107056	CED-6 protein	PID,Herpes_UL6	2.4 2.4
	417622 453655	AW298163 AW960427	Hs.82318 Hs.342874	WAS protein family, member 3 transforming growth factor, be	WH2 SS,TM,zona_pallucida	2.4
	408468	A1909712	TIS.342014	phosphatidylinositol transfer	SS,PX,PH,PLDc,PH,PLDc,PX	2.4
50	400829	14505112		C11000244:gi]11056030[ref]NP_0	SS,TM,SS,TFIID_30kD	23
	453125	AW779544	Hs.115497	hypothetical protein FLJ22655	ras	2.3
	437862	AW978107	Hs.5884	Homo sapiens mRNA; cDNA DKFZp5	HLH ·	2.3
	425462	A1491852	Hs.46783	Homo sapiens cDNA: FLJ22382 fi histamine N-methyltransferase	And CoA db	2.3 2.3
55	417094 403247	NIM_006895	TIS.0110Z	Target Exon	Acyl-CoA_dh	2.3
55	441916	AA993571		ESTs		2.3
	422746	NM_004484	Hs.119651	glypican 3	Glypican, SS ·	23
	416777	AF146760	Hs.79844	DKFZP564M1416 protein	SS,GTP_CDC,SS	2.3
60	409403	AA668224	Hs.6634	Homo sapiens cDNA: FLJ22547 fi	SS,TM SS .	2.3 2.3
oo	418956	AA234831 AW408163	Hs.58488	KIAA0788 protein catenin (cadherin-associated p	Vinculin, Stathmin	23
	410073 419461	A1452601	Hs.288869	nuclear receptor subfamily 2,	hormone_rec,zf-C4,hormone	2.3
	429319	AL023754	Hs.199068	similar to calcium/calmodulin	SS pkinase	2.2
	452123	AJ267615	Hs.38022	ESTs	SS	2.2
65	453305	R39224	Hs.267997	EHM2 gene		2.2
	416157		Hs.342874	transforming growth factor, be	zona_pellucida,SS,TM,zona Ribosomal_L18p	2.2 2.2
	406637 414466	U14966 AA349211	Hs.180946 Hs.76205	ribosomal protein L5 cytochrome P450, subfamily XIA	p450	2.2
	408915	NM_016651		heptacellular carcinoma novel	SS	2.2
70	420929	Al694143	Hs.326248	programmed cell death 4	MA3,LRR	2.2
	456972	A1054347	Hs.2017	ribosomal protein L38	SS,TM	2.2
	409549	AB029015	Hs.54886	phospholipase C, epsilon 2	C2,PH,PI-PLC-Y,PI-PLC-X	2.2
	410209	AI583661	Hs.60548	hypothetical protein PRO1635 ESTs	SS,TM,Fork_head SS,TM	2.2 2.2
75	449500 447806	AW956345 W03616	Hs.12926 Hs.10432	ESTs, Weakly similar to 138022	00,119	21
, 5	441712	AW391927	Hs.7946	KIAA1288 protein		21
	445025	A1768895	Hs.295727	ESTs, Weakly similar to ALUB_H	SS,BAG,UPF0001	2.1
	444161	N52543	Hs.142940	ESTs	SS	2.1
οΛ	427156	BE621719	Hs.173802	KIAA0603 gene product	SS,TM,TBC	21
80	436995	AI160015	Hs.125489	ESTs ESTs	SS,TM,RasGEF,actin,RasGEF SS	2.1 2.1
	408443 448274	N33937 A1268097	Hs.10336 Hs.67317	Homo sapiens cDNA FLJ11775 fis	<b>₩</b>	21
	426354		Hs.169470	dystrophin (muscular dystrophy	ZZ,CH,WW,spectrin,bZIP,SS	2.1
	443906	AA348031	Hs.7913	ESTs		2.1
			•	270		

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	444815	A 44E4F20	11- 4007	aminology/finale delta deltad	20.11.10	2.1
		AA151539	Hs.1227	aminolevulinate, delta-, dehyd	SS,ALAD	21
	420728	AA767718	Hs.93581	hypothetical protein FLJ10512	SS,TM,Sema,PSI,ig	
	404245			NM_007116*:	fibrinogen_C,fn3,SS	21
_	436420		Hs.31595	ESTs	SS,TM,PMP22_Claudin,SS,TM	21
5	410056	AL117664	Hs.58419	DKFZP586L2024 protein		2.0
	414476	AA301B67	Hs.76224	EGF-containing fibulin-like ex	EGF,TIL,SS	2.0
	424137	AA335769	Hs.16262	ESTs		2.0
	447659	AAD17472	Hs.107260	hypothetical protein DKFZp586H	SS	2.0
	444862	AI209158	Hs.143929	ESTs	SS,TM	2.0
10	426086	T94907	Hs.188572	ESTs	PH,CH,spectrin	2.0
	436080	AI684710	Hs.201645	ESTs	SS,ATP-synt_C	20
	424651	AJ493206	115.201040	ESTs	SS	20
			U- 220040			
	432939	AL038924	Hs.279849	KIAA0438 gene product	zf-C3HC4,myosin_head,DIL,	20
15	449088	AI654048	Hs.196556	ESTs	SS,MACPF,sushi,ldl_recept	20
15	428642	NM_014899		KIAA0878 protein	BTB,ras	20
	419577	L36531	Hs.91296	integrin, alpha 8	TM,integrin_A,FG-GAP	2.0
	450435	AI695975	Hs.201805	ESTs	laminin_B,laminin_EGF,lam	2.0
	450696	Al654223	Hs.16026	hypothetical protein FLJ23191	SS	2.0
	421255	BE326214	Hs.93813	ESTs	TM	2.0
20	432467	T03667	Hs.239388	Human DNA sequence from clone	SS	2.0
	408654		Hs.46721	UCC1 protein	SS,Ependymin,SS	2.0
	412611	AA732036	Hs.164478	hypothetical protein FLJ21939	oo,Eponsynantoo	20
	453355	AW295374	Hs.31412			20
				myopodin	00 TH 0	
25	424665		Hs.139851	caveolin 2	SS,TM,Caveolin,Caveolin	2.0
23	458147	AW752597		gb:lL3-CT0214-161299-045-B06 C	SS,TM,PMM	2.0
	447566	N50432	Hs.102648	ESTs		20
	414496	W73853		ESTs	SS,TM,pkinase,F5_F8_type_	2.0
	425618	AW119112	Hs.9052	Homo sapiens cDNA: FLJ22042 fi	· SS,TM	2.0
	415168	NM_003652	Hs.78068	carboxypeptidase Z	Zn_carbOpept,Fz,Dioxygena	20 ·
30	422157	AW957295	Hs.112318	6.2 kd protein	SS	2.0
	450253	AL133047	Hs.24715	Homo sapiens mRNA; cDNA DKFZp4	SH3	2.0
	418919	AA232635		ESTs	SS,DUF25	2.0
	444846	AI871055	Hs.148477	ESTs	SS,TM	2.0
	418781	T41160	Hs.8404	ESTs	33,1W	2.0
35	410/01	141100	NS.04U4	E318		2.0
22	T. D. C 0.0			•		
	TABLE 24B:					
			t identifier number			
	CAT number	: Gene cluster	number			
40	Accession: (	Senbank acces	ssion numbers			
40						
	Pkev	CAT Number	Accession			
	Pkey 408468	CAT Number		2 BE000369 AA376876 N75269 AA345398 AA34	19053 AW960062 R76169 R70638 AA054	770 Al378587 Al338002 Al762398
	Pkey 408468	CAT Number 106033_1	AI909712 AL03975	2 BE000369 AA376876 N75269 AA345398 AA34 NA74112 AW450RRO AA6RR6RA R76114 AW242		
			A1909712 AL03975 N47873 A1066549 A	2 BE000369 AA376876 N75269 AA345398 AA34 1474112 AW450680 AA668668 R76114 AW2421		
45	408468	106033_1	Al909712 AL03975 N47873 Al066549 A AW297099	A1474112 AW450680 AA668668 R76114 AW242	828 N58855 AW080313 Al378491 Al8071	02 AA417043 Al565444 AW263286
45			A1909712 AL03975; N47873 A1066549 A AW297099 AA741357 A187000	N474112 AW450680 AA668668 R76114 AW242 0 W75997 H50726 AV658709 AI498817 AL0378	828 N58855 AW080313 Al378491 Al8071 04 W67847 BE018553 Al033256 N76810	02 AA417043 Al565444 AW263286 N31548 Al032084 N36278 AW075272
45	408468	106033_1	A1909712 AL03975; N47873 A1066549 A AW297099 AA741357 A187000 A1032081 R35753 V	A1474112 AW450680 AA668668 R76114 AW242	828 N58855 AW080313 Al378491 Al8071 04 W67847 BE018553 Al033256 N76810	02 AA417043 Al565444 AW263286 N31548 Al032084 N36278 AW075272
45	408468 410295	106033_1	A1909712 AL03975; N47873 Al066549 A AW297099 AA741357 Al87000 Al032081 R35753 V W69374 AA15	N474112 AW450680 AA668668 R76114 AW2421 0 W75997 H50726 AV658709 A498817 AL0378 W93372 AA700790 A1903697 N52985 R82468 AV	828 N58855 AW080313 Al378491 Al8071 04 W67847 BE018553 Al033256 N76810 W580252 AL036760 Al052219 R36621 W	02 AA417043 AI565444 AW263286 N31548 AI032084 N36278 AW075272 07047 AA088621 AI249109 W68776
45	408468	106033_1	A1909712 AL03975; N47873 A1066549 A AW297099 AA741357 A187000 A1032081 R35753 V W69374 AA15 W73853 AA928112	N474112 AW450680 AA668668 R76114 AW2421 0 W75997 H50726 AV658709 AM98817 AL0378 V93372 AA700790 A1903697 N52985 R82468 AV W77887 AW889237 AA148524 A1749182 A1754	828 N58855 AW080313 A1378491 A18071 04 W67847 Be018553 A1033256 N76810 W580252 AL036760 A1052219 R36621 W 442 A1338392 A1253102 A1079403 A1370£	02 AA417043 AI565444 AW263286 N31548 Al032084 N36278 AW075272 07047 AA088621 AI249109 W68776 i41 AI697341 H97538 AW188021
	408468 410295	106033_1	A1909712 AL03975; N47873 A1066549 A AW297099 AA741357 A187000 A1032081 R35753 V W69374 AA15 W73853 AA928112	N474112 AW450680 AA668668 R76114 AW2421 0 W75997 H50726 AV658709 A498817 AL0378 W93372 AA700790 A1903697 N52985 R82468 AV	828 N58855 AW080313 A1378491 A18071 04 W67847 Be018553 A1033256 N76810 W580252 AL036760 A1052219 R36621 W 442 A1338392 A1253102 A1079403 A1370£	02 AA417043 AI565444 AW263286 N31548 Al032084 N36278 AW075272 07047 AA088621 AI249109 W68776 i41 AI697341 H97538 AW188021
45 50	408468 410295	106033_1	A1909712 AL03975; N47873 A1066549 A AW297099 AA741357 A187000 A1032081 R35753 V W69374 AA15 W73853 AA928112	N474112 AW450680 AA668668 R76114 AW2421 0 W75997 H50726 AV658709 AM98817 AL0378 V93372 AA700790 A1903697 N52985 R82468 AV W77887 AW889237 AA148524 A1749182 A1754	828 N58855 AW080313 A1378491 A18071 04 W67847 Be018553 A1033256 N76810 W580252 AL036760 A1052219 R36621 W 442 A1338392 A1253102 A1079403 A1370£	02 AA417043 AI565444 AW263286 N31548 Al032084 N36278 AW075272 07047 AA088621 AI249109 W68776 i41 AI697341 H97538 AW188021
	408468 410295	106033_1	AI909712 AL03975; N47873 AI066549 A AW297099 AA741357 AI87000 AI032081 R35753 V W69374 AA15 W73853 AA928112 AI927669 W72716 A	N474112 AW450680 AA668668 R76114 AW2421 0 W75997 H50726 AV658709 A498817 AL0378 V93372 AA700790 A1903697 N52985 R82468 AV W77887 AW889237 AA148524 AJ749182 AJ754 AL051402 AJ188071 AJ335900 N21488 AW77047	828 N58855 AW080313 A1378491 A18071 04 W67847 Be018553 A1033256 N76810 W580252 AL036760 A1052219 R36621 W 442 A1338392 A1253102 A1079403 A1370£	02 AA417043 AI565444 AW263286 N31548 Al032084 N36278 AW075272 07047 AA088621 AI249109 W68776 i41 AI697341 H97538 AW188021
	408458 410295 414496	105033_1 11922_2 145392_1 180623_1	AI909712 AL03975: N47873 AI066549 A AW297099 AA741357 AIB7000 AI032081 R35753 V W69374 AA15 W73853 AA928112 AI927669 W72716 AI868132 H98 AA232635 AI37370	N474112 AW450680 AA668668 R76114 AW2421 0 W75997 H50726 AV658709 A1498817 AL0378 V93372 AA700790 A1903697 N52985 R82468 AV W77887 AW889237 AA148524 AL749182 A1754 AL051402 A1188071 AL335900 N21488 AW77047 3 AA233330	828 N58855 AW080313 Al378491 Al8071 04 W67847 BE018553 Al033256 N76810 W580252 AL036760 Al052219 R36621 W 442 Al338392 Al253102 Al079403 Al3705 '8 W92522 Al691028 Al913512 Al144448	02 AA417043 AI565444 AW263286 N31548 Al032084 N36278 AW075272 D7047 AA088621 AI249109 W68776 641 AI697341 H97538 AW188021 W73819 AA604368 N28900 W95221
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50	408468 410295 414496 418919 418956	106033_1 11922_2 145392_1 180623_1 180862_1	AI909712 AL03975 N47873 AI066549 A AW297099 AA741357 AIB7000 AI032081 R35753 V W69374 AA15 W73853 AA928112 AI927669 W72716 AI868132 H98 AA232635 AI37370 AA234831 AI70030 AI868257 AIB04295	N474112 AW450680 AA668668 R76114 AW2421 0 W75997 H50726 AV658709 AI498817 AL0378 V93372 AA700790 AI903697 N52985 R82468 AV W77887 AW889237 AA148524 AI749182 AI754 AI051402 AI188071 AI335900 N21488 AW77047 3 AA233330 2 AA906216 AA776957 R49415 AI420777 AA66 6 AA897791 AA232893 AI348680 AI356232 AA23	828 N58855 AW080313 Al378491 Al8071 04 W67847 BE018553 Al033256 N76810 W580252 AL036760 Al052219 R36621 W 442 Al338392 Al253102 Al079403 Al3706 78 W92522 Al691028 Al913512 Al144448 6394 Al830619 AA779469 Al972390 N408 35138 F31396 AW079977 H16405	02 AA417043 AI565444 AW263286 N31548 AI032084 N36278 AW075272 D7047 AA088621 AI249109 W68776 I41 AI697341 H97538 AW188021 W73819 AA604358 N28900 W95221
50	408468 410295 414496 418919	105033_1 11922_2 145392_1 180623_1	AI909712 AL03975 N47873 AI066549 A AW297099 AA741357 AI87000 AI032081 R35753 V W59374 AA15 W73853 AA928112 AI927669 W72716 AI868132 H98 AA232635 AI37370 AA234831 AI700429 AI493205 AA73231	N474112 AW450680 AA668668 R76114 AW2421  0 W77597 H50726 AV658709 AI498817 AL0378  V93372 AA700790 AI903697 N52985 R82468 AV  W77887 AW889237 AA148524 AI749182 AI754  AI051402 AI186071 AI335900 N21488 AW77047  3 AA233330  2 AA2306216 AA776957 R49415 AI420777 AA666  5 AA897791 AA232893 AI34680 AI356232 AA23  5 AA344619 AA904035 AW952967 AA488889 A	828 N58855 AW080313 Al378491 Al8071 04 W67847 BE018553 Al033256 N76810 W580252 AL036760 Al052219 R36621 W 442 Al338392 Al253102 Al079403 Al3706 78 W92522 Al691028 Al913512 Al144448 6394 Al830619 AA779469 Al972390 N405 35138 F31396 AW079977 H16405 A635644 BE245127 AA669979 AA761874	02 AA417043 AI565444 AW263286 N31548 AI032084 N36278 AW075272 D7047 AA088621 AI249109 W68776 I41 AI697341 H97538 AW188021 W73819 AA604358 N28900 W95221
	408468 410295 414496 418919 418956 424651	106033_1 11922_2 145392_1 180623_1 180862_1 241981_1	AI909712 AL03975: N47873 AI066549 / AW297099 AA741357 AIB7000 AI032081 R35753 V W69374 AA15 W73853 AA928112 AI858132 H98 AA232635 AI37370 AA234831 AI70030 AI688257 AI804295 AI493206 AA73231 AA766495 W76175	N474112 AW450680 AA668668 R76114 AW2421  0 W77597 H50726 AV658709 AI498817 AL0378  V93372 AA700790 AI903697 N52985 R82468 AV  W77887 AW889237 AA148524 AI749182 AI754  AI051402 AI188071 AI335900 N21488 AW77047  3 AA233330  2 AA906216 AA776957 R49415 AI420777 AA66  5 AA897791 AA232893 AI348680 AI356232 AA23  5 AA344619 AA904035 AW952967 AA48889 A  AI521825 AA746092 AA743152 AI478562 H888	828 N58855 AW080313 Al378491 Al8071 04 W67847 BE018553 Al033256 N76810 W580252 AL036760 Al052219 R36621 W 442 Al338392 Al253102 Al079403 Al3706 78 W92522 Al691028 Al913512 Al144448 6394 Al830619 AA779469 Al972390 N405 35138 F31396 AW079977 H16405 A635644 BE245127 AA669979 AA761874	02 AA417043 AI565444 AW263286 N31548 AI032084 N36278 AW075272 D7047 AA088621 AI249109 W68776 I41 AI697341 H97538 AW188021 W73819 AA604358 N28900 W95221
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50	408468 410295 414496 418919 418956 424651 436772 438780	106033_1 11922_2 145392_1 180623_1 180862_1 241981_1 426854_1 45501_1	AJ909712 AL03975 N47873 Al066549 A AW297099 AA741357 AI87000 Al032081 R35753 V W59374 AA15 W73853 AA928112 AJ927669 W72716 A868132 H98 AA232635 AJ37370 AL634331 Al70030 AL63257 AL64295 AL93206 AA73231 AA766495 W76175 AW975688 AA7321 M54936 AL025512 AL079277 AL241318	N474112 AW450680 AA668668 R76114 AW2421 0 W75997 H50726 AV658709 A498817 AL0378 V93372 AA700790 A1903697 N52985 R82468 A1 W77887 AW889237 AA148524 AI749182 AI754 AI051402 A1186071 AI335900 N21488 AW77047 3 AA233330 2 AA906216 AA776957 R49415 AI420777 AA666 6 AA997791 AA232893 AI348680 AI356232 AA2: 5 AA344619 AA904035 AW952967 AA488889 A AI521825 AA746092 AA743152 AI478562 H888 63 N67084 AI382987 BE061777 AA089966 BE169930 T411* I BE327710 AW975215 AW896268 AA884990 BI	828 N58855 AW080313 Al378491 Al8071 04 W67847 BE018553 Al033256 N76810 W580252 AL036760 Al052219 R36621 W 442 Al338392 Al253102 Al079403 Al3706 8 W92522 Al691028 Al913512 Al144448 6394 Al830619 AA779469 Al972390 N405 35138 F31396 AW079977 H16405 A635644 BE245127 AA669979 AA761874 63 76 AW594624 BE502415 AA121893 Al261	02 AA417043 AI565444 AW263286 N31548 AI032084 N36278 AW075272 D7047 AA088621 AI249109 W68776 641 AI697341 H97538 AW188021 W73819 AA604368 N28900 W95221 D80 AI094453 AA826397 AA535994 I H28767 AA910081 AA837086
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50 55 60 65 70	408468 410295 414496 418919 418956 424651 436772 438780 441916 444931 . 451573 458147 TABLE 24C: Pkey: Unique Ref: Sequer human strand: India Nt. position: Pkey 400829 400829 403247	106033_1 11922_2 145392_1 180623_1 180862_1 241981_1 426854_1 46501_1 528799_1 62567_1 875588_1 488021_1 e number corr nce source. The chromosome sites DNA stre- lindicates nucl 8670385 7656833	A909712 AL03975: N47873 AI066549 AV297099 AA741357 AI67000 AI032081 R35753 V W69374 AA15 W69374 AA15 W73853 AA928112 AI927669 W72716 AI8568132 H98 AA232635 AI37370 AA234831 AI70030 AI868257 AI804295 AI493206 AA73231 AA766495 W76175 AW975688 AA7310 M54936 AI025217 AV652066 AA4598 AI079277 AI241318 AA993571 AA9715 AV652066 AA4598 AI268985 AI388 AW130351 AW3388 AW130351 AW3388 AW152597 AW848  esponding to an Eos ne 7 digit numbers in ne 227 Dunham, et al. and from which exons erolide positions of pr Plus Strand NL pe Plus Strand Plus	N474112 AW450680 AA668668 R76114 AW2421 0 W75997 H50726 AV658709 AJ498817 AL0378 V93372 AA700790 AJ903697 N52985 R82468 AV W77887 AW889237 AA148524 AJ749182 AJ754 AJ051402 AJ188071 AJ335900 N21488 AW77047 3 AA233330 2 AA306216 AA776957 R49415 AJ420777 AA661 AA897791 AA232893 AJ348680 AJ356232 AA22 5 AA344619 AA904035 AW952967 AA488889 A AJ521825 AA746092 AA743152 AJ478562 H888 633 N67084 AJ882987 BE061777 AA089966 BE169930 T411 BE327710 AW975215 AW896268 AA884990 BI 8 AJ937262 BO T58512 T58561 AJ651255 N49838 H87921 AV AJ871252 AJ376942 AJ740496 AA452836 AJ277 BE99 AJ803973 781 AW849062 AW848490 AW752699 AW75260 probeset this column are Genbank Identifier (GI) numbers. [1999) Nature 402489-495 were predicted ediced exons Delicon T6-152616 6-77140 9-36282,37073-37813,38946-39314,40355-4065	828 N58855 AW080313 Al378491 Al8071  04 W67847 BE018553 Al033256 N76810  N580252 AL036760 Al052219 R36621 W  442 Al338392 Al253102 Al079403 Al3706  8 W92522 Al691028 Al913512 Al144448  6394 Al830619 AA779469 Al972390 N408  35138 F31396 AW079977 H16405  A635644 BE245127 AA669979 AA761874  63  76 AW594624 BE502415 AA121893 Al269  E327514  W264447 AA428067 AA364094 AW95568  917 Al149141 AA456147 Al784566 Al003  04 AW752700  . "Dunham I. et al." refers to the publication  Dunham I. et al." refers to the publication  11,42738-43028,43391-43696,45698-4603	02 AA417043 AI565444 AW263286 N31548 AI032084 N36278 AW075272 D7047 AA088621 AI249109 W68776 AI1 AI697341 H97538 AW188021 W73819 AA604358 N28900 W95221 D80 AI094453 AA826397 AA535994 I H28767 AA910081 AA837086 D8283 T40311 AI684569 AA257011 D5 D62894 AW341452 AA243652 D875 AI245674 AI433703 AI200208 In entitled The DNA sequence of
50 55 60 65 70	408468 410295 414496 418919 418956 424651 436772 438780 441916 444931 . 451573 458147 TABLE 24C: Pkey: Unique Ref: Sequer human strand: India Nt. position: Pkey 400829 400829 403247	106033_1 11922_2 145392_1 180623_1 180862_1 241981_1 426854_1 46501_1 528799_1 62567_1 875588_1 488021_1 e number corr nce source. The chromosome sites DNA stre- lindicates nucl 8670385 7656833	A1909712 AL03975 N47873 A1068549 A AV297099 AA741357 A167000 A1032081 R35753 V W69374 AA15 W69374 AA15 A1927669 W72716 A18568132 H98 AA232635 A137370 AA234831 A170030 A1868257 A1804295 A493206 AA73231 AA766495 W76175 AW975688 AA7310 M54936 A1025512 AU97277 A1241318 AA993571 AA9715 AV652066 AA4598 A1984618 A181683 AW130351 AW388 AW130351 AW388 AW130351 AW388 AW130351 AW388 AW152597 AW848  esponding to an Eos the 7 digit numbers in a 227 Dunham, et al. and from which exons eotide positions of pr Strand Plus Strand Plus Strand Plus 1521 Minus 7662 Plus 3601 5493	N474112 AW450680 AA66868 R76114 AW2421 0 W75997 H50726 AV658709 AI498817 AL0378 V93372 AA700790 AI903697 N52985 R82468 AV W77887 AW889237 AA148524 AI749182 AI754 AI051402 AI188071 AI335900 N21488 AW77047 3 AA233330 2 AA906216 AA776957 R49415 AI420777 AA66 6 AA897791 AA232893 AI348680 AI356232 AA23 5 AA344619 AA904035 AW9522957 AA488899 AI521825 AA746092 AA743152 AI478562 H888 63 N87084 AI3822987 BE061777 AA089966 BE169330 T411* BE327710 AW975215 AW896268 AA884990 BI 8 AI937262 BO T58512 T58561 AI651255 N49838 H87921 AV I AI871252 AI376942 AI740496 AA452836 AI277 699 AI803973 781 AW849062 AW848490 AW752699 AW75260 probeset this column are Genbank Identifier (GI) numbers. (1999) Nature 402489-495 is were predicted edicted exons position 76-152618 6-77140 9-36282 37073-37813,38946-39314,40355-4055 5,55201-55509,55926-56240,56355-56672,5707	828 N58855 AW080313 Al378491 Al8071  04 W67847 BE018553 Al033256 N76810  N580252 AL036760 Al052219 R36621 W  442 Al338392 Al253102 Al079403 Al3706  8 W92522 Al691028 Al913512 Al144448  6394 Al830619 AA779469 Al972390 N408  35138 F31396 AW079977 H16405  A635644 BE245127 AA669979 AA761874  63  76 AW594624 BE502415 AA121893 Al269  E327514  W264447 AA428067 AA364094 AW95568  917 Al149141 AA456147 Al784566 Al003  04 AW752700  . "Dunham I. et al." refers to the publication  Dunham I. et al." refers to the publication  11,42738-43028,43391-43696,45698-4603	02 AA417043 AI565444 AW263286 N31548 AI032084 N36278 AW075272 D7047 AA088621 AI249109 W68776 AI1 AI697341 H97538 AW188021 W73819 AA604358 N28900 W95221 D80 AI094453 AA826397 AA535994 I H28767 AA910081 AA837086 D8283 T40311 AI684569 AA257011 D5 D62894 AW341452 AA243652 D875 AI245674 AI433703 AI200208 In entitled The DNA sequence of
50 55 60 65 70	408468 410295 414496 418919 418956 424651 436772 438780 441916 444931 . 451573 458147 TABLE 24C: Pkey: Unique Ref: Sequer human strand: India Nt. position: Pkey 400829 400829 403247	106033_1 11922_2 145392_1 180623_1 180862_1 241981_1 426854_1 46501_1 528799_1 62567_1 875588_1 488021_1 e number corr nce source. The chromosome sites DNA stre- lindicates nucl 8670385 7656833	A1909712 AL03975 N47873 A1068549 A AV297099 AA741357 A167000 A1032081 R35753 V W69374 AA15 W69374 AA15 A1927669 W72716 A18568132 H98 AA232635 A137370 AA234831 A170030 A1868257 A1804295 A493206 AA73231 AA766495 W76175 AW975688 AA7310 M54936 A1025512 AU97277 A1241318 AA993571 AA9715 AV652066 AA4598 A1984618 A181683 AW130351 AW388 AW130351 AW388 AW130351 AW388 AW130351 AW388 AW152597 AW848  esponding to an Eos the 7 digit numbers in a 227 Dunham, et al. and from which exons eotide positions of pr Strand Plus Strand Plus Strand Plus 1521 Minus 7662 Plus 3601 5493	N474112 AW450680 AA668668 R76114 AW2421 0 W75997 H50726 AV658709 AJ498817 AL0378 V93372 AA700790 AJ903697 N52985 R82468 AV W77887 AW889237 AA148524 AJ749182 AJ754 AJ051402 AJ188071 AJ335900 N21488 AW77047 3 AA233330 2 AA306216 AA776957 R49415 AJ420777 AA661 AA897791 AA232893 AJ348680 AJ356232 AA22 5 AA344619 AA904035 AW952967 AA488889 A AJ521825 AA746092 AA743152 AJ478562 H888 633 N67084 AJ882987 BE061777 AA089966 BE169930 T411 BE327710 AW975215 AW896268 AA884990 BI 8 AJ937262 BO T58512 T58561 AJ651255 N49838 H87921 AV AJ871252 AJ376942 AJ740496 AA452836 AJ277 BE99 AJ803973 781 AW849062 AW848490 AW752699 AW75260 probeset this column are Genbank Identifier (GI) numbers. [1999) Nature 402489-495 were predicted ediced exons Delicon T6-152616 6-77140 9-36282,37073-37813,38946-39314,40355-4065	828 N58855 AW080313 Al378491 Al8071  04 W67847 BE018553 Al033256 N76810  N580252 AL036760 Al052219 R36621 W  442 Al338392 Al253102 Al079403 Al3706  8 W92522 Al691028 Al913512 Al144448  6394 Al830619 AA779469 Al972390 N408  35138 F31396 AW079977 H16405  A635644 BE245127 AA669979 AA761874  63  76 AW594624 BE502415 AA121893 Al269  E327514  W264447 AA428067 AA364094 AW95568  917 Al149141 AA456147 Al784566 Al003  04 AW752700  . "Dunham I. et al." refers to the publication  Dunham I. et al." refers to the publication  11,42738-43028,43391-43696,45698-4603	02 AA417043 AI565444 AW263286 N31548 AI032084 N36278 AW075272 D7047 AA088621 AI249109 W68776 AI1 AI697341 H97538 AW188021 W73819 AA604358 N28900 W95221 D80 AI094453 AA826397 AA535994 I H28767 AA910081 AA837086 D8283 T40311 AI684569 AA257011 D5 D62894 AW341452 AA243652 D875 AI245674 AI433703 AI200208 In entitled The DNA sequence of
50 55 60 65 70	408468 410295 414496 418919 418956 424651 436772 438780 441916 444931 . 451573 458147 TABLE 24C: Pkey: Unique Ref: Sequer human strand: India Nt. position: Pkey 400829 400829 403247	106033_1 11922_2 145392_1 180623_1 180862_1 241981_1 426854_1 46501_1 528799_1 62567_1 875588_1 488021_1 e number corr nce source. The chromosome sites DNA stre- lindicates nucl 8670385 7656833	A1909712 AL03975 N47873 A1068549 A AV297099 AA741357 A167000 A1032081 R35753 V W69374 AA15 W69374 AA15 A1927669 W72716 A18568132 H98 AA232635 A137370 AA234831 A170030 A1868257 A1804295 A493206 AA73231 AA766495 W76175 AW975688 AA7310 M54936 A1025512 AU97277 A1241318 AA993571 AA9715 AV652066 AA4598 A1984618 A181683 AW130351 AW388 AW130351 AW388 AW130351 AW388 AW130351 AW388 AW152597 AW848  esponding to an Eos the 7 digit numbers in a 227 Dunham, et al. and from which exons eotide positions of pr Strand Plus Strand Plus Strand Plus 1521 Minus 7662 Plus 3601 5493	N474112 AW450680 AA66868 R76114 AW2421 0 W75997 H50726 AV658709 AI498817 AL0378 V93372 AA700790 AI903697 N52985 R82468 AV W77887 AW889237 AA148524 AI749182 AI754 AI051402 AI188071 AI335900 N21488 AW77047 3 AA233330 2 AA906216 AA776957 R49415 AI420777 AA66 6 AA897791 AA232893 AI348680 AI356232 AA23 5 AA344619 AA904035 AW9522957 AA488899 AI521825 AA746092 AA743152 AI478562 H888 63 N87084 AI3822987 BE061777 AA089966 BE169330 T411* BE327710 AW975215 AW896268 AA884990 BI 8 AI937262 BO T58512 T58561 AI651255 N49838 H87921 AV I AI871252 AI376942 AI740496 AA452836 AI277 699 AI803973 781 AW849062 AW848490 AW752699 AW75260 probeset this column are Genbank Identifier (GI) numbers. (1999) Nature 402489-495 is were predicted edicted exons position 76-152618 6-77140 9-36282 37073-37813,38946-39314,40355-4055 5,55201-55509,55926-56240,56355-56672,5707	828 N58855 AW080313 Al378491 Al8071  04 W67847 BE018553 Al033256 N76810  N580252 AL036760 Al052219 R36621 W  442 Al338392 Al253102 Al079403 Al3706  8 W92522 Al691028 Al913512 Al144448  6394 Al830619 AA779469 Al972390 N408  35138 F31396 AW079977 H16405  A635644 BE245127 AA669979 AA761874  63  76 AW594624 BE502415 AA121893 Al269  E327514  W264447 AA428067 AA364094 AW95568  917 Al149141 AA456147 Al784566 Al003  04 AW752700  . "Dunham I. et al." refers to the publication  Dunham I. et al." refers to the publication  11,42738-43028,43391-43696,45698-4603	02 AA417043 AI565444 AW263286 N31548 AI032084 N36278 AW075272 D7047 AA088621 AI249109 W68776 AI1 AI697341 H97538 AW188021 W73819 AA604358 N28900 W95221 D80 AI094453 AA826397 AA535994 I H28767 AA910081 AA837086 D8283 T40311 AI684569 AA257011 D5 D62894 AW341452 AA243652 D875 AI245674 AI433703 AI200208 In entitled The DNA sequence of

Table 25A provides UnigenelD, Unigene Title, Pkey, and Exemplar Accession for sequences in Table 26. The information in Table 25A is linked by SEQ ID NO: to Table 26.

Table 25A: Pkey: Unique Eos probeset identifier number

PCT/US02/19297 WO 02/102235

Ex. Accn: Exemplar Accession number, Genbank accession number UG ID: UniGene number Titla: UniGene title SEQ ID NO: Sequence Identification number for sequences in Table 26

5	SEQ ID NO	): Sequence Identil	ication number for s	equences in Table 26	
)	Okoni	Pu Anna	UGID	Tille .	SEQ ID NO
	Pkey 452838	Ex. Acon U65011	Hs.30743	preferentially expressed antigen in mela	SEQ ID NO: 1-2
	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	SEQ ID NO: 3-4
	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular mat	SEQ ID NO: 5-6
10	458627	AW088642	Hs.97984	SRY (sex determining region Y)-box 17 (S	SEQ ID NO: 7-8
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	SEQ ID NO: 9-10
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	SEQ ID NO: 11-12
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	SEQ ID NO: 13-22
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	SEQ ID NO: 23-24
15	451110	A1955040	Hs.265398	PAR-6 beta (partitioning defective 6 h	SEQ ID NO: 25-26
	428187	A1687303	Hs.285529	G protein-coupled receptor 49	SEQ ID NO: 27-28
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	SEQ ID NO: 29-30
	433159	AB035898	Hs.150587	kinesin-like protein 2	SEQ ID NO: 31-32
20	426427	M86699	Hs.169840	TTK protein kinase	SEQ ID NO: 33-34 SEQ ID NO: 35-38
20	425371	D49441	Hs.155981 Hs.85339	mesothelin G protein-coupled receptor 39	SEQ ID NO: 39-40
	418506 456546	AA084248 Al690321	Hs.203845	KCNK15 potassium channel, subfamily K, m	SEQ ID NO: 41-42
	427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor	SEQ ID NO: 43-44
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	SEQ ID NO: 45-46
25	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic, stratum com	SEQ ID NO: 47-48
	412078	X69699	Hs.73149	paired box gene 8	SEQ ID NO: 49-52
	409178	BE393948	Hs.50915	kallikrein 5	SEQ ID NO: 53-54
	448243	AW369771		Integrin, beta 8	SEQ ID NO: 55-56
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	SEQ ID NO: 57-58
30	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	SEQ ID NO: 59-60
	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	SEQ ID NO: 61-62
	415539	AI733881	Hs.72472	BMP-R1B	SEQ ID NO: 63-64
	423961	D13666	Hs.136348	periostin (OSF-2os)	SEQ ID NO: 65-66 SEQ ID NO: 67-68
35	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein cartilage oligomeric matrix protein (pse	SEQ ID NO: 69-70
55	422867 409542	L32137 AA503020	Hs.1584 Hs.36563	hypothetical protein FLJ22418	SEQ ID NO: 71-72
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	SEQ ID NO: 73-74
	452747	BE153855	Hs.61460	lg superfamily receptor LNIR	SEQ ID NO: 75-76
	450375	AA009647		a disintegrin and metalloproteinase doma	SEQ ID NO: 77-78
40	426215	AW963419	Hs.155223	stanniocalcin 2	SEQ 1D NO: 79-80
	430044	AA464510	Hs.152812	ESTs	SEQ ID NO: 81
	447033	Al357412	Hs.157601	ESTs	SEQ ID NO: 82-87
	410418	D31382	Hs.63325	transmembrane protease, serine 4	SEQ ID NO: 88-89
15	411274	NM_002776	Hs.69423	kallikrein 10	SEQ (D NO: 90-91
45	422260	AA315993	Hs.105484	regenerating gene type IV	SEQ ID NO: 92-93 SEQ ID NO: 94-95
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	SEQ ID NO: 96-97
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like Insulin-like growth factor 2 (somatomedi	SEQ ID NO: 98-99
	404977 427747	AW411425	Hs.180655	serine/threonine kinase 12	SEO ID NO: 100-101
50	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	SEQ ID NO: 102-103
50	431846	BE019924	Hs.271580	uroplakin 1B	SEQ ID NO: 104-105
	425465	L18964	Hs.1904	protein kinase C, iota	SEQ ID NO: 106-107
	432938	T27013	Hs.3132	steroidogenic acute regulatory protein	SEQ ID NO: 108-109
	421451	AA291377	Hs.50831	ESTs	SEQ ID NO: 110-117
55	437478	AL390172	Hs.317432	branched chain aminotransferase 1, cytos	SEQ ID NO: 118-119
	411945	AL033527	Hs.92137	L-myc-2 protein (MYCL2)	SEQ ID NO: 120-121
	424078	AB006625	Hs.139033	paternally expressed 3	SEQ ID NO: 122-123
	406400	NN 044704	Hs.184339	kallikrein 8 (neuropsin/ovasin) (KLK8)	SEQ ID NO: 124-125 SEQ ID NO: 126-127
60	428450 438167	NM_014791 R28363	Hs.24286	KIAA0175 gene product chemokine binding protein 2 (CCBP2), mRN	SEQ ID NO: 128-129
UU	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	SEQ ID NO: 130-131
	430691	C14187	Hs.157208	aristaless-related homeobox protein ARX	SEQ ID NO: 132-133
	408081	AW451597	Hs.167409	intron of basic-helix-loop-helix-PAS pro	SEQ ID NO: 134
	411773	NM 006799	Hs.72026	protease, serine, 21 (testisin)	SEQ ID NO: 135-138
65	407792	Al077715	Hs.39384	putative secreted ligand homologous to f	SEQ ID NO: 139-140
	428093	AW594506	Hs.104830	ESTs	SEQ ID NO: 141 -144
•	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	SEQ ID NO: 145-148
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospha	SEQ ID NO: 149-150
70	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	SEQ ID NO: 151-152
70	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (	SEQ ID NO: 153-154
	436972	AA284679	Hs.25640	claudin 3	SEQ ID NO: 155-156 SEQ ID NO: 157-158
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3) (NGAL) kallikrein 11	SEQ ID NO: 157-160
	410001	AB041036	Hs.57771	NGMNGM FT	Quality 110. 100-100
75	TABLE 2	58:		•	

Pkey: Unique Eos probeset identifier number CAT number: Gene duster number Accession: Genbank accession numbers

CAT Number Accession AW369771 AW748174 AA290801 AA419198 AA044331 AA127909 AW995442 Al480343 AA044582 AW956159 AA373451 AA127965 AL134913 AW994956 BE622314 BE006298 BE006312 BE006303 BE006303 AA043906 AA234175 AA479726 AA095647 AA131254 AA374293 AW954405 H04410 AW605284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532 AA190933 H03231 H59605 H01642 AA852876 AA1313768 AA626915 AA746952 Al161014 AA099554 R69067 80 Pkey 448243 450375

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TABLE 25C:
        Pkey. Unique number corresponding to an Eos probeset
        Ref. Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of
 5
             human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
        Strand: Indicates DNA strand from which exons were predicted
        Nt_position: Indicates nucleofide positions of predicted exons
                                      Nt_position
10
        404977
                  3738341
                            Minus
                                      43081-43229
                                      1553-1712,1878-2140,4252-4385,5922-6077
        406400
                  9256298
                            Plus
        Table 26
15
        Seg ID NO: 1 DNA seguence
        Nucleic Acid Accession #: NM_006115.1
        Coding sequence: 236..1765
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20
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        ACTOTOTGAG GAAAAACCAT TTTGATTATT ACTOTCAGAC GTGCGTGGCA ACAAGTGACT
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        GAGACCTAGA AATCCAAGCG TTGGAGGTCC TGAGGCCAGC CTAAGTCGCT TCAAAATGGA
                                                                                        240
25
        ACGAAGGCGT TTGTGGGGTT CCATTCAGAG CCGATACATC AGCATGAGTG TGTGGACAAG
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        CCCACGGAGA CTTGTGGAGC TGGCAGGGCA GÄGCCTGCTG AAGGATGAGG CCCTGGCCAT
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        CGGGAGACAC AGCCAGACCC TGAAGGCAAT GGTGCAGGCC TGGCCCTTCA CCTGCCTCCC
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                                                                                       1620
                                                                                       1680
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                                                                                       1860
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         GATTCTGGCT TGGGAAGTAC ATGTAGGAGT TAATCCCTGT GTAGACTGTT GTAAAGAAAC
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         Seq ID NO: 2 Protein sequence
         Protein Accession #: NP_006106.1
60
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                                  21
                                               31
                                                                         51
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         VLDLRKNSHQ DFWTVWSGNR ASLYSFPEPE AAQPMTKKRK VDGLSTEAEQ PFIPVEVLVD
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                                                                                         360
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 70
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         Seg ID NO: 3 DNA sequence
         Nucleic Acid Accession #: Eos sequence
         Coding sequence: 264..782
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                                                                                         360
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 85
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540

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				ATGTCAATCC			720
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	AAAATAGCAA	CCACCACCA	•				
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	Protein Acc	ession #: 1 11	Cos sequence 21	; 31	41	51	
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20				PSFWYFVNPA			120
	Seq ID NO: Nucleic Aci			00.			
25	Coding sequ						
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				AAGGCCAGCA			540
				AAACTTTGTG			600
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				GCACCTTCAG			960
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50				CCTGAAACCT			1380
				GACAAAGGCA			1440
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				AAGCGGCACC			1800
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	TOTOTACAC	Cyccccacac	CTCCTCCCAG	ACATGCATAG	CAATCCCCAC	ACCITTACAC	3660
	TOCTCONONC	CV000C1010	acron contra	**********	CONTRACTOR CONTRACTOR	ACCCA MACMC	
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							3960
				AATATGTACT			
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	TTTTTCTACT	TGGGGGGAAA	AAAGTCCTCA	TGTAGAAGCA	CCCACTTTTG	CAATGITGIT	4260
	CTAACCTATC	יידי ב ביי דבי	TYPACHYCATIC	ATAAAGTTCC	TTAAGCTGGT	GATTCCTAAT	4320
15				TGTATTTGGT			4380 -
13							
	AATCCTGATT	TTGGAGACTT	AAAACCAGGT	TAATGGCTAA	GAATGGGTAA	CATGACTCTT	4440
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				CTTTTGGCTA			4560
				CITITOGCIA	acmmi corri	110000111111	1500
20	AGATTTTTTA	CTACAAAAAT	G				
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	Seg ID NO:	6 Protein s	emience				
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	Protein Acc						
	1	11	21	31	41	51	
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25	1000000000	COMPATIALA	IDIAAATAEO	DETLDKVPKS	DOVOCD II DA	OCTOD DOLVIES	60
23							
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30				SAEDLCTKEC			360
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				WSACSSSTCD			480
				SPCSISCGMG			540
	PTEETEKCTV	NEECSPSSCL	MTEWGEWDEC	SATCGMGMKK	RHRMI KMNPA	DGSMCKAETS	600
35	OVERCHWEEC	HTT DCT.T.SPW	SEWSDCSVTC	GKGMRTRQRM	LKSLAELGDC	NEDLEOVEKC	660
-							720
				RTRMIQMEPQ			
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40							
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	Coding secu	ence: 205.	. 1449				
	Coding sequ			23	41	<b>C1</b>	
	Coding sequ	ence: 205.	.1449 21	31	41	51	
				31 }	41	51 }	
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45	1     GCAGTGTCAC AGAACACGGG CTCATTCCCC	11   TAGGCCGGCT CGGCGGCTTC ACCCCCTCCC	21     GGGGGCCCTG   GGGCCGGGAG   CCGGGTCGGG	 GGTACGCTGT ACCCGCGCAG GGAGGCGGCG	AGACCAGACC CCCTCGGGGC CGTCCGGCGG	) GCGACAGGCC ATCTCAGTGC AGGGTTGAGG	120 180
45	1     GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGGC	11   TAGGCCGGCT CGGCGGCTTC ACCCCCTCCC AGGCCTGGAG	21     GGGGGCCCTG   GGGCCGGGAG   CCGGGTCGGG   CGCCATGAGC	GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG	AGACCAGACC CCCTCGGGGC CGTCCGGCGG CGGGATACGC	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC	120
	1     GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGGC	11   TAGGCCGGCT CGGCGGCTTC ACCCCCTCCC AGGCCTGGAG	21     GGGGGCCCTG   GGGCCGGGAG   CCGGGTCGGG   CGCCATGAGC	GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG	AGACCAGACC CCCTCGGGGC CGTCCGGCGG CGGGATACGC	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC	120 180 240
	1     GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGGC CAGAGCCAGA	11   TAGGCCGGCT CGGCGGCTTC ACCCCTCCC AGGCCTGGAG CCCAGAGCGC	21 GGGGGCCCTG GGGCCGGAG CCGGGTCGGG CGCCATGAGC GCTGCCCGCG	GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG	AGACCAGACC CCCTCGGGGC CGTCCGGCGG CGGGATACGC GGCTGGGCCC	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG	120 180 240 300
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	1 GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGGC CAGAGCCAGA GCCGAGTCGC GGAGCACCGG	11 ) TAGGCCGGCT CGGCGGCTTC ACCCCTCCC AGGCCTGAG CCCAGAGCGC TGAGCCCAT CCGGGGCCGC	21 GGGGGCCCTG GGGCCGGGAC CCGGGTCGG GCCCATGAGC GCTGCCCGCG CCGGGACATG GGGCCGAGCC	GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGTGAAGG AAGGGCGAGT	AGACCAGACC CCCTCGGGGC CGTCCGGCGG CGGGATACGC GGCTGGGCCC GCGAGGCGCC CCCGTATCCG	J GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GGCGAACAGC GCGGCCGATG	120 180 240 300 360 420
	1 GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGGC CAGAGCCAGA GCCGAGTCGC GGAGCACCGG	11 ) TAGGCCGGCT CGGCGGCTTC ACCCCTCCC AGGCCTGAG CCCAGAGCGC TGAGCCCAT CCGGGGCCGC	21 GGGGGCCCTG GGGCCGGGAC CCGGGTCGG GCCCATGAGC GCTGCCCGCG CCGGGACATG GGGCCGAGCC	GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGTGAAGG	AGACCAGACC CCCTCGGGGC CGTCCGGCGG CGGGATACGC GGCTGGGCCC GCGAGGCGCC CCCGTATCCG	J GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GGCGAACAGC GCGGCCGATG	120 180 240 300 360
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	1 GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGGC CAGAGCCAGA GCCGAGTCGC GGAGCACCGG AACGCTTTCA CTGCACAACG	11   TAGGCCGGCT CGGCGGCTTC ACCCCTCCC AGGCCTGAG CCCAGAGCGC TGAGCCCCAT CCGGGGCCGC TGGTGTGGGC CCGAGTTGAG	21   GGGGGCCCTG GGGCCGGGAG CCGGTCGGG GCTGCCCGCG CGGGCAGCC TAAGGACGAGC TAAGGACGAG CAAGATGCTG	GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGTGAAGG AAGGGCGAGT CGCAAGCCGGC GGCAAGTCGT	AGACCAGACC CCCTCGGGGC CGTCCGGCGG CGGGATACG GGCTGGGCCC CCCGTATCCG TGGCGCAGCA GGAAGGCGCT	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCTGG GCGGACAGG GCGCCGATG GAATCCAGAC GACGCTGGCG	120 180 240 300 360 420 480 540
50	1 GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGGC CAGAGCCAGA GCCGAGTCGC GGAGCACCGG AACGCTTTCA ACGCTTTCA CTGCACAACG	11  TAGGCCGGCT CGGCGGCTTC ACCCCTCCC AGGCCTGAG CCCAGAGGCG TGAGCCCAT CCGGGCCGC TGGTGTGGG CCTTGGTGAG CCTTCGTGGA	21 ) GGGGGCCCTG GGGCCGGAG CCGCGTCGGG CGCCCCGCG CCGGGACATG GGGCCGAGCC TAAGGACGAG CAAGATGCTG GGAGCAGAG	GETACGCTGT ACCCGCGAG ACCCGGATG GTGATGGCCG AAGGTGAAGG AAGGCGAGT CGCAAGCGGC CGCTGCCCC	AGACCAGACC CCCTCGGGGC CGTCCGGCGG CGGGATACGC GCCGGATACCG CCCGTATCCG GCAGGCGCA GCAAGGCGCT TGCAGCACAT TGCAGCACAT	GCGACAGGCC ATCTCAGTGC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCTGG GCGAACAGC GCGGCCGATG GAATCCAGAC GACGCTGGCG GACGACCAC	120 180 240 300 360 420 480 540 600
	1 GCAGTGTCAC AGRACACGGG CTCATTCCCC GGAGCGGGGC CAGAGCCAGA GCCGAGTCGC GGAGCACCGG AACGCTTTCA CTCCACAACG GAGRAGCGGC CCCAACTACA	11  TAGGCCGGCT CGGCGGCTTC ACCCCTCCC AGGCCTGGAG CCCAGAGCGC TGAGCCCCAT CCGGGGCCGC TGGTTGGGC CCTTCGTGGA AGTACCGCCC	21 ) GGGGGCCCTG GGGCCGGAG CCGCATGAGC GCTGCCCGCG CCGGGACATG GGGCCGAGCC TAAGGACGAG CAAGATGCTG GGAGGCAGAG GCGCCGCGC	GETACGCTGT GETACGCTGT ACCCGCGAGC GEAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGGCAGT CGCAAGCGGC GGCAAGTCGT CGGCTGCGCG AAGCAGTGGA	AGACCAGACC CCCTCGGGGC CGTCCGGCGG CGGGATACGC GGCAGGCCC CCCGTATCCG TGGCGCAGCA GGAAGGCGCT TGCAGCACAT AGCGGCTGAA	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GCGGACAGC GCGGCCGATG GAATCCAGAC GACGCTGGCG GCAGGACCAC GCGGGCCACG	120 180 240 300 360 420 480 540 600 660
50	1 GCAGTGTCAC AGRACACGGG CTCATTCCCC GGAGCGGGGC CAGAGCCAGA GCCGAGTCGC GGAGCACCGG AACGCTTTCA CTCCACAACG GAGRAGCGGC CCCAACTACA	11  TAGGCCGGCT CGGCGGCTTC ACCCCTCCC AGGCCTGGAG CCCAGAGCGC TGAGCCCCAT CCGGGGCCGC TGGTTGGGC CCTTCGTGGA AGTACCGCCC	21 ) GGGGGCCCTG GGGCCGGAG CCGCATGAGC GCTGCCCGCG CCGGGACATG GGGCCGAGCC TAAGGACGAG CAAGATGCTG GGAGGCAGAG GCGCCGCGC	GETACGCTGT ACCCGCGAG ACCCGGATG GTGATGGCCG AAGGTGAAGG AAGGCGAGT CGCAAGCGGC CGCTGCCCC	AGACCAGACC CCCTCGGGGC CGTCCGGCGG CGGGATACGC GGCAGGCCC CCCGTATCCG TGGCGCAGCA GGAAGGCGCT TGCAGCACAT AGCGGCTGAA	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GCGGACAGC GCGGCCGATG GAATCCAGAC GACGCTGGCG GCAGGACCAC GCGGGCCACG	120 180 240 300 360 420 480 540 600
50	GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGGC CAGAGCACAGA GCCGAGTCGC GAGACACCGG AACGCTTTCA CTGCACAACG GAGAAGCGGC CCCAACTACC GGCGGCTTCC	11    TAGGCCGGCT CGGCGGCTTC ACCCCTCCC AGGCCTGGAG CCCAGAGGGC TGAGCCCCAT CGGGGCGGC CCGAGTTGAG CCTTCGTGGA AGTACCGCCT TGCACGGCCT	21 ) GGGGGCCCTG GGGCCGGGG CGCGATGAGC GCTGCCGGG CGGGACATG GGGCCGAGCC TAAGGACGAG CAAGATGCTG GGAGCAGAG GCGCGGGGC GCGTGAGCCG	GGTACGCTGT ACCCGCGCAG GCACGCGCGAGGCGCGAGGCGCGAAGGGCGAGT CGCAAGCGGCGGCAGTCGGCAAGCGGCAGCGGCAGCGGCAGCGGCCGCCGCCGCCC	AGACCAGACC CCCTCGGGGC CGTCCGGGGC CGGGATACGC GGCTGGGCCC CCCGTATCCG TGCGCGCAGCA TGCAGCACT TGCAGCACT TGCAGCACT TGCAGCACT TGCAGCACACA CGCTGGGCCC	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GCGGACAGC GCGGCCGATG GAATCCAGAC GACGCTGGCG GCAGGACCAC GCAGGTGAGG CCAGGGCCAC	120 180 240 300 360 420 480 540 600 660 720
50	1 GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGGC CAGAGCACGG GCGAGTCGC GAGCACCGG AACGCTTTCA CTGCACAACG GAGAAGCGGC CCCAACTACA GGCGGCTTCC CGCGTGGCCA	11    TAGGCCGGCT CGGCGGCTTC ACCCCTCCC AGGCCTGGAG CCCAGAGGGC TGAGCCCCAT TGGTGTGGGC CCGAGTTGAG CCTTCGTGAA AGTACCGGCC TGCACGGCCT TGGACGGCCT TGGACGGCCT	21     GGGGGCCCTG   GGGCCGGGG   CGCGTCGCG   CGGGGACATG   GGGCCGGGGG   CAAGATGCTG   GGAGCAGAG   GGGCGGGGG   GGCTGAGCC   GGCTGAGCC   GGCTCAGCC   GGCCTCCAG	GETACGCTGT GETACGCTGT ACCCGCAGC GEAGGCGCGC AGCCCGGATG GTGATGGCCG AAGGTGAAGG AAGGCAGGC GGCAAGCCGC CGCAGCGCGC AAGCAGGTGA ACAGCAGGTGA CAGGCGCCG TTCCCCGAGC	AGACCAGACC CCCTCGGGGG CGGGATACGC GGCAGGGGCC GCGAGGCGC CCCGTATCGG TGGCGCAGCA GGAAGGGCTT TGCAGCACAT AGCGGCTGAA GGGGCTTCCC AGGGCTTCCC	GCGACAGGC AGGGTTGAGG AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GCGAACAGC GCGGCGATG GAATCAGAC GACGCTGGG GAGGACAC GCGGGTGGAG CGAGGACCAC CGGGTGGAG CGAGGCCGC	120 180 240 300 360 420 480 540 600 660 720 780
50	1 GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGGG CCGAGTCGC GGAGCACCGG AACGCTTTCA GAGAAGCGGC CCCAACTACA GGCGGCTTC CGCGTGGCCA CCGCTGCTGC	11    TAGGCCGGCT CGGGGGCTTC ACCCCTCCC AGGCCTGGAG CCCAGAGGGC TGAGCCCCAT CCGGGGCGC CGGAGTTGAG CCTTCGTGGA AGTACCGGCC TGGACGGCCT TGGACGGCCT TGGACGGCCT CTCCGCACAT	21 ) GGGGGCCCTG GGGCCGGGAG CCGGTCGGG CGCCATGAGC CGGGCAGGACATG GGGCCAGGAG CAAGATGCTG GGAGCAGAG GCGCGGGGCGGG	GTTACGCTGT GGTACGCTGT ACCCGCAGC GGAGGCGGCG AGCCGGATG GTGATGGCCG AAGGTGAAGG AAGGGCGAGT CGCAAGTCGT CGCTGCGCG AAGCAGGTGA CAGCAGCGCCC TTCCCCCAGC TACCCGCACC	AGACCAGACC CCCTCGGGGC CGTCCGGCGG GGCTGGGCCC GCCGTATCGG TGGGCAC TGGGCAGCA TGGAGCACA AGGGCTTGAA AGGGCTTGAA AGGGCTTGAA AGGGCTTCCC GCCAGAGTCT	GCGACAGGCC AGGGTTGAGG CAGTGACGAC CTGCCCTGG GGCGAACAGC GCAGCCGATG GAATCCAGAC GAACGCTGGCG GCAGGACCAC	120 180 240 300 360 420 480 540 600 660 720 780
50 55	GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGGC CAGAGCACAGA GCCGAGTCGC GGAGCACCGG AACGCTTTCA CTGCACAACG CCCCAACTACA GGCGGCTTCC CGCTGGTGCCA CCGCTGCTGC	11    TAGGCCGGCT CGGCGGCTTC ACCCCTCCC AGGCCTGGAG CCCAGAGGCC TGAGCCCCAT CCGGGCGCGC CGGGTTGGGC CCGAGTTGAG CCTTCGTGGA AGTACCGGCC TGCACGGCC TGCACGGCCT TGCACGGCC TGCACGGCCT CTCCCCCACAT	21 ) GGGGGCCCTG GGGCCGGGG CGCGTCGGG GGCCCATGAGC CGGGGACATG GGGCCGAGCC TAAGGACGAG CAAGATGCTG GGAGGCCGAGC GCCGGGGG GCCTCCAG GGGCCTCCAG GGGCGCCAC	GETACGCTGT GETACGCTGT ACCCGCGCAG GCACGCGCGATG GTGATGGCCG AGCCCGGATG AGGGCGAGT CGCAAGCGGC GGCAAGTCGT CGGCTGCGGC AAGCAGGTGA CAGGCGCG ATCCCCCGAGC TCCCCGAGC TACCGCGACT GACAGGTCCC	AGACCAGACC CCCTCGGGGC CGGGATACGC GGCTGGGCGC GGCAGGCGCC CCCGTATCCG TGGCGCAGCA TGCAGCACA AGCGCCTGAA CGCTGGGCCC AGGGCTTCCC GCAGAGTCT CGCTGACGC CGCAGAGTCC CGCTGACGC	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCTGG GCGACAGC GCGGCCGATG GAATCCAGAC GACGCTGGGC GCAGGACCAC GCGGCTGGGC GCAGGACCAC GCGGCCGCCCC GCGGCCCC CGTGGACCCC	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50	GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGGC CAGAGCACAGA GCCGAGTCGC GGAGCACCGG AACGCTTTCA CTGCACAACG CCCCAACTACA GGCGGCTTCC CGCTGGTGCCA CCGCTGCTGC	11    TAGGCCGGCT CGGCGGCTTC ACCCCTCCC AGGCCTGGAG CCCAGAGGCC TGAGCCCCAT CCGGGCGCGC CGGGTTGGGC CCGAGTTGAG CCTTCGTGGA AGTACCGGCC TGCACGGCC TGCACGGCCT TGCACGGCC TGCACGGCCT CTCCCCCACAT	21 ) GGGGGCCCTG GGGCCGGGG CGCGTCGGG GGCCCATGAGC CGGGGACATG GGGCCGAGCC TAAGGACGAG CAAGATGCTG GGAGGCCGAGC GCCGGGGG GCCTCCAG GGGCCTCCAG GGGCGCCAC	GETACGCTGT GETACGCTGT ACCCGCGCAG GCACGCGCGATG GTGATGGCCG AGCCCGGATG AGGGCGAGT CGCAAGCGGC GGCAAGTCGT CGGCTGCGGC AAGCAGGTGA CAGGCGCG ATCCCCCGAGC TCCCCGAGC TACCGCGACT GACAGGTCCC	AGACCAGACC CCCTCGGGGC CGGGATACGC GGCTGGGCGC GGCAGGCGCC CCCGTATCCG TGGCGCAGCA TGCAGCACA AGCGCCTGAA CGCTGGGCCC AGGGCTTCCC GCAGAGTCT CGCTGACGC CGCAGAGTCC CGCTGACGC	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCTGG GCGACAGC GCGGCCGATG GAATCCAGAC GACGCTGGGC GCAGGACCAC GCGGCTGGGC GCAGGACCAC GCGGCCGCCCC GCGGCCCC CGTGGACCCC	120 180 240 300 360 420 480 540 600 660 720 780
50 55	GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGGC CAGAGCACGG GAACACCGG AACGCTTCA CGCAACTACG GAGAAGCGC CCCAACTACA CGCGGGTTCC CGCGTGGCCA CCGCTGCTGC CCGCTCCACG	11    TAGGCCGGCT CGGCGGCTTC ACCCCTCCC AGGCCTGGAG CCCAGAGGCGC TGAGCCCCAT TGGTGTGGGC CCGAGTTGAG CCTTGTGGA AGTACCGCCC TGGAGCGCCT TGGAGGCCT TGGACGCCT TTGGCACAT TTGTCCCCT TTGTCCCCT TTGTCCCCT TTTTTCCCCCC	21 ) GGGGGCCCTG GGGCCGGGG CGGGGACATG GGGCCCAGGG CAAGATGCTG GAGGCAGGG GCGCGGGG GGGTAGGCGG GGGTAGGCGG GGGTAGCCG GGCCCACGCC CCCAATGCCC	GETACGCTGT GEAGGCGCAG GEAGGCGCAG GEAGGCGCAG GTGATGGCCG AAGGTGAAGG AAGGCAGAT CGCAAGCGGC GGCAAGTCGT CAGCGCGCG TTCCCCGAGC TACCGCGACT GACACGTCCC GGGGACTGCCC	AGACCAGACC CCCTCGGGGG CGGGATACGC GGCAGGGCCC GCGAGGCGCC CCCTATCGG TGGCGCC GGAGGGCTTA AGCGGCTGAA AGCGGCTGAA GGGGCTTCCC GCCAGAGTTCC GCCAGAGTTCC GCCAGAGTCC CGCTGGACCC CGCGGGCCCC	GCGACAGGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GCGAACAGC GCGGCGATG GAATCAGAC GAGGCTTGAGG GAGGACAC GCGGGTTGAGG GCAGGACCAC GCGGGTGGAG CGAGGCCGC CGCCGGCCCG GGGGCGCCC CGCCGGCCCC CACCTACAGC	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50 55	1 GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGCGGG CCGAGTCGC GGAGCACCGG AACGCTTTCA CTGCACAACG GAGAAGCGGC CCCAACTACA GGCGGCTTCC CGCGTGGCCA CCGCTGGCCA CCGCTGCTGACG GACCCGGCTT TACGCGCAGG	11   TAGGCCGGCT CGGGGGCTTC ACCCCTCCC AGGCCTGAAG CCCAAAGGCC TGAGCCCCAT CCGGGGCCGC TGGTTGGGC CCTGAGTTGAG CCTTCGTGAA AGTACCGGCC TGGAACGCCT TGGAACGCCT CTCCGCACAT TCTTCGCGC TCTTCTCGCACAT	21 ) GGGGGCCCTG GGGCCGGAG CCGGTCGCG CGCGCATCAGC TAAGGACGAG CAAGATGCTG GGAGCAGAG GGCCGGGCG GGCTGAGCC GGCCTCAGC GGCCTCAGC CCCACGCC CCCATGCCC CCCGATGCCC	GSTACGCTGT GGGGCGCG GGGGCGCGAGGCGCG AGCCGGATG GTGATGGCG AAGGGGGC AAGGGCGAGT CGCAAGTCGT CAGCAGCGGC AAGCAGGTCA AAGCAGGTCA AAGCAGGTCA CAGCGCCCC GGCAACTCCC GGGGACTGCC	AGACCAGACC CCCTCGGGGC CGTCCGGCGG GGGATACGC GGCAGGGCCC GCGAGCGCCC GCGAGCGCC CCCGTATCCG TGCAGCACA AGCGCTGAA AGCGCTGAA AGCGCTGAA AGCGCTTCCC AGGGCTTCCC GCCAGAGTCT CGCAGCACGC CGGCCGGTCC CCCCGGTCC CCCCGGTCC	GCGACAGGCC AGGGTTGAGG CAGTGACGAC CTGCCCTGG GGCGAACAGC GCAGCCGATG GAACCAC GCAGGACCAC GCAGACCAC GCAGACCAC GCAGACCAC GCAGACCAC GCAGACCAC GCAGACCAC GCACACACA	120 180 240 300 360 420 480 540 600 660 720 780 840 900 1020
50 55	1 GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGGC CAGAGCCAGA GCCGAGTCGC GGAGCACCGG AACGCTTTCA GCGACACACG GACAACTACA GCGGGCTTCC CCCCTGCTGCCA CCGCTGGCCA CCGCTGCTGC GACCCGGCTT TACGCGCAGC	11   TAGGCCGGCT CGGGGGCTTC ACCCCTCCC AGGCCTGGAG CCCARAGGCC TGAGCCCCAT CGGGGCGCC TGGTTGGG AGTACCGCCT TGGACGCCT TGGACGCCT TGGACGCCT TGGACGCCT TGGACGCCT TCTCGGACAA GCTACCGGCT TCTTCGCGACAA CAGAGCCCGC	21 ) GGGGGCCCTG GGGCCGGGAG CCGGTCGGG CGCCATGAGC CGGGACATG GGCCGAGCC TAAGACCAG CAAGATGCTG GGAGCAGAG GCGCGGCGC GGCTCAGCC GGGCCTCAG GGCCTCAG GGCCGCCAC CCCATGCCC CCGATGCCC GGGTCCCTCG	GGTACGCTGT ACCCGGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGGCGAGT CGCAAGCGGC GGCAAGTCGT CAGCAGCGGC AAGCAGGTCA AAGCAGGTCA AAGCAGGTCA AAGCAGGCCCC GACACTCCC GACACTCCC GACACTCCC CCGGAGCCTC ATTCCGGGCCTC ATTCCGGGCCCA	AGACCAGACC CCCTCGGGGC CGGGATACGC GGCAGGCGC CCCGTATCCG GGCAGCGCAC GGAAGGCGCC TGCAGCACA AGCGCTGAA AGCGCTGAA AGCGCTTCAC GCCAGAGTTCC GCCAGAGTCC GCCAGAGTCT CGCTGGACGC CGCCGGGCCC CGCCCGGTCC TCCTGGCCC TCCTGGCCC TCCTGGCCC	GCGACAGGC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GCGAACAGC GCGGCCGATG GAATCCAGAC GACGCTGGCG GCAGGACCAC GCGGCCGCCC GCGGCCGCCCC GCGCCCCC CGCGCCCC CGCCGC	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020
50 55	GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGGC CAGAGCACGAG GCCGAGTCGC GCAGACTCCACACACACACACACACACACACACACACACA	11    TAGGCCGGCT CGGCGGCTTC ACCCCTCCC AGGCCTGCAG AGGCCTGAAG CCCAGAGGGC TGAGCCCCAT CGGGGTTGAG CCTTGGTGAA AGTACCGGCC TGCACGGCCT TGCACGGCCT TCCCCACAT TCTTCGCACAT TCTTCGCACAT TCTTCGCACAT ACTACCGTC TCTCGGACAT ACTACGGCCC ACAGGCCCGC ACAGGCCCGC ACAGGCCCGC ACAGGCCCGACAT ACAGGCCCGACAT ACAGGCCCGACAT ACAGGCCCGACAT ACAGGCCCGACAT ACAGGCCCGACAT ACAGGCCCGACAT ACAGGCCCGACAT ACAGGCCCGACACT ACAGGCCCCACACT ACAGGCCCCACACT ACAGGCCCCACACT ACAGGCCCCACACT ACAGGCCCCACACT ACAGGCCCCACACT ACAGGCCCCACACT ACAGGCCCACACT ACAGGCCCCACACT ACAGGCCCACACT ACAGGCCCCACACT ACAGGCCCACACT ACAGGCCCCACACT ACAGGCCCACACT ACAGGCCCCACACT ACAGGCCCACACT ACAGGCCCCACACT ACAGGCCCCAC	21 ) GGGGGCCCTG GGGCCGGAG CCGGGTCGCG GGCCCATGAGC GGGCCCATGAGC TAAGGACGAG CAAGATGCTG GGAGCCATGAGCC GGCTGAGCCG GGCTCAAGCCG CCCACGCCC CCCGATGCCC CCCGATGCCC GGGTCCCTCG GGTCCCTCG GATGGCCTCC	GETACGCTGT GEGACGCGCAG GCAGGCGCGCAGCCCGGATG GTGATGGCCG AAGGTGAAGGCGCG AAGGGCGAGT CGCAAGCGGC GGCAAGTCGT CAGCTGCCGCAGCC TCCCCGAGC TACCGCGACT GACACGTCCC GGGGACTCCC CCGGAGCCTC CCCGGAGCCTC CCCCGGGCCGC CCCCGGGCCGC	AGACCAGACC CCCTCGGGGC CGGGATACGC GGCTGGGCGC GGCATACGC GGCAGCAC GGCAGCAC TGCGCCAC TGCAGCAC AGCGCTTCCC GGCAGCAC AGCGCTCCC CCCTATCCC CCCGACC AGGCCTCCC CCCGACC CCCCGCCC CCCGGCCC CCCGGCCC CCCCGGCCC CCCCGCCC CCCCGCCC CCCCGCCC	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCTGG GCGACAGC GCGGCCGATG GAATCCAGAC GAGGTTGAGG GCAGGACCAC GCGGGTTGAGG CGAGGGCCCG CGCGGCCCC CGCGGCCCC CACCTACAGC CAGGGCCCC CACCTACAGC CCGGCCCC CCCGCCCC CCCGCCCCC CCCGCCCC	120 180 240 300 360 420 480 540 660 720 720 720 960 1020 1080 1140
50 55 60	GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGGC CAGAGCACGAG GCCGAGTCGC GCAGACTCCACACACACACACACACACACACACACACACA	11    TAGGCCGGCT CGGCGGCTTC ACCCCTCCC AGGCCTGCAG AGGCCTGAAG CCCAGAGGGC TGAGCCCCAT CGGGGTTGAG CCTTGGTGAA AGTACCGGCC TGCACGGCCT TGCACGGCCT TCCCCACAT TCTTCGCACAT TCTTCGCACAT TCTTCGCACAT ACTACCGTC TCTCGGACAT ACTACGGCCC ACAGGCCCGC ACAGGCCCGC ACAGGCCCGC ACAGGCCCGACAT ACAGGCCCGACAT ACAGGCCCGACAT ACAGGCCCGACAT ACAGGCCCGACAT ACAGGCCCGACAT ACAGGCCCGACAT ACAGGCCCGACAT ACAGGCCCGACACT ACAGGCCCCACACT ACAGGCCCCACACT ACAGGCCCCACACT ACAGGCCCCACACT ACAGGCCCCACACT ACAGGCCCCACACT ACAGGCCCCACACT ACAGGCCCACACT ACAGGCCCCACACT ACAGGCCCACACT ACAGGCCCCACACT ACAGGCCCACACT ACAGGCCCCACACT ACAGGCCCACACT ACAGGCCCCACACT ACAGGCCCACACT ACAGGCCCCACACT ACAGGCCCCAC	21 ) GGGGGCCCTG GGGCCGGAG CCGGGTCGCG GGCCCATGAGC GGGCCCATGAGC TAAGGACGAG CAAGATGCTG GGAGCCATGAGCC GGCTGAGCCG GGCTCAAGCCG CCCACGCCC CCCGATGCCC CCCGATGCCC GGGTCCCTCG GGTCCCTCG GATGGCCTCC	GGTACGCTGT ACCCGGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGGCGAGT CGCAAGCGGC GGCAAGTCGT CAGCAGCGGC AAGCAGGTCA AAGCAGGTCA AAGCAGGTCA AAGCAGGCCCC GACACTCCC GACACTCCC GACACTCCC CCGGAGCCTC ATTCCGGGCCTC ATTCCGGGCCCA	AGACCAGACC CCCTCGGGGC CGGGATACGC GGCTGGGCGC GGCATACGC GGCAGCAC GGCAGCAC TGCGCCAC TGCAGCAC AGCGCTTCCC GGCAGCAC AGCGCTCCC CCCTATCCC CCCGACC AGGCCTCCC CCCGACC CCCCGCCC CCCGGCCC CCCGGCCC CCCCGGCCC CCCCGCCC CCCCGCCC CCCCGCCC	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCTGG GCGACAGC GCGGCCGATG GAATCCAGAC GAGGTTGAGG GCAGGACCAC GCGGGTTGAGG CGAGGGCCCG CGCGGCCCC CGCGGCCCC CACCTACAGC CAGGGCCCC CACCTACAGC CCGGCCCC CCCGCCCC CCCGCCCCC CCCGCCCC	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020
50 55 60	GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGGC CAGAGCACGG GAGCACCGG AACGCTTTCA CTGCACAACC GAGAAGCGC CCCAACTACA CGCGGTTCC CCGCTGGCCA CCGCTGCTGC CCGCTCGACC CGACTCGACC CTCCACC TACCGCCT TACGCGCAGC CGACTCGCCC CTTCACGTGT ATGCAGCCG	11    TAGGCCGGCT CGGCGGCTTC ACCCCTCCC AGGCCTGCAG CCCAGAGGCGC TGAGCCCCAT TGGTGTGGGC CCGAGTTGAG CCTTCGTGAA AGTACCGCCC TTGCACACAT TGCACGGCCT TTGCACACAT TCTTCGCGCC TCTCTCGCACAT ACTACCGCCC TCTCTCGCACAT ACTACCGCCAC ACTACGGCCACAC ACTACGGCGCACACAC ACTACGGCGCACACACACACACACACACACACACACACAC	21 ) GGGGGCCCTG GGGCCGGGG CGGGGACATG GGGCCGAGGC CAAGATGCTG GAGGCCGAGCC GGCTGAGCC GGCTCCAG GGCCGACGC GGCTCCAG GCCACGCC CCCCATGCCC CGCTGGCCCC CGCTGGCCCC CGCTGGCCCC CGCTGGCCCC CGCTGGCCCC CGCTCCCCCACGCC	GETACGCTGT GEGAGGCGCG GEAGGCGGAGG GTGATGGCG AAGGCGGATG GGCAAGCGGC GGCAAGCGGC AAGGCGGCG TTCCCCGAGC TTCCCCGAGC TACCGCGACT GACAGCTGC CGGGAGCTCC CCGGAGCCTC CCGGAGCCTC CCGGAGCCTC CCGGAGCCTC CCCGGAGCCTC CCCGGGGCCC CCCGGGGCGCC	AGACCAGACC CCCCCGGG AGACCAGAC CCCCCGGG AGACCAC CCCCCCGGG AGACCAC AGAGGCCC AGGGCCC AGGCCC AGGGCCC AGGGCCC AGGCCC AGG	GCGACAGGC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GCGAACAGC GCGGCCATG GAATCCAGAC GCGGCTGGAG GCAGGACCAC GCGGGTGGAG CGAGGACCAC GCGGGCCCG GGGGGCCCT CGTGGACCCC ACCTACAGC CATGCACCC ACCCAGCCCC CGGCTCCAC CCGGCTCCAG	120 180 240 300 360 420 540 600 660 720 780 840 900 1020 1020 1140 1200
50 55	GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGC CAGAGCACAGA GCCGAGTTCA CTGCACAACG GAAAGCGGC CCCAACTACA GGCGGCTTCC CGCTGGTGCCA CGGTGGCCA CGGTTCGCC GACTACACG GACCACTACA CCGCTGCTGC CCGCTTCGACG GACCACGGCTT TACGCGCAG CGACTCGGCC CTTCACGTGT ATGCAGCCGC CTTCACGTGC CCGCTGGCCCC CTTCACGTGC	11    TAGGCCGGCT CGGCGGCTTC ACCCCTCCC ACCCCTCCC AGGCCTGGAG CCCAGAGCGC TGAGCCCCAT TCAGGCCCCAT TGACGCCC TGCACGGCCT TGCACGGCCT TCCCGCACAT TCTTCGCCACAT TCTTCGCCACAT TCTTCGCCACAT ACACCCCGC ACACACCACA ACACCACCA AACACCACCA ACACCAC	21    GGGGGCCCTG GGGCCGGGG GGCCATGAGC GCCATGAGC GGGCCGAGCC TAAGGACGAG CAAGATGCTG GGAGCCAGAGAG GCGCGAGGC GGCTCCAG GGGCCTCCAG GGCCTCCAG GGCCTCCCG GGGTCCCCC CCCATGCCC CCGATGCCC CCGATGCCC AGGCCCCC AGGCCCCAGACCCAG ACTGCCCCAG	GTTACGCTGT GCACGCCGCAG GCACGCCGCAGCCC AGCCCGCATG GCACGCCCCAGCCC AAGCCCCCAGCCCCCCCAGCCCCCCCC	AGACCAGACC CCCTCGGGGC CGGATACGC GGCAGCACC CCCGTATCGG GGCAGCACC GGCAGCACC GGCAGCACC GGCAGCACC GCCAGCACC GCCGGCAGC GCCGGCGCGC GCCGGGCGCGC GCGCGGGCGCGC TCCTGGCCCC GCGGGGCGCGC GCGGGGCGCGC GCGGGGCGCGC GCGGGGGCGCG GCGGGGCGCG	GCGACAGGC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GCGAACAGC GCGGCCGATG GAATCCAGAC GCGGCCGAC GCGGCCGCGCGCGCGCGCCGCCGCCGCCCCCCCC	120 180 240 300 360 420 480 660 720 780 840 900 960 1020 1080 1140 1200 1260
50 55 60	GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGGC GGAGCACGG AACACTTTCA CTGCACAACG GAGAAGCGGC CCCAACTACA CGCGGGTTCCC CGCGTGGCCA CGCGTGGCCA GACCACGG GACCCGGTTCACACGGCGCTTCACGGCTTCACGGCCGCTTCACGCCTTCACGTGTT ATGCGGCACGCCCCCGGGCTCCCCC	11    TAGGCCGGCT CGGCGGCTTC ACCCCTCCC AGGCCTGCAG AGGCCTGAGAG CCCAGAGGCGC TGAGCCCAT CGGGCGGC CCGAGTTGAG CCTTCGTGGA AGTACCGGC TGCACGGCCT TGCACGGCCT TCTCGGCACAT TCTTCGGCACAT TCTTCGGCACAT TCTTCGCACTAT CAGAGCCCGC ACTACGGCCG ACTACGGCGC ACTACGGCGG ACTACGGCGG ACTACGGCGG GGGAGGTGGA	21    GGGGGCCCTG GGGCCGGGG CGGGTCGGG GGCCCGGGG CGGGGACATG GGGCCGAGGC TAAGGACGA CAAGATGCTG GGAGCCTCCAG GGCCTCCAG GGCCTCCAG GGCCTCCAG GGCCTCCAG GCCCACGCCC CCCGATGCCC CAGGCCCTCCAG ACTCCCTGC CCAGCACCAC ACTCCCTGC	GETACGCTGT GETACGCTGT ACCCGCGCAG GCACGCGCGC AGCCCGGATG GTGATGGCCG AAGGGCGAGT CGCAAGCGGC GCAAGTCGT CAGCAGCGCG TTCCCCCAGC TACCCCGAGCT GACACTCCC CCGGGGCCTC ATTCCGGGCCC CCCGGGGCCGC CACCAGCACC CCGGGGCCGC CCCGGGGCCGC TTTCAACAGT	AGACCAGACC CCCTCGGGGC CGGGATACGC GGCAGGCGC GGCAGCACA GGCAGCACA GGCAGCACA AGCGCTTCAC GCCAGCACA AGCGCTTCAC GCCAGCACT CCCCGGCACC CCCCCGGCAC AGCCCTCCC GCCAGCAC CCCCCGCC CCCCCCGGC CCCCCCCGCAC ACCCCCCCGAC ACCCCCCAGA ATCTGCACT	GCGACAGGCC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GCGGACAGG GCGGCCGATG GAATCCAGAC GCGGCCGATG GCAGGACCAC GCGGCCGCCC GCGGCCGCCC CGCCGGCCCC CACCTACAGC CACCGACACA CCCCGACACA CCCCGGACAAG CCCCGGACAAG CCCCGGACAAG CCCCGGCCC CGGTTGCAAG CCCTGCGCCC CGTGTGCAAG	120 180 240 300 360 420 480 540 660 720 780 960 1020 1080 1140 1200 1260 1320
50 55 60	1     GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGGC CAGAGCACGG GCAGTCGC GAGAGCACGG AACGCTTCA CTGCACAACA CGCGGCTTCC CGCTGGCCA CCGCTGCTGC CGCTCGCGC CGACTACG CGACTCCG CGTCGCCG CGTCGCCG CTTCACGTGT ATGCACGCCC CGGTCGCCC CGGTCGCCC CGGTCCCCC CGGCTCCCC CGGCTCCCCC CGGCTCCCCC CCCCAGGATGGCCCCC CCCCAGGATGGCCCCC CCCCAGGATGGCCCCC CCCCAGGATGGCCCCC CCCCAGGATGGCCCCC CCCCAGGATGGCCCCC CCCCAGGATGGCCCCCC CCCCAGGATGGCCCCCC CCCCAGGATGGCCCCCC CCCCAGGATGGCCCCCC CCCCAGGATGGCCCCCC CAGCACCCCCC CCCCAGGATGGCCCCCC CAGCACCCCCC CAGCACCCCC CAGCACCCCC CCCCAGGATGGCCCCCC CCCCAGGATGGCCCCCCC CCCCAGCCCCCC CCCCAGCCCCCC CCCCAGCCCCCCCC	11    TAGGCCGGCTT CGGCGGCTTC CGGCGGCTTC ACCCCTCCC AGGCCCCTTGAGG CCCAGAGGCGC TGAGCCCCAT TGGTGTGGGA CCTGGTGGAG CCTGGGCGCCT TGGACGGCCT TGGACGGCCT TGCACGGCCT TCCGCACAT TCTTCGCGC TCTCGGACAA ACTACCGGCC TCTCGGACAA ACTACGGCC TCTCGGACAA CCGGGGCGACAC CCCGGAGGCGGAGCAC ACCAGCA CCCCGGAGGC GCGCGGGGGGGG	21    GGGGGCCCTG GGGCCGGGG CGGGTCGGG CGCGCACGGG CAAGATGCTG GAGCCAGGC GGGCCGCG GGCCCACGCC GGCCCCCCCACGCC CCCAATGCCC CCCAATGCCC CGGTCCCCC CCCATGCCC CCCATGCCC CCCACGCC CCACGCC CCACGCC CCACGCACCAG ACTGCCCTGCA CCACGGACCAG CCCCACGGCACCAG CCCCACGGCACCAG CCCCACGGCACCAC CCCCACGGCACCAC CCCCACGGCACCAC CCCCACGGCACCAC CCCCACGGCACCAC CCCCCACGGCACCAC CCCCCACGGCACCAC CCCCCACGGCACCAC CCCCCACGGCACCAC CCCCCACGGCACCAC CCCCCCCC	GETACGCTGT GEGAGGCGCGAGGCGCGAGGCGCGAGGCGCGAGCCGCGAGCCCCCGGGGAGCCCCCC	AGACCAGACC CCCTCGGGGC CGCGATACGC GGCAGGGCC CCCTATCGG GGAGGGCC CCCTATCGG TGCAGCACA AGGGCTTCA AGGGCTTCA AGGGCTTCCC GCAGAGTTCC GCAGAGTTCC GCCAGAGTTCC TGCTGACGC CGCCGGCC CGCCGGCC AGGCCTCC TCCTGCGCC AGGCCTCC TCCTGCGCC AGGCCTCC TCCTGCCCC TCCTCCCCC TCCTCCCC TCCTCCCCC TCCTCC	GCGACAGGC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GCGAACAGC GCGGCCATG GAATCAGAC GCAGGCCACG GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC CACCTACAGC CACCTACAGC CACCTACAGC CACCTACAGC CCAGCCCCC CCGGCTCCAC CCCGGACAG CCAGCCAGCCC CCGGTTGCAAC CCAGCCACC CCGTGTGCAAC CCAGCCACC CCGTGTGCAAC CCAGCACAC CCAGCCACC CCGTGTGCAAC CCACCACCAC CCAGCACAC CCACACAC CCACAC CCACACAC CCACACAC CCACACAC CCACACAC CCACACAC CCACACAC CCACAC CCACACAC CCACACAC CCACACAC CCACAC CCACACAC CCACAC	120 180 240 300 360 420 540 660 660 720 780 840 960 1020 1140 1260 1320 1380
50 55 60	1     GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGGC CAGAGCACGG GCAGTCGC GAGAGCACGG AACGCTTCA CTGCACAACA CGCGGCTTCC CGCTGGCCA CCGCTGCTGC CGCTCGCGC CGACTACG CGACTCCG CGTCGCCG CGTCGCCG CTTCACGTGT ATGCACGCCC CGGTCGCCC CGGTCGCCC CGGTCCCCC CGGCTCCCC CGGCTCCCCC CGGCTCCCCC CCCCAGGATGGCCCCC CCCCAGGATGGCCCCC CCCCAGGATGGCCCCC CCCCAGGATGGCCCCC CCCCAGGATGGCCCCC CCCCAGGATGGCCCCC CCCCAGGATGGCCCCCC CCCCAGGATGGCCCCCC CCCCAGGATGGCCCCCC CCCCAGGATGGCCCCCC CCCCAGGATGGCCCCCC CAGCACCCCCC CCCCAGGATGGCCCCCC CAGCACCCCCC CAGCACCCCC CAGCACCCCC CCCCAGGATGGCCCCCC CCCCAGGATGGCCCCCCC CCCCAGCCCCCC CCCCAGCCCCCC CCCCAGCCCCCCCC	11    TAGGCCGGCTT CGGCGGCTTC CGGCGGCTTC ACCCCTCCC AGGCCCCTTGAGG CCCAGAGGCGC TGAGCCCCAT TGGTGTGGGA CCTGGTGGAG CCTGGGCGCCT TGGACGGCCT TGGACGGCCT TGCACGGCCT TCCGCACAT TCTTCGCGC TCTCGGACAA ACTACCGGCC TCTCGGACAA ACTACGGCC TCTCGGACAA CCGGGGCGACAC CCCGGAGGCGGAGCAC ACCAGCA CCCCGGAGGC GCGCGGGGGGGG	21    GGGGGCCCTG GGGCCGGGG CGGGTCGGG CGCGCACGGG CAAGATGCTG GAGCCAGGC GGGCCGCG GGCCCACGCC GGCCCCCCCACGCC CCCAATGCCC CCCAATGCCC CGGTCCCCC CCCATGCCC CCCATGCCC CCCACGCC CCACGCC CCACGCC CCACGCACCAG ACTGCCCTGCA CCACGGACCAG CCCCACGGCACCAG CCCCACGGCACCAG CCCCACGGCACCAC CCCCACGGCACCAC CCCCACGGCACCAC CCCCACGGCACCAC CCCCACGGCACCAC CCCCCACGGCACCAC CCCCCACGGCACCAC CCCCCACGGCACCAC CCCCCACGGCACCAC CCCCCACGGCACCAC CCCCCCCC	GETACGCTGT GEGAGGCGCGAGGCGCGAGGCGCGAGGCGCGAGCCGCGAGCCCCCGGGGAGCCCCCC	AGACCAGACC CCCTCGGGGC CGCGATACGC GGCAGGGCC CCCTATCGG GGAGGGCC CCCTATCGG TGCAGCACA AGGGCTTCA AGGGCTTCA AGGGCTTCCC GCAGAGTTCC GCAGAGTTCC GCCAGAGTTCC TGCTGACGC CGCCGGCC CGCCGGCC AGGCCTCC TCCTGCGCC AGGCCTCC TCCTGCGCC AGGCCTCC TCCTGCCCC TCCTCCCCC TCCTCCCC TCCTCCCCC TCCTCC	GCGACAGGC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GCGAACAGC GCGGCCATG GAATCAGAC GCAGGCCACG GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC CACCTACAGC CACCTACAGC CACCTACAGC CACCTACAGC CCAGCCCCC CCGGCTCCAC CCCGGACAG CCAGCCAGCCC CCGGTTGCAAC CCAGCCACC CCGTGTGCAAC CCAGCCACC CCGTGTGCAAC CCAGCACAC CCAGCCACC CCGTGTGCAAC CCACCACCAC CCAGCACAC CCACACAC CCACAC CCACACAC CCACACAC CCACACAC CCACACAC CCACACAC CCACACAC CCACAC CCACACAC CCACACAC CCACACAC CCACAC CCACACAC CCACAC	120 180 240 300 360 420 480 540 660 720 780 960 1020 1080 1140 1200 1260 1320
50 55 60	1     GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGGC CAGAGCACGG GCGAGTCGC GAGACACCGG AACGCTTTCA CTGCACAACG GAGAAGCGGC CCCAACTACA CGCGTGGCCA CCGCTGGCCA CGACTGGCC CTTCACGTGT ATGCAGCAGG CCGTCGCCC CTTCACGTGT CCGTCGCCC CTTCACGTGT CCGTCGCCC CTTCACGTGT CCGTCGCCC CCTCAGCAGG CCGTCGCCCC CGAGCTCCTCGC CCGTCGCCCC GAGCTCCTCGC CCTCAGATGG CCTCGAGATGG CCGTCGCCCC GAGCTCCTCG CCTCAGATGG CGGCCCATTT	11   TAGGCCGGCT CGGCGGCTTC CGGCGGCTTC ACCCCTCCC AGGCCCAT CCCAGAGGCC TGAGCCCCAT CGGGGGCTTCAGGC CCTGAGTTGAG CCTTCGTGAA AGTACCGGCCT TGCACGGCCT TCTCGCACAT TCTTCGCGCC TCTCGCACAT CAGAGCCCGC TCTCGCACAT CAGAGCCCGC TCTCGGACT CAGAGCCCGC TCTCGGACT CCCGGAGCT CCCGGAGGC CCCCCCCTA CCTCCGGTGGT CCTCCGGTGGT	21    GGGGGCCCTG GGGCGGGAG CCGGTCGGG GCCATGAGC CGGGGACATG GGGCCGAGGCC TAAGGACGAG CAAGATGCTG GGAGCAGAG GGCTGAGCC GGGCTGAGCC CCCATGCC CCACGCC CCACGCACAG ACTGCCCTGG CCACGGAC ACTGCCCTGC CCGCACGGAC ACTGCCCTGC CCGCACGGAC CCACGGAC CCACGGACAC GTCCAACGCC CTCCAACGCC CTCCAACGCC CTCCAACGCC CTCCAACGCC CTCCAACGCC CTCCAACGCC CTCCAACGCC CTCCAACGCC CTCCAACGCC CTCCCAACGCC CTCCAACGCC CTCCAACGC CTCCAACGCC CTCCAACCC CTCCAACC CTCCAACCC	GSTACGCTGT GGTACGCTGT ACCCGCAGG GGAGGCGGCG AGCCGGATG GTGATGGCG AAGGTGAAGT CGCAAGTGGC CGGCAGTGCGCG AAGCAGGTGA CAGCAGCGCC TTCCCGAGC TACCCCGAGC TACCCGCACC GGGACTGCC CCGGAGCCTC ATTCCGGGCC CCCGGGCCGC CACCGGCCC CCGGGCCGCC CACCGCCCC CGGCACCTC ATTCCGGGCC CCGCGCGCC CACCGCCCC CGGCACCTC ATTCCGGCCC CCGCGCCGCC CACCCCCCCCCC	AGACCAGACC CCCTCGGGGC CGGGATACGC GGCTGGGCCC GGCTGGCCC CCCGTATCCG GGCAGGCCC TGCAGCACA AGCGCTGAA AGCGCTGAA AGCGCTTCCC GCCAGAGTCT CGCTGGACGC CGCCGGTCC TCCTGGCCCC TCCTGGCCCC TCCTGGCCCC TCCTGGCCC TCCTGGCCCC TCCTGGCCCC TCCTGGCCCC TCCTGCCCCAG ATCTACACTT TCTACACTT TCTACACTT TCTATATTACTG TCTTTACTGCCC TATATTACTG	GCGACAGGC ATCTCAGTGG AGGGTTGAGG CAGTGACGAC CTGCCCTGG GGCGAACAGC GCAGCCCATG GAACCAC GCAGGACCAC CACCTACAGC CACCTACAGC CCAGGACCAC CCAGGACCAC ACCTACAGC CCAGGACCAC CCAGCACCAC CCAGCACCAC CCAGCACCAC CCAGCACCAC CCAGCACCAC CCAGCACCAC CCACTACCAC CCACTACCAC CCACTACCAC CCACTACCAC CCACTACCAC CCACCACCAC CCACTACCAC CCACTACCAC CAACTATCCT	120 180 240 300 360 420 660 660 720 780 840 900 1020 1020 1140 1200 1260 1380 1440
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGC CAGAGCACAGA GCCGAGTCGC GGAGCACCGG AACGCTTTCA CTGCACAACG CCCCAACTACA CGGTGGCCA CCGCTGCTGC CCGCTCGACG GACCCGGCTT TACGGCCGC CTTCACGTGGC CGACTCGGCC CGTGCTCGCCC CGAGCTCCTCG GACTCGCCC	11    TAGGCCGGCT CGGCGGCTTC ACCCCTCCC ACCCCTCCC AGGCCTGGAG CCCAGAGCGC TGAGCCCCAT CCGGGGCCGC TGGATTGGGC CGGAGTTGAG CCTTCGTGGA AGTACCGCCT TGCACGGCCT TCTCGGACTA TCTTCGGACTA CTTCGGACTA CTTCGGACTA CTCCGACTA CTCCGGACTA CTCCGGACTA CTCCGGACGC ACTACGGCC ACTACGCC ACTACGCC ACTACGCC ACTACGCC ACTACGCC ACTACGCC ACTACGCC ACTACGCC ACTACGCC ACTACC ACTACGCC ACTACGC ACTACGCC ACTACGC ACT	21  GGGGGCCCTG GGGCCGGGG GGCCGGGG GGCCGAGGC CGGGGACATG GGGCCGAGGC CAAGATGCTG GGGCCGAGGC GGCCTCAGG GGCCTCAG GGGCCTCAG GGGCCTCCAG GGGCCTCCAG GGGCCTCCG CCCATGCCC CCGATGCCC CCGATGCCC CCGATGCCC CCAGCACACAC GCCACACACAC GCCACACACAC	GETACGCTGT GETACGCTGT GEAGGCGCG AGCCCGGATG GEAGGCGCG AAGCCGGATG AAGGGCGCG AAGCAGTCGT CGCAAGTCGT CAGCAGCTGCGCG AAGCAGGTCA AAGCAGGTCA CAGCAGCTCCC GAGCACTCCC CCCGAGCCTC ATTCCCGGCC CCCCGAGCCTC ATTCCCGGCCC CCCGGGCCGC CACCAGCACC CCGGGACGCC TTTGAACAGT GACTCCCGCG AGCTCCCGCGGCCC CCGGGACGCCC CCGCGACGCCC CCGCGACGCCC CCGCGACGCCC CCGCGACGCCC CCGCGACGCCC CCGCGACGCCC CCCGCGACCCC CCCGCGCCCCCCCC	AGACCAGACC CCCTCGGGGC CGGATACGC GGCAGCACC CCCGTATCCG GGCAGCACC GGCAGCACC GGCAGCACC GGCAGCACC GCCAGCACC GCCGGCAGCA AGGCCTTCC GCCGGCGCC GCCAGAGTCT TCCTGGCCC CCCCCGGC CCCCCGGCACC TCCTGGCCCC TCCTGGCCC TCCTGGCCCC TCCTGGCCCC TCCTGCCCC TCCTGCCCC TCCTGCCCC TCCTGCACCT TCAATATACTGCACTT AGAAGCAGTG	GCGACAGGC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GCGAACAGC GCGGCCGATG GAATCCAGAC GCGGCCGAC GCGGCCGCGCGCCGCCGCCGCCCC CGCGGCCCC CACCTACAGC CACCTACAGC CACCTACAGC CACCTACAGC CCGGCCCC CCGGCCCC CCGGCCCC CCGGCCCC CCGGACAC CCACCTACAGC CCACTACCC CCTGTCCAAC CCACTACCC CCACTACCC CCACTACCC CCACTACCC CCACTACCC CCACTACCC CCACTACCC CCACTACCC CCACTACCC CTGTCCAAC CCACTACCC CTACTACCC CTACTACC CTACTAC CTACT	120 180 240 300 360 420 480 540 660 720 780 960 1020 1140 1260 1320 1320 1340 1500
50 55 60	GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGGC CAGAGCACGAG GCCGAGTCGC GCAGACTCGC GCAGACTCCA CCCCAACTACA GGCGGCTTCC CCCCAACTACA GCGGCTTCC CCGCTGCGCG CCGCTCGCC CCTCCACGAG ATGCACAGG CCTCCACGGCT ATGCACGGCCCCC CGGTCGCCCC CGGGCCTCTCC CCTCGACGG CCTCGACGGC CCTCGACGGCCCCCC CCTCGACGAGTCCCCCC CCTGAGATGG CCCTGAGATGG CCCTGAGATGG CCCTGAGATGG CCCTGGAGGAGG	11    TAGGCCGGCT CGGCGGCTTC ACCCCTCCC AGGCCTGCAG AGGCCTGAAG CCCAGAGGCC TGAGCCCCAT CCGGGCGCGC CCGAGTTGAG CCTTCGTGGA AGTACCGGCC TGCACGGCCT TGCACGGCCT TCTCGGACAT TCTTCGCACAT TCTTCGCACAT ACTACCGGTC CCTCGGACAT CCTCGGACAT CCTCGGACAT CCTCGGACAT CCTCGGAGGC ACACCAGCA CTCCGGAGGC CTCCGGAGGA GCCTCCCCTA CCTCGGTGGT AGGTCCCTGA CCTAAGGAAT CTAAGGAAAT CCTCCCTCCCCTC	21    GGGGGCCCTG GGGCCGGAG CCGGGTCGGG GGCCCATGAGC GGGCCGAGAG CAGATGCTG GGAGCAGAG CAAGATGCTG GGAGCAGAG GGCGACAGAG GGCCACAGAC CCCAACACC CCCGATGCCC GGGTCCCTCG GATGGCCTCG GATGGCCTCG GATGCCCTCG CCGCACGAC CCGACACAC CCGACACAC CCGCACACAC CCGCCCAGACC CCGCACGAC CCGCACGAC CCGCACGAC CCGCACGAC CCGCCCAGAC CCTCCACACC CCTCCCCCAGACCC CCCCCACACAC CCTCCCCCCAC	GETACGCTGT GEAGGCGCAG GEAGGCGCAG GEAGGCGCAG GEAGGCGCAG AGGCGCAGCAGCAGCAGCAGCAGCACCACCAGCACCCCCGGAGCCTCCCCGAGCCCCCCGGAGCCTCCCCCGGAGCCTCCCCGGAGCCTCCCCGGAGCCTCCCCGGAGCCTCCCCGGAGCCTCCCCGGAGCCTCCCCGGAGCCCCCCGGAGCCCCCCGGAGCCCCCCCGGAGCCCCCC	AGACCAGACC CCCTOGGGGC CGCAGAGCCACACACACACACACACACACACACA	GCGACAGGC AGGGTTGAGG AGGGTTGAGG CAGTGACGAC GCGACAGG GCGACAGC GCAGGCCATG GAATCAGAC GCAGGCCACG GCAGGACAC GCAGGACAC GCAGGACAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCACTACAGC CACTACAGC CACTACAGC CCAGCCAC CCAGCACAC CCAGCACAC CCAGCACAC CCAGCACAC CCAGCACC CTCAGCACC CCTGTGCAAC CCAGCACC CCTGTGCAAC CCAGCACC CTTACACAC CTACACC CTTACACAC CTACACC CTACACC CTTTACACACT TTACACACTT TTACACACTT	120 180 240 300 360 420 540 660 720 780 960 1020 1080 1140 1260 1320 1380 1440 1500 1560
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGGC CAGAGCACGAG GCCGAGTCGC GCAGACTCGC GCAGACTCCA CCCCAACTACA GGCGGCTTCC CCCCAACTACA GCGGCTTCC CCGCTGCGCG CCGCTCGCC CCTCCACGAG ATGCACAGG CCTCCACGGCT ATGCACGGCCCCC CGGTCGCCCC CGGGCCTCTCC CCTCGACGG CCTCGACGGC CCTCGACGGCCCCCC CCTCGACGAGTCCCCCC CCTGAGATGG CCCTGAGATGG CCCTGAGATGG CCCTGAGATGG CCCTGGAGGAGG	11    TAGGCCGGCT CGGCGGCTTC ACCCCTCCC AGGCCTGCAG AGGCCTGAAG CCCAGAGGCC TGAGCCCCAT CCGGGCGCGC CCGAGTTGAG CCTTCGTGGA AGTACCGGCC TGCACGGCCT TGCACGGCCT TCTCGGACAT TCTTCGCACAT TCTTCGCACAT ACTACCGGTC CCTCGGACAT CCTCGGACAT CCTCGGACAT CCTCGGACAT CCTCGGAGGC ACACCAGCA CTCCGGAGGC CTCCGGAGGA GCCTCCCCTA CCTCGGTGGT AGGTCCCTGA CCTAAGGAAT CTAAGGAAAT CCTCCCTCCCCTC	21    GGGGGCCCTG GGGCCGGAG CCGGGTCGGG GGCCCATGAGC GGGCCGAGAG CAGATGCTG GGAGCAGAG CAAGATGCTG GGAGCAGAG GGCGACAGAG GGCCACAGAC CCCAACACC CCCGATGCCC GGGTCCCTCG GATGGCCTCG GATGGCCTCG GATGCCCTCG CCGCACGAC CCGACACAC CCGACACAC CCGCACACAC CCGCCCAGACC CCGCACGAC CCGCACGAC CCGCACGAC CCGCACGAC CCGCCCAGAC CCTCCACACC CCTCCCCCAGACCC CCCCCACACAC CCTCCCCCCAC	GETACGCTGT GEAGGCGCAG GEAGGCGCAG GEAGGCGCAG GEAGGCGCAG AGGCGCAGCAGCAGCAGCAGCAGCACCACCAGCACCCCCGGAGCCTCCCCGAGCCCCCCGGAGCCTCCCCCGGAGCCTCCCCGGAGCCTCCCCGGAGCCTCCCCGGAGCCTCCCCGGAGCCTCCCCGGAGCCTCCCCGGAGCCCCCCGGAGCCCCCCGGAGCCCCCCCGGAGCCCCCC	AGACCAGACC CCCTOGGGGC CGCAGAGCCACACACACACACACACACACACACA	GCGACAGGC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GCGAACAGC GCGGCCGATG GAATCCAGAC GCGGCCGAC GCGGCCGCGCGCCGCCGCCGCCCC CGCGGCCCC CACCTACAGC CACCTACAGC CACCTACAGC CACCTACAGC CCGGCCCC CCGGCCCC CCGGCCCC CCGGCCCC CCGGACAC CCACCTACAGC CCACTACCC CCTGTCCAAC CCACTACCC CCACTACCC CCACTACCC CCACTACCC CCACTACCC CCACTACCC CCACTACCC CCACTACCC CCACTACCC CTGTCCAAC CCACTACCC CTACTACCC CTACTACC CTACTAC CTACT	120 180 240 300 360 420 480 540 660 720 780 960 1020 1140 1260 1320 1320 1340 1500
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGGC CAGAGCACGG GCGAGTCGC GAGACACCG GAGAGCACGG AACGCTTCA CGCGTGGCCA CGCGGGTCCC CGCTGGCGC CGCTCGCGC CGTCGCGC CTCCACGTAC ATGCACGCTTCA CGGTGGCCA CTCCACGTGTGC CTTCACGTGT ATGCAGCGC CGGTCGCCC CGGCTCCCCC CGGCTCTCG CCTCGAGGGG CCTCGAGGAGG CCTCGAGGAGG CCTCGAGGAGG CCTGGAGGAGG TTAAAAGGTG TTAAAAGGTG	11    TAGGCCGGCT CGGCGGCTTC ACCCCTCCC AGGCCGCT CCCAGAGGCGC TGAGCCCCAT CCGGGGGCGC CCGAGTTGAG CCTGATGAG AGTACCGCCC TGCAGCGCT TGCACGGCCT TGCACGGCCT TCCTCGCACAT TCTTCGCGC TCTCGGACTA ACTACCGCT CCTCGGACTA ACTACCGCT CCTCGGACTA ACTACGGCC ACTACGGGCG ACCCCCTA CCTCGGTGGT AGGTCCCTCA CCTCGGTGGT AGGTCCCTCA CTCAGGAAT TGTTGGCATA	21    GGGGGCCCTG GGGCCGGGAG CCGGGTCGGG CGCGCACTGAGC CGGGGACATG GGGCCCAGGG CAAGATGCTG GGAGCCAGGC GGCTCCCAG GGCCCACGCC CCCAATGCCC CCCAATGCCC CGCTCCCCAG ACTGCCCCAG ACTGCCCTGAC CCAGCACCAG ACTGCCCCCAGC CCGCACGGAC CCCGCACGCAC CCCCCAGGCCC CCGCACGCA	GETACGCTGT GEGAGGCGGAG GEAGGCGGAGG AGCCAGGAGG AGGCGGAGG AGGCGGAGG AGGCGGAGG CGGCAGGCGGAGGCGAGCGCAGCAGCAGCAGCAGCAGCAG	AGACCAGACC CCCTCGGGGC CGCGGATACGC GGCAGGGCCC GCGGAGGCCC CCCTATCGG GGAGGGCCC TGCAGCACAT AGGGGTTCCC GCCAGAGTTCC GCCAGAGTTCC GCCAGAGTTCC GCCAGAGTTT CGCTGGCCC TCCTGGCCC CCGCCGGCCC AGGCCCAG ACCCCCGG ACCCCCGG ACCCCCGG ACCCCCAG ATTACATACCC TATATTACTG AGAAGCAGTT TGAATCTCCC TTGCTGCCAC TTGTTGCCAC TTGTTGCCAC	GCGACAGGCC AGGGTTGAGG CAGTGACGAC GCGCCATG GCGACACAG GCGCCATG GACGCTGGAG GCAGCCGATG GAAGACCAC GCGGCCGATG GCAGGACCAC GCGGCCGATG GCAGGACCAC GCGGCCCG GCGCCCG GCGCCCG CACCTACAGC CACCTACAGC CACCTACAGC CCGGCTCCAC CCGGCTCCAC CCGGCTCCAC CCGGCTCCAC CCGCTTCCAC CCACTACAGC CACTACAGC CAACTATCC TTACACACTT TTGCACACTT TTGCACACTT	120 180 240 300 360 420 540 660 660 720 780 960 1020 1140 1200 1240 1320 1380 1440 1560 1620
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGC CAGAGCACAGA GCCGAGTTCA CTGCACAACG GAGAGCACAGA GCCGAGTCGC CCCAACTACA GGCGGCTTCC CCCCACTACA CGCTGGCCA GACCACTACA CGCTGCTGC CCCCACTACA GACCACTTCC CCCTACACA GCGCTTCC CCCTCGACG GACCCGCTCGACG CTTCACGTGT ATGCAGCAG CCGTCCCCC GAGCTCCTCG CCTTCAGATGG CCGTCCCCC GAGCTCCTCG CTTGAGATGG CTGAGATGG TTAAAAGGTC TTGAGGGGG TTAAAAGGTC TTGGGGGGGTT	11    TAGGCCGGCT CGGCGGCTTC ACCCCTCCC ACCCCTCCC AGGCCTGGAG CCCAGAGGCC TGAGCCCCAT TGAGGCCCAT TGAGGCCCAT TGACGGCC TGCACGGCCT TGCACGCCT TCTCGCGACAT TCTTCGACTA ACACCACCA ACACCAGCA	21    GGGGGCCCTG GGGCCGGAG CCGGGTCGGG GGCCTGAGGC GGGCCGAGGC TAAGGACGAG CAGAGACGAGAG GCGCGAGGC GGCTCAGGC GGCCTCAG GGCCTCCAG GGCCTCCAG GCCACGCC CCGATGCCC CCGATGCCC CCGATGCCC CCGATGCCC CCGCACGCCC CCGCACGCCC CCGCACGCCC CCGCACGCCC CCGCACGCCC CCGCACGCCC CCGCACGCCCC CCGCACGCCCC CCGCACGCCCC CCGCACGCCCC CCGCACGCCCC CCGCACGCCCC CCGCACGCCCC CCCCCAGGCCCC TCCCCCCAG CCTCAGACTC TCCCCCCAG CCTCAGACTC TAATTTATGG TAAAATTTGT	GTTACGCTGT GGTACGCTGT ACCCGCAGC GGAGGCGCG AGCCGGATG GTGATGGCCG AAGGTGAAGTCGT CGCAAGCGGC GGCAAGTCGT CAGCAGCAGC TACCGCGACT GACACGTCCC GGGACTGCC CCCGGGGCG ATTCCGCGCC TTCCGCGCC TTCCGGGCC CCCGGGCGCG TTTGAACAGT GACTCCCGCGCC CTGCAGCC CTGCAGCC CTGCAGCC TTTGAACAGT TTGAACAGT TACTTTTTTT TCAGAGATTT TCAGAGATTT	AGACCAGACC CCCTCGGGGC CGGGATACGC GGCTGGGCCC CCCGTATCCG GGCAGGCCC CCCGTATCCG TGCAGCACA AGCGCTGACA AGCGCTTCCC GCCAGAGTCT CGCTGGCCC CCGGGCGCGC CCGGGCCCCG CCGGCGCGCC TCCTGGCCC TCCTGGCCC TCCTGGCCC TCCTGGCCC TCTTCCCACA TTGACTTT	GCGACAGGCC ATCTCAGTGG AGGGTTGAGG CAGTGACGAC CTGCCCTGG GCGACAGC GCGGCCGATG GAATCCAGAC GCGGCGCGATG GAAGCCAC GCGGGCCCG GCGGCCCG GCGGCCCG CGCGGCCCG CACCTACAGC CCAGCCCC CCGGCTCCAG TCAGCCCCC CCTGTGCAAG CCACCTACAGC CAACTATCCT TTACACACTT TTGTTGTTTTT TTGTACAGTTT GTTGGATTGT	120 180 240 300 360 420 480 540 660 720 780 960 1020 1140 1260 1320 1320 1340 1500 1500 1620 1680
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	1     GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGGC CAGAGCACAGA GCCGAGTCGC GAGACACCGG AACGCTTTCA CTGCACAACG GAGAAGCGGC CCCAACTACA CGCGGCTTCC CGCGTGGCCA CGCTTCGACACG GACCACTACA CGCTGCTCG CCGTTCGACGGCGCT TACGGCACGG CTTCACGGTT ATGCAGCAGG CGACTTCGCCC CGGGTTCCTCG CCTGAGATGG GGGGCCATTT GACGTGTGAC CCTGGAGAGG CTTGAAAGGTG TTAAAAGGTG TGGGGGGGTG CCAAAACCCTA	11    TAGGCCGGCT CGGCGGCTTC ACCCCTCCC ACCCCTCCC AGGCCTGCAG CCCAGAGGCC TGAGCCCCTT CGGGGCGC CCGAGTTGAG CCTTCGTGGA AGTACCGGC TGCACGGCCT TCCGGCACAT TCTTCGGCACAT TCTTCGGACTA CCAGAGCCCCGACCGCCGACCACCCGTCCCCCACACT TCTCGGCCACAT TCTTCGCACTA CCAGAGCCCCCCCCCC	21    GGGGGCCCTG GGGCCGGGG CGGGTCCGGG GGCCCGCG CGGGGACATG GGGCCCGAGGC CAAGATGCTG GGAGCCGAGGC GGCTGAGCC GGCCTCAGGCC CCGATGCCC CCGATGCCC CCGATGCCC CCGATGCCC CCGATGCCC CCGATGCCC CCGATGCCC CCGCACGCCC CCGCACGCCC CCGCACGCCC CCGCACGCCC CCGCACGCCC CCGCCCCGGACCCAGGCCC CCCCCCCGCACGCCC CCCCCCCC	GTTACGCTGT GACACGCCC AGCCCGGATG GGAGGCGCC AGCCCGGATG GTGATGGCCC AAGCGCGCC AAGCGCGCC GGCAAGTCGT CGCTGCGCC AAGCAGGTCA CAGCAGCCC CAGCAGCCCC CCCGGGGCCC CCCCGGGCCC CCCCGGGCCC CCCCGGCCC CCCCGGCCC CCCCGGCCC CCCCGCCCC CCCCGCCCC CCCCGCCCC CCCCGCCCC CCCCGCCCC CCCCGCCCC CCCCGCCCC CCCCGCCCC CCCCGCCCC CCCCCC	AGACCAGACC CCCTCGGGGC CGGGATACGC GGCAGGCACC CCCGTATCCG GGCAGCACC GGCAGCACA GGCAGCACA AGCGCTGACA AGCGCTGACA AGCGCTTCCC GCCAGAGTTCCC GCCAGAGTCT CGCTGGACGC GCCAGAGTCT CGCTGGACGC ACCCCCGGG ACCCCCGGG ACCCCCAGAGTCT TGAATCTCCC ATATATACCT AGAAGCAGTG GTTGTGCCCACA GTTCCCCACA GTTCCCCACA	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GCGACAGC GCGGCCGATG GAATCCAGAC GCGGCTGAG GCAGGACCAC GCGGCCGCCC GCGGCCCC CGCGGCCCC CACCTACAGC CTGGACCCC CTGGACCC CTGGACCC CTGTGCAAG CCACTACCT TTAGACACTT TTGTTGTTTT TTGAACACTT TTGTTGTTTT ACACCCTT ACACCCTC ACCAGCTCCT ACCACCTC CACCTACCTC CACCTACCTC CACCTACCT	120 180 240 300 360 420 660 720 780 960 1020 1080 1140 1260 1320 1380 1440 1500 1560 1680 1740
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	1     GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGGC CAGAGCACAGA GCCGAGTCGC GAGACACCGG AACGCTTTCA CTGCACAACG GAGAAGCGGC CCCAACTACA CGCGGCTTCC CGCGTGGCCA CGCTTCGACACG GACCACTACA CGCTGCTCG CCGTTCGACGGCGCT TACGGCACGG CTTCACGGTT ATGCAGCAGG CGACTTCGCCC CGGGTTCCTCG CCTGAGATGG GGGGCCATTT GACGTGTGAC CCTGGAGAGG CTTGAAAGGTG TTAAAAGGTG TGGGGGGGTG CCAAAACCCTA	11    TAGGCCGGCT CGGCGGCTTC ACCCCTCCC ACCCCTCCC AGGCCTGCAG CCCAGAGGCC TGAGCCCCTT CGGGGCGC CCGAGTTGAG CCTTCGTGGA AGTACCGGC TGCACGGCCT TCCGGCACAT TCTTCGGCACAT TCTTCGGACTA CCAGAGCCCCGACCGCCGACCACCCGTCCCCCACACT TCTCGGCCACAT TCTTCGCACTA CCAGAGCCCCCCCCCC	21    GGGGGCCCTG GGGCCGGGG CGGGTCCGGG GGCCCGCG CGGGGACATG GGGCCCGAGGC CAAGATGCTG GGAGCCGAGGC GGCTGAGCC GGCCTCAGGCC CCGATGCCC CCGATGCCC CCGATGCCC CCGATGCCC CCGATGCCC CCGATGCCC CCGATGCCC CCGCACGCCC CCGCACGCCC CCGCACGCCC CCGCACGCCC CCGCACGCCC CCGCCCCGGACCCAGGCCC CCCCCCCGCACGCCC CCCCCCCC	GTTACGCTGT GACACGCCC AGCCCGGATG GGAGGCGCC AGCCCGGATG GTGATGGCCC AAGCGCGCC GACAGCGCC GGCAAGTCGT CGCTGCGCC AAGCAGGTCA CAGCAGCCC CAGCAGCCCC CCCGGGGCCC CCCCGGGCCC CCCCGGGCCC CCCCGGCCC CCCCGGCCC CCCCGGCCC CCCCGCCCC CCCCGCCCC CCCCGCCCC CCCCGCCCC CCCCGCCCC CCCCCC	AGACCAGACC CCCTCGGGGC CGGGATACGC GGCAGGCACC CCCGTATCCG GGCAGCACC GGCAGCACA GGCAGCACA AGCGCTGACA AGCGCTGACA AGCGCTTCCC GCCAGAGTTCCC GCCAGAGTCT CGCTGGACGC GCCAGAGTCT CGCTGGACGC ACCCCCGGG ACCCCCGGG ACCCCCAGAGTCT TGAATCTCCC ATATATACCT AGAAGCAGTG GTTGTGCCCACA GTTCCCCACA GTTCCCCACA	GCGACAGGCC ATCTCAGTGG AGGGTTGAGG CAGTGACGAC CTGCCCTGG GCGACAGC GCGGCCGATG GAATCCAGAC GCGGCGCGATG GAAGCCAC GCGGGCCCG GCGGCCCG GCGGCCCG CGCGGCCCG CACCTACAGC CCAGCCCC CCGGCTCCAG TCAGCCCCC CCTGTGCAAG CCACCTACAGC CAACTATCCT TTACACACTT TTGTTGTTTTT TTGTACAGTTT GTTGGATTGT	120 180 240 300 360 420 480 540 660 720 780 960 1020 1140 1260 1320 1320 1340 1500 1500 1620 1680
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGGC CAGAGCACGG GCGAGTCGC GAGAGCACCGG ACCACTACA GGCGGCTTCCA CGCGTGCCCA CGCTCGCGC CGCTCGCGCGCGC CGCTCGCCCC CTCACGACG CGGCCCCCC CTCGACGGCCCCC CGGCTCCCCC CGGCTCCCCC CTCGACGGCCTCCCCCC CTCGACGGCCTCCCCCC CTCGACGGCCTCCCCCC CCTCGACGCCCCC CCTCGACGCCCCC CCTCGACGCCCCC CCTCGACGCCCCC CCTCGACGCCCCC CCTCGACGCCCCC CCTCGACGCCCCC CCTCGACGCCCCC CCTCGACGCCCCC CCTCGCCCCC CCTCGACGACGCCCCCCC CCTCGACGACCCCTCCCCCCCCCC	11    TAGGCCGGCTT CAGCGCTCCC CAGCGGCTTC ACCCCTCCCC AGGCCTGCAG CCCAGAGGCC TGAGCCCCAT CCGGGCCGC CCGAGTTGAG CCTTCGTGGA AGTACCGCCC TGCACGGCCT TGCACGGCCT TGCACGGCCT TCTCGGCACAT TCTTCGCGC TCTCGGACAT ACTACCGCT CCCGAGGCT CCCGAGGCT CCCGAGGC ACACCAGCA CTCCGGAGGT CCTCGGAGGT ACACCAGCA CTCCGGAGGT CCTCCCTA AGGTTCCAT TCTTGGCATA AGGTTCATT TTTCCAAGTT AAGTTTCATT AAAGTTTATT	21    GGGGGCCCTG GGGCCGGGG CGGGGTCGCG CGGGGACATG GGGCCGGGG CAGGACATG GGAGCCAGGG CAAGATGCTG GGAGCCAGGC GGCTCCAG GGCCACGCC CCCAATGCCC CCCAATGCCC GGTTGCCCCG GGTCCCTCG GGATGCCCTCG CCAGCCCCCCCCCC	GETACGCTGT GEGAGGCGCG GEAGGCGCGAGGCGCGAGGCGCGCGAGCCGCGAGCCGCGAGCCCCGGAGCCCCCGGGACCCCCC	AGACCAGACC CCCTCGGGGC CGCGGGATACGC GGCAGGGCC GCGAGGCGC CCCTATCGG GGAGGGCC TGCAGCACT TGCAGCACT AGGGGCTT TGCAGCACT AGGGCTTCC GCAGAGTTCC GCCAGAGTTCC GCCAGAGTTCC TCCTGGCGCC TCCTGGCGCC TCCTGGCGCC TCCTGGCGCC TCCTGGCGCC TCTTGCACT TGAACCACT TGAACCACT TGAACCCCT TTGATTACTG GTGACCCCT TTGTTCCCCACA TGTTCCCCACA GGGTGTTTT	GCGACAGGC ATCTCAGGG AGGGTTGAGG CAGTGACGAC CTGCCCTGG GCGAACAGC GCGGCCATG GAATCAGAC GCAGGCCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC CACCTACAGC CACCTACAGC CACCTACAGC CCAGCTCCAC CCAGCACAC CCAGCACC CTCTGGACCC CCTGTGGACC CCAGTGCACC CACTACACC CTACAGCC CATGTGCACC CTTTCAACCTT TTCAACACTT TTGAACAGTT TTGAACAGTT TTGAACAGTT TTCAACACTT TTTCAACACTT TTTCAACACTT	120 180 240 300 360 420 660 720 780 960 1020 1080 1140 1260 1320 1380 1440 1500 1560 1680 1740
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGGC CAGAGCACGG GCGAGTCGC GAGAGCACCGG ACCACTACA GGCGGCTTCCA CGCGTGCCCA CGCTCGCGC CGCTCGCGCGCGCGCGCGCGCCCCC CTCACGACT ATGCAGCGGC CTTCACGTGTGC CTTCACGTGTGC CTTCACGTGTGCCCC CGGCTCCCCC CGGCTCCTCCCCC CTCGCCCCC CTCGCCCCC CTCGAGGACG GGGCCATTT GACGTGTGAC CTTCAGGTGT CTCGAGGAGG CTTCAGGTGT CCTTCGAGGAGG CTTCAGGTGTCCTCC CCTGGAGGAGG CTTCAGGTGTCCTCCCCCC CCTGGGCGCTCCCCCC CCTGGGCGCTCTCCCCCC CCTGGAGGAGG CTTAAAAGGTC CGGGGGGGTT CAAAACCCTA CCATTTCCTG	11    TAGGCCGGCTT CAGCGCTCCC CAGCGGCTTC ACCCCTCCCC AGGCCTGCAG CCCAGAGGCC TGAGCCCCAT CCGGGCCGC CCGAGTTGAG CCTTCGTGGA AGTACCGCCC TGCACGGCCT TGCACGGCCT TGCACGGCCT TCTCGGCACAT TCTTCGCGC TCTCGGACAT ACTACCGCT CCCGAGGCT CCCGAGGCT CCCGAGGC ACACCAGCA CTCCGGAGGT CCTCGGAGGT ACACCAGCA CTCCGGAGGT CCTCCCTA AGGTTCCAT TCTTGGCATA AGGTTCATT TTTCCAAGTT AAGTTTCATT AAAGTTTATT	21    GGGGGCCCTG GGGCCGGGG CGGGGTCGCG CGGGGACATG GGGCCGGGG CAGGACATG GGAGCCAGGG CAAGATGCTG GGAGCCAGGC GGCTCCAG GGCCACGCC CCCAATGCCC CCCAATGCCC GGTTGCCCCG GGTCCCTCG GGATGCCCTCG CCAGCCCCCCCCCC	GTTACGCTGT GACACGCCC AGCCCGGATG GGAGGCGCC AGCCCGGATG GTGATGGCCC AAGCGCGCC GACAGCGCC GGCAAGTCGT CGCTGCGCC AAGCAGGTCA CAGCAGCCC CAGCAGCCCC CCCGGGGCCC CCCCGGGCCC CCCCGGGCCC CCCCGGCCC CCCCGGCCC CCCCGGCCC CCCCGCCCC CCCCGCCCC CCCCGCCCC CCCCGCCCC CCCCGCCCC CCCCCC	AGACCAGACC CCCTCGGGGC CGCGGGATACGC GGCAGGGCC GCGAGGCGC CCCTATCGG GGAGGGCC TGCAGCACT TGCAGCACT AGGGGCTT TGCAGCACT AGGGCTTCC GCAGAGTTCC GCCAGAGTTCC GCCAGAGTTCC TCCTGGCGCC TCCTGGCGCC TCCTGGCGCC TCCTGGCGCC TCCTGGCGCC TCTTGCACT TGAACCACT TGAACCACT TGAACCCCT TTGATTACTG GTGACCCCT TTGTTCCCCACA TGTTCCCCACA GGGTGTTTT	GCGACAGGC ATCTCAGGG AGGGTTGAGG CAGTGACGAC CTGCCCTGG GCGAACAGC GCGGCCATG GAATCAGAC GCAGGCCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC CACCTACAGC CACCTACAGC CACCTACAGC CCAGCTCCAC CCAGCACAC CCAGCACC CTCTGGACCC CCTGTGGACC CCAGTGCACC CACTACACC CTACAGCC CATGTGCACC CTTTCAACCTT TTCAACACTT TTGAACAGTT TTGAACAGTT TTGAACAGTT TTCAACACTT TTTCAACACTT TTTCAACACTT	120 180 240 300 360 420 660 720 780 960 1020 1080 1140 1260 1320 1380 1440 1500 1560 1680 1740
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGC CAGAGCACAGA GCCGAGTGGC GAGAGCACCGG AACGCTTTCA CTGCACÀACG GAGAGCGGC CCCAACTACA CGGTGGCCA CCGCTGCTGC CCGCTCGACG GACCCGGCTT TACGGCCGC CTTCACGTGT CACGTGGCC CGTCGACGG CTTCACGTGT ATGCAGCCGC CTTCACGTGT CTGAGATGG CTGGAGAGG CTTGAGATGG CTGGAGAGG TTAAAAGGT TTAAAAGGT CTGGAGGGG CTTGGAGGAG TTAAAAGGT CCATTTCCTG CAAAACCCTA CCATTTCCTG	11    TAGGCCGGCT CGGCGGCTTC ACCCCTCCC ACCCCTCCC AGGCCTGGAG CCCAGAGCGC TGAGCCCCAT CCGGGGCCGC TGGAGTTGAG CCTTCGTGGA AGTACCGCC TGCACGGCCT TCTCGGACTA TCTTCGGACTA CCTACCGGC ACTACGGCC ACTACGGACT AGGTCCCCTA AGGTTCCAT AGGTTCATT TTTCCAAGTT AAAGTTTATT AAATCTGGAAT	21    GGGGGCCCTG GGGCCGGAG CCGGGTCGGG GGCCCAGGCC CGGGGACATG GGGCCGAGGC TAAGGACGAG GCGAGGCG GGGCTCCAG GGGCCTCAG GGGCCTCAG GGGCCCC CCGATGCCC CCGATGCCC CCGATGCCC CCGCACGCCC CCGCACGCCC CCGCACGCCC CCGCACGCCC CCGCACGCCC CCGCACGCCC CCGCACGCCC CCGCACGCCC CCGCACGCCC CCGCACGCA	GETACGCTGT GEGAGGCGCG GEAGGCGCGAGGCGCGAGGCGCGCGAGCCGCGAGCCGCGAGCCCCGGAGCCCCCGGGACCCCCC	AGACCAGACC CCCTCGGGGC CGCGGGATACGC GGCAGGGCC GCGAGGCGC CCCTATCGG GGAGGGCC TGCAGCACT TGCAGCACT AGGGGCTT TGCAGCACT AGGGCTTCC GCAGAGTTCC GCCAGAGTTCC GCCAGAGTTCC TCCTGGCGCC TCCTGGCGCC TCCTGGCGCC TCCTGGCGCC TCCTGGCGCC TCTTGCACT TGAACCACT TGAACCACT TGAACCCCT TTGATTACTG GTGACCCCT TTGTTCCCCACA TGTTCCCCACA GGGTGTTTT	GCGACAGGC ATCTCAGGG AGGGTTGAGG CAGTGACGAC CTGCCCTGG GCGAACAGC GCGGCCATG GAATCAGAC GCAGGCCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC CACCTACAGC CACCTACAGC CACCTACAGC CCAGCTCCAC CCAGCACAC CCAGCACC CTCTGGACCC CCTGTGGACC CCAGTGCACC CACTACACC CTACAGCC CATGTGCACC CTTTCAACCTT TTCAACACTT TTGAACAGTT TTGAACAGTT TTGAACAGTT TTCAACACTT TTTCAACACTT TTTCAACACTT	120 180 240 300 360 420 660 720 780 960 1020 1080 1140 1260 1320 1380 1440 1500 1560 1680 1740
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGC CAGAGCACAGA GCCGAGTGGC GAGAGCACCGG AACGCTTTCA CTGCACÀACG GAGAGCGGC CCCAACTACA CGGTGGCCA CCGCTGCTGC CCGCTCGACG GACCCGGCTT TACGGCCGC CTTCACGTGT CACGTGGCC CGTCGACGG CTTCACGTGT ATGCAGCCGC CTTCACGTGT CTGAGATGG CTGGAGAGG CTTGAGATGG CTGGAGAGG TTAAAAGGT TTAAAAGGT CTGGAGGGG CTTGGAGGAG TTAAAAGGT CCATTTCCTG CAAAACCCTA CCATTTCCTG	11    TAGGCCGGCTT CAGCGCTCCC CAGCGGCTTC ACCCCTCCCC AGGCCTGCAG CCCAGAGGCC TGAGCCCCAT CCGGGCCGC CCGAGTTGAG CCTTCGTGGA AGTACCGCCC TGCACGGCCT TGCACGGCCT TGCACGGCCT TCTCGGCACAT TCTTCGCGC TCTCGGACAT ACTACCGCT CCCGAGGCT CCCGAGGCT CCCGAGGC ACACCAGCA CTCCGGAGGT CCTCGGAGGT ACACCAGCA CTCCGGAGGT CCTCCCTA AGGTTCCAT TCTTGGCATA AGGTTCATT TTTCCAAGTT AAGTTTCATT AAAGTTTATT	21    GGGGGCCCTG GGGCCGGAG CCGGGTCGGG GGCCCAGGCC CGGGGACATG GGGCCGAGGC TAAGGACGAG GCGAGGCG GGGCTCCAG GGGCCTCAG GGGCCTCAG GGGCCCC CCGATGCCC CCGATGCCC CCGATGCCC CCGCACGCCC CCGCACGCCC CCGCACGCCC CCGCACGCCC CCGCACGCCC CCGCACGCCC CCGCACGCCC CCGCACGCCC CCGCACGCCC CCGCACGCA	GETACGCTGT GEGAGGCGCG GEAGGCGCGAGGCGCGAGGCGCGCGAGCCGCGAGCCGCGAGCCCCGGAGCCCCCGGGACCCCCC	AGACCAGACC CCCTCGGGGC CGCGGGATACGC GGCAGGGCC GCGAGGCGC CCCTATCGG GGAGGCGC TGCAGCACA AGGGCTTCA AGGGCTTCA AGGGCTTCA GCGGGCC CGCGGGCGC CGCGGGCGC ACCCCCGGG ACCCCCGGG ACCCCCGGG TGAGCACT TGAGCACT TGAGCACT TGAGCCC TATATTACTG AGAGCATTCC TGTTGCTCC TGTTGCTCAC GGTTGCTCCCACA GGGTGTTTCCCACA GGGTGTTTTCCCACA GGGTGTGTTT	GCGACAGGC ATCTCAGGG AGGGTTGAGG CAGTGACGAC CTGCCCTGG GCGAACAGC GCGGCCATG GAATCAGAC GCAGGCCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC CACCTACAGC CACCTACAGC CACCTACAGC CCAGCTCCAC CCAGCACAC CCAGCACC CTCTGGACCC CCTGTGGACC CCAGTGCACC CACTACACC CTACAGCC CATGTGCACC CTTTCAACCTT TTCAACACTT TTGAACAGTT TTGAACAGTT TTGAACAGTT TTCAACACTT TTTCAACACTT TTTCAACACTT	120 180 240 300 360 420 660 720 780 960 1020 1080 1140 1260 1320 1380 1440 1500 1560 1680 1740
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	1     GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGGC CAGAGCACAGA GCCAGTCGC GAGAGCACGG AACGCTTTCA CTGCACAACG GGAGAGCGGC CCCAACTACA CGCGGCTTCC CGCTGGCCA GACCACTACA CGGCGCTTCACACGGC CGCTTCGACGT TACGGCACGG CGACTCGCCC CTTCACGTGT ATGCAGCGC CTTCACGTGT ATGCAGCGC CTTCACGTGT CTGAGATGG GGGCCATTT GACGTGTGAC CCTGGAGAGG TTAAAAGGTG TGACGTGTGAC CCTGGAGGAG TTAAAAGGTG CCAAACCCTA CCATTTCCTG CTAAAAAATA Seq ID NO:	11    TAGGCCGGCT CGGCGGCTTC ACCCCTCCC ACCCCTCCC AGGCCTGCAG CCCAGAGGCC TGAGCCCCTT CGGGCGCT CGGGGCGCC TGGTTTGGGA AGTACCGCCC TGCACGGCCT TGCACGGCCT TGCACGGCCT TCTCGGCACAT TCTTCGCACAT CCTCCGACCAT CCTCCGACCAT CCTCCGACCAT TCTTCGCACCAT TCTTCGCACCAT TCTTCGCACCAT TCTTCGCACCAT TCTTCGCACCAT ACACACACCAC CCTCCCCTAA CCTCCCCTAA CCTCCCCTAA CCTCCCCTAA TGTTGGCATA AGGTTCATT AAAGTTTATT AAATCTGGAA  8 Protein	21    GGGGGCCCTG GGGCCGGGG CGCGGTCGGG CGCGGCGCGCGGGC CGGGCCGCGGGCGCGGGCGGC	GETACGCTGT GEGAGGCGCG GEAGGCGCGAGGCGCGAGGCGCGCGAGCCGCGAGCCGCGAGCCCCGGAGCCCCCGGGACCCCCC	AGACCAGACC CCCTCGGGGC CGCGGGATACGC GGCAGGGCC GCGAGGCGC CCCTATCGG GGAGGCGC TGCAGCACA AGGGCTTCA AGGGCTTCA AGGGCTTCA GCGGGCC CGCGGGCGC CGCGGGCGC ACCCCCGGG ACCCCCGGG ACCCCCGGG TGAGCACT TGAGCACT TGAGCACT TGAGCCC TATATTACTG AGAGCATTCC TGTTGCTCC TGTTGCTCAC GGTTGCTCCCACA GGGTGTTTCCCACA GGGTGTTTTCCCACA GGGTGTGTTT	GCGACAGGC ATCTCAGGG AGGGTTGAGG CAGTGACGAC CTGCCCTGG GCGAACAGC GCGGCCATG GAATCAGAC GCAGGCCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC CACCTACAGC CACCTACAGC CACCTACAGC CCAGCTCCAC CCAGCACAC CCAGCACC CTCTGGACCC CCTGTGGACC CCAGTGCACC CACTACACC CTACAGCC CATGTGCACC CTTTCAACCTT TTCAACACTT TTGAACAGTT TTGAACAGTT TTGAACAGTT TTCAACACTT TTTCAACACTT TTTCAACACTT	120 180 240 300 360 420 660 720 780 960 1020 1080 1140 1260 1320 1380 1440 1500 1560 1680 1740
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	1     GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGGC CAGAGCACAGA GCCAGTCGC GAGAGCACGG AACGCTTTCA CTGCACAACG GGAGAGCGGC CCCAACTACA CGCGGCTTCC CGCTGGCCA GACCACTACA CGGCGCTTCACACGGC CGCTTCGACGT TACGGCACGG CGACTCGCCC CTTCACGTGT ATGCAGCGC CTTCACGTGT ATGCAGCGC CTTCACGTGT CTGAGATGG GGGCCATTT GACGTGTGAC CCTGGAGAGG TTAAAAGGTG TGACGTGTGAC CCTGGAGGAG TTAAAAGGTG CCAAACCCTA CCATTTCCTG CTAAAAAATA Seq ID NO:	11    TAGGCCGGCT CGGCGGCTTC ACCCCTCCC AGGCCGCT CCCAGAGGCC TGAGCCCCAT CCGGGGCGCC CCGAGTTGAG CCTTGTGGA AGTACCGCCC TGCAGGCCT TGGACGCCT TGCACGGCCT TGCACGGCCT TCTCGGCACAT TCTTCGCGC ACTACCGCT CTCGGCACAT ACTACCGCT CTCGGACAT TCTTCGCGC ACTACGGACAT ACTACGGCC CTCCGGAGGC ACCCCCTA ACGCCCCTA ACGCTCCCTA AGGTTCCATT TTTCCAGTT TTTCCAGTT AAAGTTTATT AAATCTGGAA  8 Protein CCCCGGGCTTCAA	21    GGGGGCCCTG GGGCCGGGAG CCGGGTCGGG GGGCCATGAGC GGGCCGAGACATG GGAGCCAGGAC CAAGATGCTG GGAGCCAGGC GGCTCCAG GGGCCCCCCCATGCCC CCCAATGCCC CCCAATGCCC CCGATGCCC CCGATGCCC CCGATGCCC CCTGCACGCC CTGCACGCC CTGCACGCC TCCGCCCAGA CTGCCCTGC TCAGACTC TAATTTATGG TAAAATTTGT CAAGTTAACT GATCAAAGAA TCCTGAAAAAA  Bequence NP_071899	GETACGCTGT GEGAGGCGCG AGCCCGGATG AGCCGGATG AGGCGCGCG AAGGTGAAGCGG AAGGCGGCG CGGCAGTGCCC AAGCAGCTGC CGGCAGCTCCCCGAGC TTCCCCGAGC TTCCCGAGC TTCCCGGGCGC CCCGGAGCTCC CCGGAGCTTC ATTCCGGCC CCTGCAGC TTTCAACAGT GACTCCCC CTGCAGCC CTGCAGC CTGCAGCC CTGCAGC	AGACCAGACC CCCTCGGGGC CGTCCGGGGC CGGGATACGC GGGAGGGCC CCCGTATCGG GGAGGGCCC CCCGTATCGG GGAGGGCT TGCAGCACAT AGGGGTTCCC AGGGCTTCCC GCCAGAGTTT CGCTGGACGC CCGCCGGCCGC CCGCCGGCCC CCGCCGGCCC TCCTGGCCCC TCCTGGCCCC TCCTGCCCCC TCCTGCACT TGAATCTCCC TATATTACTG AGAACCACTG CTTGTCCCACA GTGTCCCCACA GTGTCCCACA GTGTCCCCACA GTGTCCCCCCCCCC	GCGACAGGCC ATCTCAGTGG AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GCGAACAGC GCAGCCCATG GAAGTCCAGAC GCAGGCCCAC GCAGGCCCG GCAGGCCCG GCGCCCG GCGCCCG GCGCCCG CACCTACAGC CACCTACAGC CACCTACAGC CACTACAGC CAGCCCC CGGTTGCAG CCAGCCCC CGGTTCCAG CCAGCCCC CGTTGCACC CACTACAGC CAACTATCCT TTACACACTT TTGAACAGTT GTTGGATTGT AAA	120 180 240 300 360 420 660 720 780 960 1020 1080 1140 1260 1320 1380 1440 1500 1560 1680 1740
50 55 60 65 70	1     GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGGC CAGAGCACAGA GCCAGTCGC GAGAGCACGG AACGCTTTCA CTGCACAACG GGAGAGCGGC CCCAACTACA CGCGGCTTCC CGCTGGCCA GACCACTACA CGGCGCTTCACACGGC CGCTTCGACGT TACGGCACGG CGACTCGCCC CTTCACGTGT ATGCAGCGC CTTCACGTGT ATGCAGCGC CTTCACGTGT CTGAGATGG GGGCCATTT GACGTGTGAC CCTGGAGAGG TTAAAAGGTG TGACGTGTGAC CCTGGAGGAG TTAAAAGGTG CCAAACCCTA CCATTTCCTG CTAAAAAATA Seq ID NO:	11    TAGGCCGGCT CGGCGGCTTC ACCCCTCCC ACCCCTCCC AGGCCTGCAG CCCAGAGGCC TGAGCCCCTT CGGGCGCT CGGGGCGCC TGGTTTGGGA AGTACCGCCC TGCACGGCCT TGCACGGCCT TGCACGGCCT TCTCGGCACAT TCTTCGCACAT CCTCCGACCAT CCTCCGACCAT CCTCCGACCAT TCTTCGCACCAT TCTTCGCACCAT TCTTCGCACCAT TCTTCGCACCAT TCTTCGCACCAT ACACACACCAC CCTCCCCTAA CCTCCCCTAA CCTCCCCTAA CCTCCCCTAA TGTTGGCATA AGGTTCATT AAAGTTTATT AAATCTGGAA  8 Protein	21    GGGGGCCCTG GGGCCGGGG CGCGGTCGGG CGCGGCGCGCGGGC CGGGCCGCGGGCGCGGGCGGC	GETACGCTGT GEGAGGCGCG GEAGGCGCGAGGCGCGAGGCGCGCGAGCCGCGAGCCGCGAGCCCCGGAGCCCCCGGGACCCCCC	AGACCAGACC CCCTCGGGGC CGCGGGATACGC GGCAGGGCC GCGAGGCGC CCCTATCGG GGAGGCGC TGCAGCACA AGGGCTTCA AGGGCTTCA AGGGCTTCA GCGGGCC CGCGGGCGC CGCGGGCGC ACCCCCGGG ACCCCCGGG ACCCCCGGG TGAGCACT TGAGCACT TGAGCACT TGAGCCC TATATTACTG AGAGCATTCC TGTTGCTCC TGTTGCTCAC GGTTGCTCCCACA GGGTGTTTCCCACA GGGTGTTTTCCCACA GGGTGTGTTT	GCGACAGGC ATCTCAGGG AGGGTTGAGG CAGTGACGAC CTGCCCTGG GCGAACAGC GCGGCCATG GAATCAGAC GCAGGCCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC CACCTACAGC CACCTACAGC CACCTACAGC CCAGCTCCAC CCAGCACAC CCAGCACC CTCTGGACCC CCTGTGGACC CCAGTGCACC CACTACACC CTACAGCC CATGTGCACC CTTTCAACCTT TTCAACACTT TTGAACAGTT TTGAACAGTT TTGAACAGTT TTCAACACTT TTTCAACACTT TTTCAACACTT	120 180 240 300 360 420 660 720 780 960 1020 1080 1140 1260 1320 1380 1440 1500 1560 1680 1740
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	1     GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGGC CAGAGCACGG ACGACTTCA CTGCACACG GAGCAGCGG GCGAGTCGC CCCCAACTACA GGCGGCTTCC CCGCTGGCCA GGCGGCTTCC CGCTGGCCA GACCCGGCTT TACGGCAGGC CGACTCGCCC CTTCACGTGT ATGCAGCAGG CGACTCGCCC CTTCACGTGT ATGCAGCGC CTTCACGTGT ATGCAGCGC CTTCACGTGT CTGAGATGG CGACTTCTCC CCTGAGAGAG TTAAAAGGTG TGACGTGTGAC CCATTTCCTG CTAAAAAATA Seq ID NO: Protein Ac 1	11    TAGGCCGGCT CGGCGGCTTC ACCCCTCCC AGGCCTGCAG AGGCCTGGAG CCCAGAGGGC TGAGCCCCT TGGTGTGGGA AGTACCGCCC TGCACGGCCT TGCACGGCCT TGCACGGCCT TCTCGGACTA CCTCCGACAT TCTTCGCACAT ACTACCGTCGT TCTCGGACTA ACTACCAGCA CTCCCGAGGCC GCGAGGTGA GCCTCCCCTA CCTCCGAGGT ACTACGAGAC CCTCCCGAGGT ACTACGAGAAT TGTTGGCATA AGGTTCATT AAATCTGGAA  8 Protein Cession #: 11	21    GGGGGCCCTG GGGCCGGGG CGCGGTGGGG CGCGGGGCGGGGCGGGGCGGGGGGGG	GETACGCTGT GETACGCTGT ACCCGCAGA GCAGGCGCG AGCCCGGATG GTGATGGCCG AAGGTGAAG AAGGCAGGTGA ACGCGGCG TTCCCCGAGC TACCGCGACT GACACGTCC CGGAGCTCC CCGGAGCTCC CCGGGGCGC CCCCGGGGCGC CCCCGGGCCGC CCTGCAGCC CCTGCAGCC CCTGCAGCC CCTGCAGCC CTGCAGCC CTGCCTTTTT AAAAAAAAAA	AGACCAGACC CCCTCGGGGC CGCGGGATACGC GGCAGGGCCC CCCTATCGG GGCAGGCCC CCCTATCGG TGCAGCACA AGGGCTTCCC GCAGAGTTCCC GCAGAGTTCCC GCAGAGTTCCC GCAGAGTTCCC GCAGAGTTCCC TGCTGGACGC CGGCGGGGCCGA ACCCCCGGG CGGGCGGGGCCGA ACCCCCGGG TTGAATATACTG TTGAATCTCCC TATATTACTG TTTTCCCACA TGTTCCCACA GGGTTTCCCAAA GGGTTGTTT AAAAAAAAAA	GCGACAGGC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GCGGAACAGC GCGGACCAC GCGGCCATG GCAGGCCAC GCGGCCCC GCGGCCCCG GCGGCCCCC CACCTACAGC CACCTACAGC CCGGCCCCC CCGGCCCCC CCGGCCCCC CCGCCCCC CCGCCCCC CCGCCCCC CCGCCCCC CCCCCC	120 180 240 300 360 420 660 720 780 960 1020 1080 1140 1200 1320 1380 1440 1500 1560 1680 1740 1800
50 55 60 65 70	1   GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGGC CAGAGCACGG GCGAGTCGC GGAGCACGG GCGAGTCGC GGAGCACCG CCCAACTACA CGCGGCTTCCA CGCTGCTGC CCGCTGCTGC CCGCTCGCG GACTCGGC CTTCACGTGT ATGCAGCAG ATGCACCAG CTTCACGTGTT ATGCAGCAG CTTCACGTGTT CACGTGTGCCCC CCTCGACG CCTCGCCCC CCTCGCCCC CCTCGCCCC CCTCGCCCC CCTCGAGATGG GGGCCATTT GACGTGTGA CTTAAAAGGTC TGGGGGGGT CTAAAAACCCTA CCATTTCCTG CTAAAAAATA Seq ID NO: PTOtein AC 1   MSSPDAGYAS	11    TAGGCCGGCTT CAGGCGGCTTC ACCCCTCCC AGGCCGCT CCAGAGGCC TGAGCCCCAT CCGGGGCGCC CCGAGTTGAG CCTTGTGGA AGTACCGCCC TGGACGCCT TGGACGCCT TGGACGCCT TGGACGCCT TGCACGGCC TCTCGGCACAT TCTTCGCGC ACTACCGCT CTCGGACAT CCTCGGACAT TCTTCGCGC ACTACCGATT TCTTCGCGC ACTACCGATT TCTTCGCGC ACTACCGATT AGGTCCCTA AGGTCCCTA AGGTTCCATT TTTCCAGTT TAAAGTTTATT AAATCTGGAA  8 Protein CCESSIOn #: 11  DDQSQTQSAI	21    GGGGGCCCTG GGGCCGGGGG CGGGTCGCG CGGGGACATG GGGCCGGGGACATG CGAGCCGGGCGCG CGGGGACATG GGAGCCAGGC GGCTCCAG GGGCGCCC CCCAATGCCC CCCAATGCCC CGCTGGCCCC CCCAATGCCC CAGCACCCC CCACACCCC CCCCACACCC CCCCCAGACCC CCCCACACCC TAATTTATGG TAAAATTTGT CAAGTTAACT CAACTTAAACA Sequence NP_071899 21    PAVMAGLGPC	GETACGCTGT GETACGCTGT ACCCGCAGA GEAGGCGCG AGCCCGGATG GTGATGCCC AAGGTGAAGCGG AAGGCGGCG CGGCAGTCC CGGCAGCT TCCCCGAGC TACCGCGACT CCGGAGCTCC CCGGAGCCT CCCGGAGCCT ATTCCGGGC CCCGGAGCTT ATTCAACAGT GACTCCCGG CCTGCAGC CTGCAGCC CTGCAGCT TAAACAGT TAAATTATTT TCAGACATTT AGCTTTGAAC ATTTGAACAGT TAATTTATTT AGCTTTGAAC AAAAAAAAAA	AGACCAGACC CCCTCGGGGC CGTCCGGGGC CGGGAGGGCC CCCTATCGG GGAGGGCC CCCTATCGG GGAGGGCCC GGAGGCCCT TGCAGCACAT AGGGGTTCCC GCCAGAGTTCC GCCAGAGTTCC GCCAGAGTCT CGCTGGCCCC TCCTGGCCCC TCCTGGCCCC TCCTGGCCCC TCCTGGCCCC TCCTGGCCCC TCCTGCCCCAG ACCCCCCGG TCCTCCCAGAGTCT TGAATCTCCC TATATTACTG AGAAGCAGTTG TGTTTCCCACA GTTTCCCACA GGGTTTTCCAAA GGGTTTTTCCAAA GGGTTTGTTT AAAAAAAAAA	GCGACAGGCC ACTCAGGG AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GCGAACAGC GCGGCCGATG GAAGTCCAGAC GCGGCCGATG GCAGGCCCC GCGGGCCCG GCGGCCCG CGCGGCCCG CACCTACAGC CACCTACAGC CACCTACAGC CACCTACAGC CACTACAGC CAACTATCCT TTACACACTT TTGAACAGTT TTGAACAGTT TTTCAATCTT AAA  51	120 180 240 300 360 420 660 660 720 780 960 1020 1020 1140 11200 1140 11500 1560 1620 1620 1620 1620 1620
50 55 60 65 70	1   GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGGC CAGAGCACGG GCGAGTCGC GGAGCACGG GCGAGTCGC GGAGCACCG CCCAACTACA CGCGGCTTCCA CGCTGCTGC CCGCTGCTGC CCGCTCGCG GACTCGGC CTTCACGTGT ATGCAGCAG ATGCACCAG CTTCACGTGTT ATGCAGCAG CTTCACGTGTT CACGTGTGCCCC CCTCGACG CCTCGCCCC CCTCGCCCC CCTCGCCCC CCTCGCCCC CCTCGAGATGG GGGCCATTT GACGTGTGA CTTAAAAGGTC TGGGGGGGT CTAAAAACCCTA CCATTTCCTG CTAAAAAATA Seq ID NO: PTOtein AC 1   MSSPDAGYAS	11    TAGGCCGGCTT CAGGCGGCTTC ACCCCTCCC AGGCCGCT CCAGAGGCC TGAGCCCCAT CCGGGGCGCC CCGAGTTGAG CCTTGTGGA AGTACCGCCC TGGACGCCT TGGACGCCT TGGACGCCT TGGACGCCT TGCACGGCC TCTCGGCACAT TCTTCGCGC ACTACCGCT CTCGGACAT CCTCGGACAT TCTTCGCGC ACTACCGATT TCTTCGCGC ACTACCGATT TCTTCGCGC ACTACCGATT AGGTCCCTA AGGTCCCTA AGGTTCCATT TTTCCAGTT TAAAGTTTATT AAATCTGGAA  8 Protein CCESSIOn #: 11  DDQSQTQSAI	21    GGGGGCCCTG GGGCCGGGGG CGGGTCGCG CGGGGACATG GGGCCGGGGACATG CGAGCCGGGCGCG CGGGGACATG GGAGCCAGGC GGCTCCAG GGGCGCCC CCCAATGCCC CCCAATGCCC CGCTGGCCCC CCCAATGCCC CAGCACCCC CCACACCCC CCCCACACCC CCCCCAGACCC CCCCACACCC TAATTTATGG TAAAATTTGT CAAGTTAACT CAACTTAAACA Sequence NP_071899 21    PAVMAGLGPC	GETACGCTGT GETACGCTGT ACCCGCAGA GEAGGCGCG AGCCCGGATG GTGATGCCC AAGGTGAAGCGG AAGGCGGCG CGGCAGTCC CGGCAGCT TCCCCGAGC TACCGCGACT CCGGAGCTCC CCGGAGCCT CCCGGAGCCT ATTCCGGGC CCCGGAGCTT ATTCAACAGT GACTCCCGG CCTGCAGC CTGCAGCC CTGCAGCT TAAACAGT TAAATTATTT TCAGACATTT AGCTTTGAAC ATTTGAACAGT TAATTTATTT AGCTTTGAAC AAAAAAAAAA	AGACCAGACC CCCTCGGGGC CGTCCGGGGC CGGGAGGGCC CCCTATCGG GGAGGGCC CCCTATCGG GGAGGGCCC GGAGGCCCT TGCAGCACAT AGGGGTTCCC GCCAGAGTTCC GCCAGAGTTCC GCCAGAGTCT CGCTGGCCCC TCCTGGCCCC TCCTGGCCCC TCCTGGCCCC TCCTGGCCCC TCCTGGCCCC TCCTGCCCCAG ACCCCCCGG TCCTCCCAGAGTCT TGAATCTCCC TATATTACTG AGAAGCAGTTG TGTTTCCCACA GTTTCCCACA GGGTTTTCCAAA GGGTTTTTCCAAA GGGTTTGTTT AAAAAAAAAA	GCGACAGGCC ACTCAGGG AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GCGAACAGC GCGGCCGATG GAAGTCCAGAC GCGGCCGATG GCAGGCCCC GCGGGCCCG GCGGCCCG CGCGGCCCG CACCTACAGC CACCTACAGC CACCTACAGC CACCTACAGC CACTACAGC CAACTATCCT TTACACACTT TTGAACAGTT TTGAACAGTT TTTCAATCTT AAA  51	120 180 240 300 360 420 660 720 780 960 1020 1080 1140 1200 1320 1380 1440 1500 1560 1680 1740 1800
50 55 60 65 70	1     GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGC CAGAGCCAGA GCCGAGTCGC GGAGCACCGG AACGCTTTCA CTGCACACAC GGCGGCTTCC CCCAACTACA CCGCTGGCCA GACCGCTTCC GACTGCTGC CCGCTCGACG GACCCGCTTCACACAC GACCCGCTTCACACAC GACCTCGACG GACCCGCTTCGACG GACCCGCCCC GAGCTCCTCG CTTCACGTGT CCTTCACGTGT CCTTCACGTGT CCGTTGCCCC GAGCTCCTCG CCGTGCCCC CCGTGGCCCC CCTTCACGTGT CCACTTCCTCG CCGTCGCCCC CCTTCACATGG CCGTCCCCC CCTTCACATGG CCGTCCCCC CCTTCACATGG CCGTCCCCC CCTTCACATGG CCATTTCCTCG CTAAAAAAAAA Seq ID NO: Protein Ac 1   MSSPDAGYAS BAKGESEIRR	11    TAGGCCGGCT CGGCGGCTTC ACCCCTCCC ACCCCTCCC AGGCCTGGAG CCCAGAGGCC TGAGCCCAT CCGGGGCCGC TGGAGGCCC TGGACGCCT TGGACGCCT TGCACGCCT TCTCGGACTA CCTACCCGTT TCTTCGACTA CCTACCCGTT TCTTCGACTA ACTACCGCC TCCCGAGCA ACACCAGCA	21    GGGGGCCCTG GGGCCGGAG CCGGGTCGGG GCCCATGAGC GGGCCGAGAC CCGGGACATGCC GGGCCTCAGGC GGGCCTCAGG GGCCTCAGGC GGCCTCAGGC GGCCTCAGGCC CCGATGCCC CCGATGCCC CCGATGCCC CCGATGCCC CCCTCAGGCCAC GCCACGCCAC	GGTACGCTGT ACCCGCAGG GGAGGCGGCG AGCCGGATG GTGATGGCCG AAGGTGAAGTCGC CGCAAGTCGC CAGCAGGTCG TTCCCCGAGC TTCCCCGAGC TTCCCCGAGC TTCCCGAGC TTCCCGAGC TTCCCGAGC TTCCCGAGC CCGGACTCC CCGGGCCGC CTGCAGCCC CTGCAGCC CTGCAGCCC CTGCAGCC CTGCAGCCC CTGCAGCC CTGCAGCCC CTGCAGCC CTGCAGCC CTGCAGCC	AGACCAGACC CCCTCGGGGC CGCTCCGGGGC GGCTGGGCCC GGCTGGCCC CCCGTATCCG TGCGGCACCA AGCGGCTGACACA AGCGGCTGACACA AGCGGCTTCCC GCCAGAGTCT CGCTGGACGC CCGCCGGTCC TCCTGGCCCC TCCTGGCCCC TCCTGGCCCC TCCTGGCCCC TCCTGGCCCC TCCTGCCCCAA ACCCCCCGGGCCC TCCTGCCCCAA ACCCCCCGGGCCC TCCTGCCCCAA ACCCCCCGGGCCC TCCTGCCCCAA ACCCCCCGGGCCC TCCTGCCCCAA ACCCCCCAAA ACCCCCCAAA ACCCCCCAAA ACCCCCC	GCGACAGGCC ACGTTGAGG CAGTGACGAC CTGCCCTGG GGCGACAGG CAGTGACGAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCCC CACCTACAGC CACCTACAGC CAGCACCC ACCTACAGC CAGCACCC CACCTACAGC CAGCACCC CACCTACAGC CCAGCACC CACCTACAGC CCAGCACC CACCTACAGC CCAGCACC CCAGCACC CCAGCACC CACCTACAGC CCAGCACC CACTTCCAAC TTACACACTT TTGTGTTTT TTGTATCTT TTTCAATCTT TTTCAATCTT TACACACTT TTACACACTT TACACACTT TTACACACTT TTACACACTT TACACACTT TTACACACTT TACACACTT TACACACTT TACACACTT TACACACTT TACACACT TACACACT ACAC ACACACAC	120 180 240 300 360 420 480 540 660 720 780 960 1020 1140 1120 1320 1320 1440 1500 1680 1740 1800
50 55 60 65 70	1   GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGCGGG CAGAGCACGG AACGCTTCA CGCGGGCTTCC CGCGTGGCCA CGCTCGACGG GACCACTACA CGCGGGTTCC CGCGTGGCCA CGCTCGACGGC CGTCGCCC CGGCTCGCCC CGGGTCCCCC CGGGTTCTACAGGCGG CGACTCGGCC CTTCACGGT ATGCAGCGG CGACTCGGCC CTGAGATGG GGGCCATTT GACGTGTAAAAGGTT TAAAAGGTT TAAAAGGTT CAAAAAATA CGTTAAAAAATA Seq ID NO: Protein Ac 1   MSSPDAGYAS RAKGESRIRR AAGRICAGACCAAACCCTA CCATTCCTG CTAAAAAATA AACACCTA ACGCGGCGGGTGCCCC CAGGTCGCCCC CAGGTCTCCCC CAGGTCCCCC CAGGTCCCCC CTGAGATGG CGGGGCCATTT CACGTGTAAAAAGGTG TGAAAAAATA CCATTTCCTG CTAAAAAATA ACGTGCAGGGGGTG CAAAACCCTA CCATTCCTG CAAAAAATA AACACCTA ACACCCTA CCATTCCTG CAAAAAATA AACACCTA CCATTCCTG CAAAAAATA AACACCTA AACACCTA AACACCCTA CCATTCCTG CAAAAACCCTA CCATTCCTG CAAAAAATA AACACCTA AACACCCTA AACACCCTA AACACCCTA CCATTCCTG CAAAAAATA AACACCCTA AACACCCTA AACACCCTA AACACCCTA CAAAAAATA AACACCCTA AACACCCTA AACACCCTA AACACCCTA CCATTCCTG CAAAAAAATA AACACCCTA AACACCCTA AACACCCTA AAAAAATA AACACCCTA AAAAAAAA	11    TAGGCCGGCT CGGCGGCTTC ACCCCTCCC ACCCCTCCC AGGCCTGCA AGGCCTGAAG CCTAGAAGCC TGAAGCCCTT TGGTGTAGA CCTTCGTGGA AGTACCGCC TGCACGGCCT TCTCGGACTA TCTTCGCACTA TTTCCAAGTT AAAGTTTATT AAATCTGGAA  8 Protein CCSGCGGAGGC 11 DDQSCTGSAI DDQSCTGSAI DMAPMVWAF DMAPMVWAF DMAPMVWAF DMAPMVWAF DMAPMVWAF DMAPMVWAF DMAPMVWAF DMAPMVWAF	21    GGGGGCCCTG GGGCCGGAG CCGGGTCGGG GGCCCATGAGC CGGGACATGCG CGGGACATGCC CGGGACCT TAAGGACGAG GGCCTCAG GGCCTCAG GGCCTCAG GGCCACGCC CCGATGCCC CCGATGCCC CCGATGCCC CCGATGCCC CTGACCCTG GATEGCCTCG GATEGCCTCG CCGCACGGCC CCTCAGACTC TAATTTATGG TAAATTTATGG TAAATTTATGG TAAATTTATGG CTCACGCCCAG CCTCAGACTC TAATTTATGG CTCAACGCC TCAGCTCC CAGTTAACT CAAGTTAACT GATCAAAAAA SEQUENCE NP_071899 21    PAVMAGLEPC DERKRLAQQX RRKQVKRLKG	GSTACGCTGT GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCGGATG AGGGCGGCG AAGGTGAAGTCGT CGCAAGCGGC GACAGTCGT CAGCAGCGCG TTCCCCGAGC TTCCCGAGC TTCCCGAGC TTCCCGAGC TTCCGGGCCG ACCAGCACT CCCGGAGCTTC ATTCCGGGCC CCGGAGCTTC ATTCAACAGT GACTCCGGGC CTGCAGGCC CTGCAGGCC CTGCAGCCC CTGCATTTT TAGACAGT TTCAACAGT TAGACATTT TAGACAGT TAGACATTT AGCTTTGAAT ATGTTGTCCT AAAAAAAAAA	AGACCAGACC CCCTCGGGGC CGCTCCGGGGC CGGATACGC GGCTGGGCCC CCCGTATCCG TGGGCACC CCCGTATCCG TGGAGCACA AGCGCTGACA AGCGCTGACA AGCGCTTCCC CCCAGAGTCT CGCCAGAGTCT TCCTGGCCC CCCGGGCCGC CGGCGGGCGC ACCCCCGGG ACCCCCGGACCT TGAACACT TGAACACT TGAACTCCC ATCTTGCACT TGAACTCCCACA ATCTCCCCACA ACCCCCAGACTTC AGAACACTT AAAAAAAAAA	GGGACAGGCC ATCTCAGTIGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GGCGAACAGC GCGGCCGATG GAATCCAGAC GCGGCTGGAG GCAGGACCAC GCGGGCCGC GGGCGCCC GGGGCCCC CGTGGACCCC CATCTACAGC CACCTACAGC CCAGCACC ACCCAGCGCC CCGGCGCCC TCAGCACC CCGGGTCCAC TCAGCCCC ACCCAGCCC TCAGCCCC TTACACACTT TTGTTGTTTT TTGAACAGTT GTTGGATTGT AAA  51   NSGAPAGAAG LAEKRPFVEE GGRVAMDGLG	120 180 240 300 360 420 660 720 780 960 1020 1080 1140 1260 1320 1380 1440 1500 1560 1680 1740 1800
50 55 60 65 70	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGGC CAGAGCACGAG GCCGAGTCGC GCAGACTCGC CGCAGCACTACA GGCGGCTTCC CGCTGCTGC CGCTGCGCG GACCCGGCTTCC CGCTGCGCG CGACTCGC CGCTGCGCC CGCTGCGCC CTTCACATGT ATGCAGCAGG CGACTCCCC CGAGCTCCCC CGAGCTCCCCC CCTGAGCAGG CTCACACTACA CCTTCACGTGT ATGCAGCAGG CCTTCACGTGT ATGCAGCAGG CCTTCACCTCT CCTAGAGATGG CAAACCCTA CCATTTCCTG CTAAAAAATA Seq ID NO: Protein Ac 1 MSSPDAGYAS RAKGESRIRE AERLRVQHMQ LQFPEQGFPA	11    TAGGCCGGCT CGGCGGCTTC ACCCCTCCC ACCCCTCCC AGGCCTGCAG CCCAGAGGCC TGAGCCCCTTGAGG CCTGAGGCCT TGGTGTGGGC TGGACGGCCT TGCACGGCCT TGCACGGCCT TCTCGGACAT TCTTCGCACAT TCTTCGCACAT TCTTCGCACAT TCTTCGCACAT TCTTCGCACAT TCTTCGCACAT TCTTCGCACAT TCTTCGCACAT TCTTCGCACAT ACACAGCAC TCCCGAGGCC TCCCGAGGCT CTCCGAGGCT TCTCGCAGGCT TCTCGCAGGCT TCTCGCAGGCT ACACAGCAC TCCCGAGGCT TCTCGCAGGCT TCTCGCAGGT TCTTCCAGTT AAATTTATT DDQCGTCAAT PNNAPWWARE DDDQCGTCAAT GPPLLPPHMC GPPLLPPHMC GPPLLPPHMC GPPLLPPHMC	21    GGGGGCCCTG GGGCCGGAG CCGGGTCGGG GGCCCATGAGC GGGCCGAGGC CGGGACATGAGC CAAGATGCTG GGAGCCATGAGC GGGCGCGCG GGCTCCAG GGCCACGCC CCCGATGCC CCCGATGCC CCGATGCC CCGATGCC CCGATGCC CTCAGCCC CCTCAGCCC CCTCAGCCC CCTCAGCCC CCTCAGACTC CCTCAGACTC TAATTTATGG TAAAATTTG TAAATTTATG TAATTTATGG TAAAATTGC TAAATTTATGG TAAAATTGC TAATTTATGG TAAAATTGC TAAATTTATGG TAAAATTGC TAAATTTATGG TAAAATTGC TAAATTTATGG TAAAATTGC TAATTTATGG TAAAATTGC TAATTTATGG TAAAATTGC TAAATTTATGG TAAAATTGC TAATTTATGG TAAAATTGC TAAAATTGC TAATTTATGG TAAATTTATGG TAAATTTATGG TAATTTATGG TAATTTATGG TAAATTTATGG TAATTTATGG TAATTTAT	GGTACGCTGT GGAGGCGCG GGAGGCGCG AGCCCGGATG GTGATGCCCG AAGGTGAAGCGG AAGGCGGCG CGCAAGCCGC TACCGCGACT GACACGTCC CGGGACTGC CCGGAGCTTCCCGAGC TACCGCGACT ATTCCGGCCC CCGGAGCCTC CCCGGGACTCC CCGGAGCCTC CCCGGGCGCGC CACCAGCACC CCGGGACTGCC CTGCGTTTT TAATTTATTT TCAGACATTT AGCTTTGAAT AAAAAAAAAA	AGACCAGACC CCCTCGGGGC CGCGGGATACGC GGCAGGGCCC GCGAGGCCC CCCTATCGG GGAGGCGCC GCGAGGCCC AGGGCTTCCC GCAGAGTTCC GCCAGAGTTCC GCCAGAGTTCC GCCAGAGTTCC GCCAGAGTTCC GCCAGAGTTCC TCTGGCCC TCTTGGCCC TCTTGCCCC TCTTGCCCC TATATTACTG AGAGCATTT TGAATCTCC TGTTGCTCC TGTTTCCCACA GGGTTTCCCCACA GGGTTTCCCCACA GGTTTCCCCACA GGTTTCCCCACA TTCCACACT TATATACTG TTGATCCCC TTTCCCACACT TTCCCACACT TTCCCACACT TTCCACACT TTCCCACACT TTCCACACT TTCCA	GCGACAGGCC ACGTTGAGG CAGTGACGAC CTGCCCTGG GGCGACAGG CAGTGACGAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCCC CACCTACAGC CACCTACAGC CAGCACCC ACCTACAGC CAGCACCC CACCTACAGC CAGCACCC CACCTACAGC CCAGCACC CACCTACAGC CCAGCACC CACCTACAGC CCAGCACC CCAGCACC CCAGCACC CACCTACAGC CCAGCACC CACTTCCAAC TTACACACTT TTGTGTTTT TTGTATCTT TTTCAATCTT TTTCAATCTT TACACACTT TTACACACTT TACACACTT TTACACACTT TTACACACTT TACACACTT TTACACACTT TACACACTT TACACACTT TACACACTT TACACACTT TACACACT TACACACT ACAC ACACACAC	120 180 240 300 360 420 480 540 660 720 780 960 1020 1140 1120 1320 1320 1440 1500 1680 1740 1800

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					AAGAAGCTGG		300
					TCCCTGTTAT		360
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					AAGGTTTGGA		480
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					TGAAATATTC		1740
					GCAAGGAAAC		1800
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					AAAATCCAGA		1980
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						TCCACTAGCA	
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70						ATCAGTTTTA	
						GGTCTTATAA CACAATAGCC	
						TTTTATTTCC	
7.5	TATTTCTTTA	GGGAGTGCTA	CAAATGTTTG	TCACTTAAAT	TTCAAGTTTC	TGTTTTAATA	3960
75						AGTAGTAAAT	
•				ATTAGTAAGA	ACTTTGTAAA	TAAATACCTA	4080
	MANCCCAAAA	AAAAAAAAA	nnnAA				
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	1	11	21	31	41	51 I	
	MARNSVI.TCT	   TGRTSLADSS	   IFDSKUTETS	KENLLIGSTS	I YVEEEMPOIE	TRVILVQEAG	60
0.5	KQEELTKALK	DIKVGFVKME	SVEEFEGLDS	PEFENVFVVT	DFQDSVFNDL	YKADCRVIGP	
85	PVVLNCSQKG	EPLPFSCRPI	YCTSMMNLVL	CFTGFRKKEE	LVRLVTLVHH	MGGVIRKOFN	180

	SKVTHLVANC	TOGERFRYAV	SLGTPIMKPE	WIYKAWERRN	EQDFYAAVDD	FRNEFKVPPF	240
	OPCIRCULOR	SDEEKTNMEE	MERMOCCIOT.	מו כחפס כיישו.	WITCH TIRE	DEEDGAMI AM	300
	Cherranda	SDEEKINGER	HIENGGGKIE	PLODERCIAL	AAPPRITATO	PPEPSKKLIV	
	VKQEWFWGSI	QMDARAGETM	YLYEKANTPE	LKKSVSMLSL	NTPNSNRKRR	RLKETLAQLS	360
	PHTHUSPPPP	RKRPSAEHSL	SIGSLIDISN	TPESSINYGD	TPKSCTKSSK	SSTPVPSKOS	420
5							
J		QTESNYVNIL					480
	HTKIKDDLED	LIVNWDESKS	IGDIFLKYSK	DLVKTYPPFV	NFFEMSKETI	IKCEKOKPRF	540
		PECGROSLVE					600
	KEVMTHINED	KRKTEAOKQI	FDVVYEVDGC	PANLLSSKRS	LVQRVETISL	GEHPCDRGEQ	660
	UPLELEMBOL.	ELARKRHKVI	CTERSPHOOT	RPPAST.KHTH	LMPLSOTKKV	LOTRETEDCH	720
10	AIRLINDCH	PTHYKKURYAT	GIEKDEMGQI	AL LADDICIAN	THE DOOR THE		
10	NAFALLVRPP	TEQANVLLSF	OMISDELPKE	NWLKMLCRHV	ANTICKADAE	NLIYTADPES	780
	FRUNTKOMOS	TLSRASRAIK	KTSKKVTRAF	SFSKTPKRAL	RRALMTSHGS	VEGRSPSSND	840
		SSLAGIPSPS					
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	Character Control	GCCATGCCTA	GTCTAGTGGT	ATCTGGAATA	ATGGAAAGAA	ATGGGGGCTT	60
20		GGATGTTTCG					120
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	CGCCCTTCAG	CTGGCTCTCG	ATCAACTCTG	CCTCCTGGGT	TTGGGGGAGC	CCCCCCCCCCC	180
	. CARROCCOCC	GAGGACGGGG	CACCTCCCCC	GGGCGGCGCC	CCCGCCCAGC	CGACAGCCCC	240
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		GCGCCGCCGC					300
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		ACAGGGCGAC					600
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30	CCCTCCTCCTT	CTGCCCGGCC	AGGTGACCAT	COGTGTGCGG	GTGCCCTACC	GCGTGGTGGG	720
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	COMO CO COCO	GCGCGCGAGG	ACATCCACAC	CCACATCCCC	CTCCCCACTC	CCAACATCCT	900
	CGAGTACAAC	AATGAAAACG	ACTTCCTGGC	GGGGAGCCCC	GACGCAGCAA	TCGATAGCCG	960
35	CTACTCCGAC	GCCTGGCGGG	TGCACCAGCC	CGGCTGCAAG	CCCCTCTCCA	CCTTCCGGCA	1020
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40		CCCACCTCCG					1260
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		CTGCGGAGCC					1440
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		AGGACGGACC					1560
45							
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	CTGGACCTGT	TTTCCACTAA	AGCCTTTTGG	AAAGCGGTGA	TTTGAGGGGC	AAGGTGCTTA	1680
		CTCGCTGGGG					1740
	TTTCAGAGCC	TCTGGTCACC	CTGTCCTGGA	AAGATTGGGA	GGGGGCCAGA	CIGAAAATIT	1800
	TACTAGAGTT	<b>ACAACTCTGA</b>	TACCTCAACA	CACCCTTAAA	TCTGGAAGCA	GCTAAGAGAA	1860
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		ACTCCACCCC					1980
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		CTGTCTTGTT					2100
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		TTATTGATGG					2280
		TAAAGGGTCA					2340
	TAGTTCTTCC	GCTGGATTTT	CTGGTTGTGG	AAGTGGGGGC	GCCAGAGTAG	TGTGTCTGCT	2400
		GCAGGAAAGG					2460
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		TGTGGTTGAG					2640
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		GGGGAGGTGG					2700
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65						GGAGATCCTT	2820
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						TCCAGAGTCC	
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						GGAGGGGTGG	3000
70						CCGCCTATGT	3060
70	GAGCCATCCT	GAGATGTCTG	TACAATAGAA	ACCAAACCAA	ATGGGCACCC	TCGGTTGCCG	3120
						CCCTCCCCCT	3180
						CAAATTCAAT	3240
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75	AGAAAACAAA	AATAGCAAAA	AAAAAAAAAA .	AAAGCAGTTC	TTTATAATTT	AATATTCTAT	3420
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	FCFAMPSIAN	SGIMERNGGE	GELGCFGGG		ALOLALDOLO	LIGIGEPPAP	60
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						PKGASDAKLC	
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85	FMVTGRREDV	/ ATARREIIS	AEHFSMIRAS	RNKSGAAFGV	/ APALPGOVTI	RVRVPYRVVG	240
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5	KARAGPPGAH	RSPATSAGPE	LAGLPRRPPG	eplogfsklg Vchitatoai	GGGLRSPGGG	RDCMVCFESE	480
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	ATGGTTTTCT	CTGTCAGGCA	GTGTGGCCAT	GTTGGCAGAA	CTGAAGAAGT	TTTACTGACG	60
	TTCAAGATAT	TCCTTGTCAT	CATTTGTCTT	CATGTCGTTC	TGGTAACATC	CCTGGAAGAA	120
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				CTTCAGTGTG			660
				TTTTCTTCCA			720 780
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23				GECATTGACA			900
				TCCGGCACCC			960
				AATGTCAACA			1020
				TCTGATCTTG			1080
30				CCTAACCTCG			1140
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				AACTTTTCAA			1260
				GTGAATGCCA			1320
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				TTTGAAACAC			1500
				GTCATATCAT			1560
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70				CTATCTAGGA			1800
				GGTTGTGGGC			1860
				AAGATCCGGA			1920
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45				ATCTCAGTGG			2040
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	AAAGTATTTA	ATACTTACAT	CCGAAAATAC	ATCCTTAAAT	TCTGCATTGT	CGGTTGGGGG	2160
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60				AATGGGAAAG		TCTCAGAAGG	2940
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		VGRTEEVLLT	FKIFLVIICL	HVVLVTSLEE	DTDNSSLSPP	PDVTLSLLPS	60
	NETEKTKITI	VKTPNASGVK	PORNICNLSS	ICNDSAFFRG	EIMPQYDKES	TVPQNQHITN	120
~~						NTMNACAVIA	180
70						FSSSQSIPVV	240
				PIGEIQPLSP			300
						SDLENQVLQM	360
	EKALSLGSLE	PNLAGEMINQ	VSRLLHSPPD	MLAPLAQRLL	KVVDDIGLQL	NESNTTISLT	420
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50 55	CTCAGAAGGA  Seq ID NO: Protein Acc	CTTCAAAGCG  18 Protein 11	GGGAAGCTTA Sequence 20 sequence 21   FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV	CACTTTATTG  31  HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRLLKVVDDI APENSIGTIN APENSIGTIN CTCSHLTSFG	AGCAAATGTG  41    DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSSG ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLE LPSSLMNLH VLLDLSRTSV	51	60 120 180 240 300 360 420 480 540
50 55	CTCAGAAGGA Seq ID NO: Protein Acc 1   WYFSVRQCGH VTLSLLPSNE LSLSELKRSE IRPMEHCCCS SQVPKATSFA OTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFMFFETPAL VFWDLGRNGG ITTIGCGLSS	CTTCAAAGCG  18 Protein ression #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EPPDYSPVTH VKASFSSPTV WKNQVSRLLH NTTTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY	GGGAAGCTTA  sequence 21   FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKIQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI LAFEKIRRDY	CACTTTATTG  31    HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVI APENSIGTIT ANLITVRNLTR CTCSHLTSFG PSKILIQLCA	41    DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP NVTVTLKHIN VLLDLSRTSV ALLILLNLVFL	51	60 120 180 240 300 360 420 480 540 600
50	CTCAGAAGGA Seq ID NO: Protein Acc	CTTCAAAGCG  18 Protein ression #: 1  11  VGRTEEVLLT TGVKPQRNIC LNRTLQTLSE EPPDYSPVTH VKASFSSPTV MINQVSRLLH MINGVSRLLH MITTIFVAQDP FQDPSLENLS RGGWSDNGCS IPLSVTLUTY LHYFLLVSFT	GGGAAGCTTA  sequence 20 sequence 21   FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAFEKIRRDY WMGLEAFHMY	CACTITATIG  31  HVVLVISLEE FFRGEIMPQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRLLKVVDDI APENSIGTIT ANLIVRNLTR CTCSHLISFG FSKILIQLCA LALVKVFNTY	AGCAAATGTG  41  DTDNSSLSPP DKESTVPQNQ IKLNNTMNAS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP NVTVTLKHIN VILDLSRTSV ALLLLNLVFL IRKYILKPCI	51   PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTF LDSWHALYKM VGWGVPAVVV	60 120 180 240 300 420 480 540 600 720
50 55	CTCAGAAGGA  Seq ID NO: Protein Acc  I   MVFSVRQCGH VTLSLLPSNE LSLSELKRSE IRPMEHCCCS SQVPKATSFA QTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFMFFETPAL VFMDLGRNGG ITYIGCGLSS QGLCISVAVF TIILTISPDN	CTTCAAAGCG  18 Protein 12 protein 11 protein 12 protein 13 protein 14 protein 15 protein 16 protein	GGGAAGCTTA  Sequence 20 sequence 21   FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAFEKIRRDI MMGLEAFHMY NGSPDDFCWI	CACTTTATTG  31  HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRLLKVVDDI APENSIGTIT ANLTVRNLTR CTCSHLTSFG PSKILIQLCA LALVKVFNTY NNNAVFYITV	AGCAAATGTG  41    DTDNSSLSPP DKESTVPQNQ IKLINITMNAC RGPPPSSSQS ASSPAIDMPP TSSISDLENQ GLQLINFSNTLP LPSSLMNNLP LPSSLMNNLP NVTVTLKHIN VILDLSRTSV ALLLLINLVFL IRKYILKPCI VGYFCVIFLL	51       PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTF LDSWIALYKM VGWGVPAVVV NVSMFIVVLV	60 120 180 240 300 360 420 480 540 600 720 780
50 55	CTCAGAAGGA  Seq ID NO: Protein Acc  I   MVFSVRQCGH VTLSLLPSNE LSLSELKRSE IRPMEHCCCS SQVPKATSFA QTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFMFFETPAL VFMDLGRNGG ITYIGCGLSS QGLCISVAVF TIILTISPDN	CTTCAAAGCG  18 Protein 12 protein 11 protein 12 protein 13 protein 14 protein 15 protein 16 protein	GGGAAGCTTA  sequence 20 sequence 21   FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAFEKIRRDY WMGLEAFHMY	CACTTTATTG  31  HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRLLKVVDDI APENSIGTIT ANLTVRNLTR CTCSHLTSFG PSKILIQLCA LALVKVFNTY NNNAVFYITV	AGCAAATGTG  41    DTDNSSLSPP DKESTVPQNQ IKLINITMNAC RGPPPSSSQS ASSPAIDMPP TSSISDLENQ GLQLINFSNTLP LPSSLMNNLP LPSSLMNNLP NVTVTLKHIN VILDLSRTSV ALLLLINLVFL IRKYILKPCI VGYFCVIFLL	51       PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTF LDSWIALYKM VGWGVPAVVV NVSMFIVVLV	60 120 180 240 300 360 420 480 600 660 720 840
50 55	CTCAGAAGGA  Seq ID NO: Protein Acc  I WYFSVRQCGH VTLSLLPSNE LSLSELKRSE IRPMEHCCCS SQVPKATSFA QTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFMFFETPAL VFWDLGRNGG ITTIGCGLSS QGLCISVAVF TIILTISPDN QLCRIKKKKQ	CTTCAAAGCG  18 Protein 18 Protein 19 Protein 11	GGGAAGCTTA  Sequence 20 sequence 21   FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKIQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAFEKIRDY WMGLEAFHMY MGSPDDFCWI DLRSIAGLTF	CACTTTATTG  31  HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRLLKVVDDII APENSIGTII APLIKVVDDII ACTCSHLTSFG FSKILIQLCA LALVKVFNTY LLGITWGFAF	41   DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSSQ ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLF UPSSLMNLF VILDLSRTSV ALLLLNLVPL IRKYILKPCL IRKYILKPCL FAWGPVNVTF	51	60 120 180 240 300 360 420 480 540 600 720 780
50 55	CTCAGAAGGA  Seq ID NO: Protein Acc  I   WYFSVRQCGH VTLSLLPSNE LSLSELKRSE IRPMEHCCCS SQVPKATSFA OTHVSGTPPP GSLEPNLAGE AVIRVNASSF OFMFFETPAL VFWDLGRNGG ITTIGCGLSS QGLCISVAVF TILLTISPDN DLCRIKKKQ QGFFIFIFYC	CTTCAAAGCG  18 Protein ression #: 1 11   VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EPPDYSPVTH VKASFSSPTV VKASTSSPT VKASTSSPT VKASTSSPT VKASTSSPT VKASTST VKASTS VKASTST VKASTS VKASTST VKASTST VKASTST VKASTST VKASTST VKASTST VKASTS VKASTS VKASTST VKASTS VKAS	GGGAAGCTTA  sequence 20 sequence 21  FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI LAFEKIRRDY WMGLEAFHMY NGSPDDFCWI RTYLCCGKLR	CACTTTATTG  31  HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN APENSIGTIT ANLTVRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVFYITV LIGITWGFAF LAENSGNAST	41   DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSSQ ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLF UPSSLMNLF VILDLSRTSV ALLLLNLVPL IRKYILKPCL IRKYILKPCL FAWGPVNVTF	51	60 120 180 240 300 360 420 480 600 660 720 840
50 55 60	CTCAGAAGGA  Seq ID NO: Protein Acc  I   WYFSVRQCGH VTLSLLPSNE LSLSELKRSE IRPMEHCCCS SQVPKATSFA OTHVSGTPPP GSLEPNLAGE AVIRVNASSF OFMFFETPAL VFWDLGRNGG ITTIGCGLSS QGLCISVAVF TILLTISPDN DLCRIKKKQ QGFFIFIFYC	CTTCAAAGCG  18 Protein ression #: 1 11   VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EPPDYSPVTH VKASFSSPTV VKASTSSPT VKASTSSPT VKASTSSPT VKASTSSPT VKASTST VKASTS VKASTST VKASTS VKASTST VKASTST VKASTST VKASTST VKASTST VKASTST VKASTS VKASTS VKASTST VKASTS VKAS	GGGAAGCTTA  Sequence 20 sequence 21   FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKIQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAFEKIRDY WMGLEAFHMY MGSPDDFCWI DLRSIAGLTF	CACTTTATTG  31  HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN APENSIGTIT ANLTVRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVFYITV LIGITWGFAF LAENSGNAST	41   DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSSQ ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLF UPSSLMNLF VILDLSRTSV ALLLLNLVPL IRKYILKPCL IRKYILKPCL FAWGPVNVTF	51	60 120 180 240 300 360 420 480 600 660 720 840
50 55	CTCAGAAGGA  Seq ID NO: Protein Acc  I   MVFSVRQCGH VTLSLLPSNE LSLSELKRSE IRPMEHCCCS SQVPKATSFA QTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFMFFETPAL VFWDLGRNGG ITYIGCGLSS QGLCISVAVP TILLTISPDN QLCRIKKKKQ QGFFIFIFYC GKQHMFNEKB	CTTCAAAGCG  18 Protein 18 Protein 19 Protein 11	GGGAAGCTTA  Sequence 20 sequence 21   FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKIQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRLNETI IAFEKIRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL	CACTTTATTG  31  HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN APENSIGTIT ANLTVRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVFYITV LIGITWGFAF LAENSGNAST	41   DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSSQ ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLF UPSSLMNLF VILDLSRTSV ALLLLNLVPL IRKYILKPCL IRKYILKPCL FAWGPVNVTF	51	60 120 180 240 300 360 420 480 600 660 720 840
50 55 60	CTCAGAAGGA  Seq ID NO: Protein Acc  I   WYFSVRQCGH VTLSLLPSNE LSLSELKRSE IRPMEHCCCS SQVPKATSFA OTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFMFFETPAL VFWDLGRNGG ITTIGCGLSS QGLCISVAVF TILLTISPDN DLCRIKKKQ QGFFIFFYC GKQHMFNEKB  Seq ID NO:	CTTCAAAGCG  18 Protein ession #: 1 11   VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EPPDYSPVTH VKASFSSPTV WKASFSSPTV WKNOVSRLLH NTTTFVAQDP FOPPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSPT YGLGSYGKFP VAKENVRKQW DSCNGKGRMA 19 DNA seq	GGGAAGCTTA  sequence 21   FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI LISYVISSSV VKDRRLNETI LIAFEKIRRDY WMGLEAFHMY NGSPDDFCWI RRYLCCGKLR LRRTSKRGSL uence	CACTTTATTG  31  HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN APENSIGTIT ANLITVRNLTR CTCSHLTSFG PSKILIQLCA LALVKVFNTY NNNAVFYITY NNNAVFYITY LLGITWGFAF LAENSGNAST HFIEQM	41   DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSSQ ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLF UPSSLMNLF VILDLSRTSV ALLLLNLVPL IRKYILKPCL IRKYILKPCL FAWGPVNVTF	51	60 120 180 240 300 360 420 480 600 660 720 840
50 55 60	CTCAGAAGGA  Seq ID NO: Protein Acc  I   WYFSVRQCGH VTLSLLPSNE LSLSELKRSE IRPMEHCCCS SQVPKATSFA OTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFMFFETPAL VFWDLGRNGG ITTIGCGLSS QGLCISVAVF TILLTISPDN DLCRIKKKQ QGFFIFFYC GKQHMFNEKB  Seq ID NO:	CTTCAAAGCG  18 Protein ession #: 1 11   VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EPPDYSPVTH VKASFSSPTV WKASFSSPTV WKNOVSRLLH NTTTFVAQDP FOPPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSPT YGLGSYGKFP VAKENVRKQW DSCNGKGRMA 19 DNA seq	GGGAAGCTTA  Sequence 20 sequence 21   FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKIQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRLNETI IAFEKIRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL	CACTTTATTG  31  HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN APENSIGTIT ANLITVRNLTR CTCSHLTSFG PSKILIQLCA LALVKVFNTY NNNAVFYITY NNNAVFYITY LLGITWGFAF LAENSGNAST HFIEQM	41   DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSSQ ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLF UPSSLMNLF VILDLSRTSV ALLLLNLVPL IRKYILKPCL IRKYILKPCL FAWGPVNVTF	51	60 120 180 240 300 360 420 480 600 660 720 840
50 55 60	CTCAGAAGGA  Seq ID NO: Protein Acc	CTTCAAAGCG  18 Protein ression #: 1  11  VGRTEEVLLT TGVKPQRNIC LNRTLQTLSE EPPDYSPVTH VKASFSSPTV MINQVSRLLH MINQVSRLLH MINTIFFVAQDP FQDPSLENLS RGGWSDNGCS IPLSVTLVTY LHYFLLVSPT YGLGSYGKFP LGAQRKTSIQ DSCNGKGRMA  19 DNA seq id Accessio	GGGAAGCTTA  sequence 20 sequence 21   FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI LIAFEKIRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL uence n #: Eos se	CACTTTATTG  31  HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN APENSIGTIT ANLITVRNLTR CTCSHLTSFG PSKILIQLCA LALVKVFNTY NNNAVFYITY NNNAVFYITY LLGITWGFAF LAENSGNAST HFIEQM	41   DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSSQ ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLF UPSSLMNLF VILDLSRTSV ALLLLNLVPL IRKYILKPCL IRKYILKPCL FAWGPVNVTF	51	60 120 180 240 300 360 420 480 600 660 720 840
50 55 60	CTCAGAAGGA  Seq ID NO: Protein Acc	CTTCAAAGCG  18 Protein lession #: 1  11    VGRTEEVLLT TGVKPQRNIC LNRTLQTLSE VRIPCPSSPE EPPDYSEVTH VKASFSSPTV MINQVSRLLH NTTTFVAQDP FQDPSLENLS RGGWSDNGCS IPLSVTLVTT YGLGSYGKFP LGAQRKTSIQ VAKENVRCQW DSCNGKGRMA  19 DNA seq id Accessio Lence: 13	GGGAAGCTTA  sequence 20 sequence 21   FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAFEKIRRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLL LRRTSKRGSL LRTTSKRGSL UMENCE m #: EOS Seconds	CACTTTATTG  31  HVVLVTSLEE FFRGEIMPQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRILKVVDDIT ANLITVRNLTR CTCSHLISFG PSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAF LAENSGNAST HFIEQM  QUENCE	AGCAAATGTG  41    DTDNSSLSPP DKESTVPQNQ IKLINITMNAC RGPPPFSSQS ASSPAIDMPP TSSISDLENQ GLQLINFSNTLP LPSSLMNNLP NVTVTLKHIN VILLDLSRTSV ALLLLINLVFL IRKYILKPCI VGYFCVIFLL FAWGPVNVTF ERNGVSFSVQ	A  51    PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSLASL AHDMELASRV PSQDELTVRC LPAQMMALTF LDSWIALYKM VGWGVPAVVV NVSMFIVVLV MYLFAIRNTL NGDVCLHDFT	60 120 180 240 300 360 420 480 600 660 720 840
50 55 60 65	CTCAGAAGGA  Seq ID NO: Protein Acc	CTTCAAAGCG  18 Protein ression #: 1  11  VGRTEEVLLT TGVKPQRNIC LNRTLQTLSE EPPDYSPVTH VKASFSSPTV MINQVSRLLH MINQVSRLLH MINTIFFVAQDP FQDPSLENLS RGGWSDNGCS IPLSVTLVTY LHYFLLVSPT YGLGSYGKFP LGAQRKTSIQ DSCNGKGRMA  19 DNA seq id Accessio	GGGAAGCTTA  sequence 20 sequence 21   FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI LIAFEKIRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL uence n #: Eos se	CACTTTATTG  31  HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN APENSIGTIT ANLITVRNLTR CTCSHLTSFG PSKILIQLCA LALVKVFNTY NNNAVFYITY NNNAVFYITY LLGITWGFAF LAENSGNAST HFIEQM	41   DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSSQ ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLF UPSSLMNLF VILDLSRTSV ALLLLNLVPL IRKYILKPCL IRKYILKPCL FAWGPVNVTF	51	60 120 180 240 300 360 420 480 600 660 720 840
50 55 60	CTCAGAAGGA  Seq ID NO: Protein Acc	CTTCAAAGCG  18 Protein lession #: 1  11    VGRTEEVLLT TGVKPQRNIC LNRTLQTLSE VRIPCPSSPE EPPDYSEVTH VKASFSSPTV MINQVSRLLH NTTTFVAQDP FQDPSLENLS RGGWSDNGCS IPLSVTLVTT YGLGSYGKFP LGAQRKTSIQ VAKENVRCQW DSCNGKGRMA  19 DNA seq id Accessio Lence: 13	GGGAAGCTTA  sequence 20 sequence 21   FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAFEKIRRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLL LRRTSKRGSL LRTTSKRGSL UMENCE m #: EOS Seconds	CACTTTATTG  31  HVVLVTSLEE FFRGEIMPQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRILKVVDDIT ANLITVRNLTR CTCSHLISFG PSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAF LAENSGNAST HFIEQM  QUENCE	AGCAAATGTG  41    DTDNSSLSPP DKESTVPQNQ IKLINITMNAC RGPPPFSSQS ASSPAIDMPP TSSISDLENQ GLQLINFSNTLP LPSSLMNNLP NVTVTLKHIN VILLDLSRTSV ALLLLINLVFL IRKYILKPCI VGYFCVIFLL FAWGPVNVTF ERNGVSFSVQ	A  51    PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSLASL AHDMELASRV PSQDELTVRC LPAQMMALTF LDSWIALYKM VGWGVPAVVV NVSMFIVVLV MYLFAIRNTL NGDVCLHDFT	60 120 180 240 300 360 420 480 600 660 720 840
50 55 60 65	CTCAGAAGGA  Seq ID NO: Protein Acc	CTTCAAAGCG  18 Protein ression #: 1  1  VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EPPDYSPVTH VKASFSSFTV MINQVSRLLH MTTTFVAQDP FQDPSLENLS RGGWSDNGCS IPLSVTLVTY LHYFLLVSFT YGLGSYGKFP LGAQRKTSIQ UAKENVRQW DSCNGKGRMA  19 DNA seq id Accessio uence: 13  1	GGGAAGCTTA  sequence 20 sequence 21   FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKORRLNETI LIAFEKIRRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLFI ERRICCGKLR LRRTSKRGSL uence n #: Eos seco45 21	CACTTTATTG  31  HVVLVTSLEE FFRGEIMPQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRLLKVVDDI APENSIGTIT ANLTVRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVFYITA LLGITWGTAF LLGITWGTAF LLGITWGTAF HFIEQM  Quence  31	AGCAAATGTG  41    DTDNSSLSPP DKESTVPQNQ IKLINITMNAC RGPPPSSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP NVTUTLKHIN VILDLSRTSV ALLILINLVPL IRKYILKPCI VGYFCVIFLF FAWGPVNVTL FAWGPVNVTL FAWGPVNVTL FAWGPVNVTL 41	51    PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL OSETISSPMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTM VGWGVPAVVV NVSMFIVVLV MYLFAIFNTL NGDVCLHDFT  51	60 120 180 240 300 360 420 480 600 660 720 840
50 55 60 65	CTCAGAAGGA  Seq ID NO: Protein Acc	CTTCAAAGCG  18 Protein Pession #: 1  11    VGRTEEVLLT TGVKPQRNIC LNRTLQTLSE VRIPCPSSPE EPPDYSEVTH VKASFSSPTV MINQVSRLLH MINGVSRLLH MINTTFVAQDP FQDPSLENLS RGGWSDNGCS IPLSVTLVTT YGLGSYGKPP LGAQRKTSIQ DSCNGKGRMA  19 DNA seq id Accessio Lence: 13  11    CTGTCAGGCA	GGGAAGCTTA  sequence 20 sequence 21   FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA LISYVISSSV VKDRRINETI IAFEKIRRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL  uence n #: Eos se 045 21   GTGTGGCCAT	CACTTTATTG  31	AGCAAATGTG  41    DTDNSSLSPP DKESTVPQNQ IKLINITMIAC RGPPPFSSQS ASSPAIDMPP TSSISDLENQ GLQLINFSNIT LPSSLMNILP NVIVILKHIN VILLDLSRTSV ALLLLLNLVPL IRKYILKPCI VGYFCVIFLL FAWGPVNVTF ERNGVSFSVQ  41    CTGAAGAAGT	51   PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTF LDSWIALYKM VGWGVPAVVV NVSMFIVVLV MYLPAIFNTL NGDVCLHDFT  51   TTTACTGACG	60 120 180 240 300 360 420 540 600 720 780 840 900
50 55 60 65	CTCAGAAGGA  Seq ID NO: Protein Acc	CTTCAAAGCG  18 Protein lession #: 1  11    VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPIV MINQVSKLLH NTTTFVAQDP FQDPSLENLS RGGWSDNGCS IPLSVTLVTY LHYFLLVSFT YGLGSYGKFP LGAQRKTSIQ VAKENVRKQM DSCNGKGRMA  19 DNA seq id Accessio lence: 13  11    CTGTCAGGCA TCCTGTCAGCA TCCTGTCATCAT	GGGAAGCTTA  Sequence 20 sequence 21   FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKIQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRLNETI IAFEKIRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL LRRTSKRGSL uence n #: Eos se 045 21   GTGTGGCCAT CATTTGTCTT	CACTTTATTG  31  HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRILKVVDDI APENSIGTIT ANLTVRNLTR CTCSHLTSFG PSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAF LAENSGNAST HFIEQM  Quence  31    GTTGGCAGAA CATGTCGTTC	AGCAAATGTG  41    DTDNSSLSPP DKESTVPQNQ IKLINITMNAC RGPPFSSSQS ASSPAIDMPP TSSISDLENQ GLQINFSNTT LPSSLMNNTL LPSSLMNNTL LPSSLMNTL LPSSLMNTL LPSSLMNTL ENSYLVET LPSSLMNTL FAWGPVNVTF ERNGVSFSVQ  41    CTGAAGAAGT TGGTAACATC	51	60 120 180 240 300 360 420 540 600 660 720 780 840 900
50 55 60 65	CTCAGAAGGA  Seq ID NO: Protein Acci      MVFSVRQCGH VTLSLLPSNE LSLSELKRSE IRPMEHCCCS SQVPKATSFA OTHVSGTPPP GSLEPNLAGE AVIRVNASSF OFMFFETPAL VFWDLGRNGG ITTIGCGLSS QGLCISVAVP TILLTISPDN QLCRIKKKKQ QGFFIFIFYC GKQHMFNEKB Seq ID NO: Nucleic Acc Coding sequil   ATGGTTTTCT TTCAAGATAT GATACTGATA	CTTCAAAGCG  18 Protein lession #: 1 11   VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EPPDYSPVTH VKASFSSPTV VKASFSSPTV VKASFSSPTV VKASFSSTV VKASFSSTV VKASFSSTV VKASFSSTV VKASFSSTV VKASFSSTV VKASFSSTV VKASFSSTV VKASFSSTV VKASTSV LHYFLLVSFT YGLGSYGKFP VGASTV VAKENVRKOM DSCNGKGRMA  19 DNA seq id Accessio uence: 13 11   CTGTCAGGCA TCCTTGTCAGTA ATTCCAGTTT	GGGAAGCTTA  sequence 20 sequence 21   FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SSPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI LIAFEKIRRDY WMGLEAFHMY NGSPDDFCWI LIRTSKRGSL LRRTSKRGSL LRRTSKRGSL uence n #: Eos se 045 21   GTGTGGCCAT GTCACCACCA	CACTTTATTG  31  HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN APENSIGTIT ANLTVRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVFYITV NNNAVFYITV LLGITWGFAF LAENSGNAST HFIEQM  31  GTTGGCAGAA CATGTCGTTC CCTGCTAAAT	AGCAAATGTG  41    DTDNSSLSPP DKESTVPQNQ IKLNNITMAG RGPPPSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP NVTVTLKHIN VLLDLSRTSV ALLLLINLVFL IRKYILKFCI VGYFCVIFLL FAWGPVVTF ERNGVSFSVQ  41    CTGAAGAAGT TGGTAACATC TATCTGTTGT	51   PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTF LDSWIALYKM VGWGVPAVVV NVSMFIVVLV NVSMFIVVLN NGDVCLHDFT  51   TTTACTGACG CCTGGAAGAA CAGTTTTGCC	60 120 180 240 300 360 420 480 540 600 720 780 900
50 55 60 65 70	CTCAGAAGGA  Seq ID NO: Protein Acci      MVFSVRQCGH VTLSLLPSNE LSLSELKRSE IRPMEHCCCS SQVPKATSFA OTHVSGTPPP GSLEPNLAGE AVIRVNASSF OFMFFETPAL VFWDLGRNGG ITTIGCGLSS QGLCISVAVP TILLTISPDN QLCRIKKKKQ QGFFIFIFYC GKQHMFNEKB Seq ID NO: Nucleic Acc Coding sequil   ATGGTTTTCT TTCAAGATAT GATACTGATA	CTTCAAAGCG  18 Protein lession #: 1 11   VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EPPDYSPVTH VKASFSSPTV VKASFSSPTV VKASFSSPTV VKASFSSTV VKASFSSTV VKASFSSTV VKASFSSTV VKASFSSTV VKASFSSTV VKASFSSTV VKASFSSTV VKASFSSTV VKASTSV LHYFLLVSFT YGLGSYGKFP VGASTV VAKENVRKOM DSCNGKGRMA  19 DNA seq id Accessio uence: 13 11   CTGTCAGGCA TCCTTGTCAGTA ATTCCAGTTT	GGGAAGCTTA  Sequence 20 sequence 21   FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKIQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRLNETI IAFEKIRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL LRRTSKRGSL uence n #: Eos se 045 21   GTGTGGCCAT CATTTGTCTT	CACTTTATTG  31  HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN APENSIGTIT ANLTVRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVFYITV NNNAVFYITV LLGITWGFAF LAENSGNAST HFIEQM  31  GTTGGCAGAA CATGTCGTTC CCTGCTAAAT	AGCAAATGTG  41    DTDNSSLSPP DKESTVPQNQ IKLNNITMAG RGPPPSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP NVTVTLKHIN VLLDLSRTSV ALLLLINLVFL IRKYILKFCI VGYFCVIFLL FAWGPVVTF ERNGVSFSVQ  41    CTGAAGAAGT TGGTAACATC TATCTGTTGT	51   PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTF LDSWIALYKM VGWGVPAVVV NVSMFIVVLV NVSMFIVVLN NGDVCLHDFT  51   TTTACTGACG CCTGGAAGAA CAGTTTTGCC	60 120 180 240 300 360 420 540 600 660 720 780 840 900
50 55 60 65 70	CTCAGAAGGA  Seq ID NO: Protein Acci    WYFSVRQCGH VTLSLLPSNE LSLSELKRSE IRPMEHCSE SQVPKATSFA OTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFNFFETPAL VFWDLGRNGG ITYIGCGLSS QGLCISVAVF TILLTISPDN QLCRIKKKG QGFFIFIFYC GKQHMFNEKB  Seq ID NO: Nucleic Ac. Coding sequil ATGGTTTTCT TTCAAGATAT CCCTCCTCCA	CTTCAAAGCG  18 Protein ression #: 1  11    VGRTEEVLLT TGVKPQRNIC LNRTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV MINQVSRLLH MINQVSRLLH MINTUFVAQDP FQDPSLENLS RGGWSDNGCS IPLSVTLVTY LHYFLLVSFT YGLGSYGKPP LGAGYKFP LGAGYTGAG  19 DNA seq id Accessio Lence: 13  11  CTGTCAGGCA TCTTGTCATT ATGAGGTTGA	GGGAAGCTTA  sequence 20s sequence 21   FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKORRINETI IAFEKIRRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCGKLR LRRTSKRGSL uence n #: Eos se 045 21   GTGTGGCCAT CATTTGTCTT GTCACCACCA AACAACAAGC	CACTTTATTG  31  HVVLVTSLEE FFRGEIMPQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRLLKVVDDI ANLIVRNLTR CTCSHLISFG FSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAST HFIEQM  QUENCE  31  GTTGGCAGAA CATGTCGTTC CCCTGCTAATG	AGCAAATGTG  41    DTDNSSLSPP DKESTVPQNQ IKINTMNAC RGPPPFSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP NVTVTLKHIN VILDLSRTSV ALLLLNLVFL IRKYILKPCI VGYFCVIFIL FAWGPVNVTF ERNGVSFSVQ  41    CTGAAGAAGT TGGTAACATC TGTTATGTT	51   PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTF LDSWIALYKM VGWGVPAVVV NVSMFIVVLV MYLPAIPNTL NGDVCLHDFT  51   TTTACTGACG CCTGGAAGAA ACAGTTTTGCC CTTACTCCCT	60 120 180 240 300 360 420 540 600 720 780 840 900
50 55 60 65	CTCAGAAGGA  Seq ID NO: Protein Acc  I   MVFSVRQCGH VTLSLLPSNE LSLSELKRSE IRPMEHCCCS SQVPKATSFA QTHVSGTPPP GSLEPNLAGE ITYIGCGLSS QGLCISVAVF TILLTISPDN QLCRIKKKKQ QGFFIFIFYC GKQHMFNEKB Seq ID NO: Nucleic Ac Coding seq I   ATGGTTTTCT TTCAAGATAT GATACTGATA CCCTCCTCA TCAAACGAAAA	CTTCAAAGCG  18 Protein Pession #: 1  11    VGRTEEVLLT TGVKPQRNIC LNRTLQTLSE VRIPCPSSPE EPPDYSEVTH VKASFSSPTV MINQVSRLLH NTTTFVAQDP FQDPSLENLS RGGWSDNGCS IPLSVTLVTT YGLGSYGKFP LGAQRKTSIQ VAKENVRCQW DSCNGKGRMA  19 DNA seq id Accessio Lence: 13  11    CTGTCAGGCA TCCTGTCATT ATCAGGTTCA CAGAAAAAAC CAGAAAAAAAC CAGGAAAAAAC CAGGAAAAAAAC CAGGAAAAAAAC CAGGAAAAAAAC CAGGAAAAAAAC CAGGAAAAAAC CAGGAAAAAAC CAGGAAAAAAAC CAGGAAAAAAAC CAGGAAAAAAAC CAGGAAAAAAC CAGGAAAAAAC CAGGAAAAAAAC CAGGAAAAAAAA	GGGAAGCTTA  Sequence 20 sequence 21   FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLOVSLETQ LISYVISSSV VKDRRLNETI IAFEKIRRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLE LERTSKRGSL UEDCE 045 21   GTGTGGCCAT GTTACCACCA AACAACAGC	CACTTTATTG  31    HVVLVTSLEE FFRGEIMPQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN APENSIGTIT ANLTVRNLTR CTCSHLTSFG PSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAF LAENSGNAST HFIEQM  QUENCE 31    GTTGGCAGAA CATGTCGTTC CCTGCTAAATT CTCAATGATG ATAGTRAAAAA	AGCAAATGTG  41    DTDNSSLSPP DKESTVPQNQ IKLINITMIAC RGPPPSSSQS ASSPAIDMPP TSSISDLENQ GLQLINFSNTI- LPSSLMNNLP NVTVTLKHIN VILLDLSRTSV ALLLLINLVFL IRKYILKPCI VGYFCVIFLL FAWGPVNVTF ERNGVSFSVQ  41    CTGAAGAAGT TGGTAACATC TATCTGTTGT TTACTTTAAG CCTTCAATGC	51	60 120 180 240 300 360 420 600 600 720 780 840 900
50 55 60 65 70	CTCAGAAGGA  Seq ID NO: Protein Acci      WYFSVRQCGH VTLSLLPSNE LSLSELKRSE LSRSES SQVPKATSFA OTHVSGTPPP GSLEPNLAGE AVIRVNASSF OFMFFETPAL VFWDLGRNGG ITTIGCGLSS QGLCISVAVF TILLTISPDN DLCRIKKKQ QGFFIFIFYC GKQHMFNEKB Seq ID NO: Nucleic Acc Coding seq 1   ATGGTTTTCT TTCAAGATAT CCCTCCTCAA TCAAACGAAA AAACCCCAGAA	CTTCAAAGCG  18 Protein lession #: 1 11   VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EPPDYSPVTH VKASFSSPTV VKASFSSPTV WINGVSRLLH NTTTFVAQDP FOPPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKFPL VAKENVRKQN DSCNGKGRMA  19 DNA seq id Accessio ence: 13 11   CTGTCAGCCA TCCTTGTCAT ATTCCAGTTT ATGCAGTTTA ATGAGAATAAC GAAATATCTG GAAATATCTG	GGGAAGCTTA  sequence 21   FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI LIAFEKIRRDY WMGLEAFHMY NGSPDDFCWI LIRSTIGGLEF RRYLCCGKLR LRRTSKRGSL UENCE ##: EOS Se	CACTITATIG  31   HVVLVISLEE FFRGEIMFQY AQSTINCTFI DPIVCLADHP PLSPQPSAPI APPVQTDIVI APENSIGTIT ANLITVRNLTR CTCSHLISFG PSKILIQLCA LALVKVFNTY NNNAVFIIT LALVKVFNTY NNNAVFITH LAENSGNAST HFIEQM  QUEENCE  31   GTTGGCAGAA CATGTCGTTC CCTGCTAAAT CTCAATGAAAA TCTATITGCA	AGCAAATGTG  41    DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPPSSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP NVTVTLKHIN VILDLSRTSV ALLLLINLVFL IRKYILKPCI VGYFCVIFL FAWGPVNVTF ERNGVSFSVQ  41    CTGAAGAAGT TGGTAACATC TATCTGTTGT TTACTTTAAG ACTCAAGC ATGACTCAGC	51   PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSIAL AHDMELASRV PSQDELTVRC LPAQMMALTF LDSWIALYKM VGWGVPAVVV NVSMFIVVLV MYLFAIFNTL NGDVCLHDFT  51   TTTACTGACG CCTGGAAGAA CAGTTTTGCC CTTTACTCCCT ATTCTTACTACTA	60 120 240 300 360 420 480 540 660 720 780 900
50 55 60 65 70	CTCAGAAGGA  Seq ID NO: Protein Acci      WYFSVRQCGH VTLSLLPSNE LSLSELKRSE LSRSES SQVPKATSFA OTHVSGTPPP GSLEPNLAGE AVIRVNASSF OFMFFETPAL VFWDLGRNGG ITTIGCGLSS QGLCISVAVF TILLTISPDN DLCRIKKKQ QGFFIFIFYC GKQHMFNEKB Seq ID NO: Nucleic Acc Coding seq 1   ATGGTTTTCT TTCAAGATAT CCCTCCTCAA TCAAACGAAA AAACCCCAGAA	CTTCAAAGCG  18 Protein lession #: 1 11   VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EPPDYSPVTH VKASFSSPTV VKASFSSPTV WINGVSRLLH NTTTFVAQDP FOPPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKFPL VAKENVRKQN DSCNGKGRMA  19 DNA seq id Accessio ence: 13 11   CTGTCAGCCA TCCTTGTCAT ATTCCAGTTT ATGCAGTTTA ATGAGAATAAC GAAATATCTG GAAATATCTG	GGGAAGCTTA  Sequence 20 sequence 21   FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLOVSLETQ LISYVISSSV VKDRRLNETI IAFEKIRRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLE LERTSKRGSL UEDCE 045 21   GTGTGGCCAT GTTACCACCA AACAACAGC	CACTITATIG  31   HVVLVISLEE FFRGEIMFQY AQSTINCTFI DPIVCLADHP PLSPQPSAPI APPVQTDIVI APENSIGTIT ANLITVRNLTR CTCSHLISFG PSKILIQLCA LALVKVFNTY NNNAVFIIT LALVKVFNTY NNNAVFITH LAENSGNAST HFIEQM  QUEENCE  31   GTTGGCAGAA CATGTCGTTC CCTGCTAAAT CTCAATGAAAA TCTATITGCA	AGCAAATGTG  41    DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPPSSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP NVTVTLKHIN VILDLSRTSV ALLLLINLVFL IRKYILKPCI VGYFCVIFL FAWGPVNVTF ERNGVSFSVQ  41    CTGAAGAAGT TGGTAACATC TATCTGTTGT TTACTTTAAG ACTCAAGC ATGACTCAGC	51   PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSIAL AHDMELASRV PSQDELTVRC LPAQMMALTF LDSWIALYKM VGWGVPAVVV NVSMFIVVLV MYLFAIFNTL NGDVCLHDFT  51   TTTACTGACG CCTGGAAGAA CAGTTTTGCC CTTTACTCCCT ATTCTTACTACTA	60 120 180 240 300 360 420 600 600 720 780 840 900
50 55 60 65 70	CTCAGAAGGA  Seq ID NO: Protein Acc  I   WYFSVRQCGH VTLSLLPSNE LSLSELKRSE ERPMEHCCCS SQVPKATSFA OTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFNFFETPAL VFMDLGRNGG ITTIGCGLSS QGLCISVAVF TILLTISPDN QLCRIKKKQ QGFFIFIFYC GKQHMFNEKB  Seq ID NO: Nucleic Acc Coding sequil ATGGTTTTCT TTCAAGATAT GGTACTGATA CCCTCCTCCA TCAAACGAAA AAACCCCAGA GGTGAGATCA	CTTCAAAGCG  18 Protein ression #: 1  1  VGRTEEVLLT TGVKPQRNIC LNRTLQTLSE EPPDYSPVTH VKASFSSFTV MINQVSRLLH MITTFVAQDP FQDPSLENLS RGGWSDNGCS IPLSVTLVTY LHYFLLVSFT YGLGSYGKFP LGAQRKTSIQ UAKENVRQW DSCNGKGRMA  19 DNA seq id Accessio uence: 13  1  CTGTCAGGCA ATTCCAGTTT ATGAGGTTGA CAGAAAAAAAC CAGAATATCTG TGTTTCATA	GGGAAGCTTA  sequence 20 sequence 21   FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRINETI LIAFEKIRTDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL uence n #: Eos se 045 21   GTGTGGCCAT CATTTGTCTT GTCACCACCA AACAACAAGCA CAATTGTCA CAATGAAAGAA	CACTTTATTG  31  HVVLVTSLEE FFRGEIMPQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRLLKVVDDI ANLTVRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVFYITV LUGITWGFAF LAENSGNAST HFIEQM  QUENCE  31  GTTGGCAGAA CATGTCGTTC CCTGCTAAAT CTCAATGATG ATAGTAAAAAA ATCTAATTGCA AGCACTGTTC	AGCAAATGTG  41    DTDNSSLSPP DKESTVPQNQ IKLINITMNAC RGPPPSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP NVTUTLKHIN VILDLSRTSV ALLLLINLVPL IRKYILKPCI VGYFCVIFLL FAWGPVNVTL FAWGPVNVTL FAWGPVNVTL TGGTAAGAAGT TGGTAACATC TTACTTGTTGT TTACTTTAAG CCTTCAATGC CCCAGAATCA	51   PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL OSETISSPMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTR LDSWIALYKM VGWGVPAVVV NVSMFIVVLV MYLFAIFNTL NGDVCLHDFT  51   TITACTGACG CCTTGGAAGGA CAGTTTTGCC CTTACTCCCT TTCAGGCGTT ATTTTTTTAGA ACATATAACG	60 120 240 300 360 420 480 540 660 720 780 900
50 55 60 65 70	CTCAGAAGGA  Seq ID NO: Protein Acci    WYPSVRQCGH VTLSLLPSNE LSLSELKRSE LSLSELKRSE SQVPKATSFA OTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFNFFETPAL VFMDLGRINGG ITYIGCGLSS QGLCISVAVF TILLTISPDN QLCRIKKKKQ QGFPIFIFYC GKQBMFNEKB  Seq ID NO: Nucleic Ac. Coding sequity ATGGTTTTCT TTCAAGATAT GATACTGATA CCCTCCTCCA TCAAACGAAA AAACCCCAGA AAACCCCAGA AATGGCACCT	CTTCAAAGCG  18 Protein Pession #: 1  11    VGRTEEVLLT TGVKPQRNIC LNRTLQTLSE VRIPCPSSPE VRIPCPSSPE VRIPCPSSPTV MINQVSRLLH MINQVSRLLH MINQVSRLLH MINTTFVAQDP FQDPSLENLS RGGWSDNGCS 1PLSVTLVTY LHYFLLVSFT YGLGSYGKPP LGAQRKTSIQ DSCNGKGRMA  19 DNA seq id Accessio Dence: 13  11    CTGTCAGGCA TCTTGTCATT ATGAGGTTCA CAGAAAAAAC GAAATATCTG GTTTTCAATT TAACTGGAGT	GGGAAGCTTA  Sequence 20 sequence 21   FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRINETI IAFEKIRRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL  uence n #: Eos se 045 21 GTGTGGCCAT CATTTGTCTT GTCACCACCA AACAACAAGC TAAAATCACT CAATTTGTCTA TGAAAATCACT CAATTTGTCA TGAAAATCACT CAATTTGTCA TGAAAAACAA	CACTTTATTG  31  HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRLLKVVDDI ANENSIGTIT ANLTVRNLTR CTCSHLTSFG PSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAS HFIEQM  QUENCE  31  GTTGGCAGAA CATGTCGTTA CTCAATGATGA ATAGTAAAAA ATCTTATTTGCA ATGGTATTA	AGCAAATGTG  41    DITDNSSLSPP DKESTVPQNQ IKLINITMIAC RGPPPFSSQS ASSPAIDMPP TSSISDLENQ GLQLINFSNTT LPSSLMNILP NVTVTLKHIN VILLDLSRTSV ALLLLINLVFL IRKYILKPCI VGYFCVIFIL FAWGPVNVTF ERNGVSFSVQ  41    CTGAAGAAGT TGGTAACATC TATCTGTTGT TTACTTTTAAG CCTTCAATGC ATGACTCAGA AACGCTCAGA	51   PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL OSETISSPMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTF LDSWIALYKM VGWGVPAVVV NVSMFIVVLV MYLFAIFNTL NGDVCLHDFT  51   TTTACTGACG CCTGGAAGAA ACAGTTTTGCC CTTCAGGCGTC ATTTTTTAGG GCTCAACAAAA	60 120 180 300 360 420 540 600 720 780 840 900
50 55 60 65 70	CTCAGAAGGA  Seq ID NO: Protein Acci      WYFSVRQCGH VTLSLLPSNE LSLSELKRSE IRPMEHCCCS SQVPKATSFA OTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFNFFETPAL VFWDLGRNGG ITTIGCGLSS QGLCISVAVF TILLTISPDN OLCRIKKKKQ QGPFIFIFYC GKQBMFNEKB Seq ID NO: Nucleic Ac: Coding seq 1     ATGGTTTTCT TTCAAGATAT GATACTGATA CCCTCCTCAT ATGGCACCT AATGGCACA AATGGCACCT ACCCTGCAAA	CTTCAAAGCG  18 Protein lession #: 1 11   VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EPPDYSPVTH VKASFSSPTV WKASFSSPTV WKNOVSRLLH NTTTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFILVSFT YGLGSYGKPP JGAGRKTSIQ VAKENVRKQW DSCNGKGRMA  19 DNA seq id Accessio ence: 13 11   CTGTCAGGCA TCCTTGTCAT ATTCCAGTTT ATGAGGTTTCA ATTCCAGTTT ATGAGGTTCA CAGAAAAAAAC GAAATATCTG TGTTTCAATGA TAACTGGAGT CCCTAAGGAT CCCTAAGAT CCCTAAGGAT CCCTA	GGGAAGCTTA  sequence Eos sequence 21   FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKIQCDLQ NVPSPIGEIQ SAPANVNITS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAFEKIRRDY MMGLEAFHMY NGSPDDFCWI LRSTSAGLTF RRYLCCGKLR LRRTSKRGSL UENCE ##: EOS SE 045 21   GTGTGGCCAT GTTACCTT GTCACCACCA AACAACAAGC TAAAATCACT CAATTTGTCAT	CACTITATIG  31    HVVLVISLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVI APENSIGTIT ANLITVRNLTR CTCSHLISFG PSKILIQLCA LALVKVFNTY NNNAVFYITV LIGITWGFAF LAENSGNAST HFIEQM  31    GTTGGCAGAA CATGTCGTTC CCTGCTAAAT CTCAATGATAAAA TCTATTTGCA AGCACTGTTC AGTGAATTAAA ATTATTGTG	41    DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSSQS ASSPAIDMPP TSSISDLEND GLQLNFSNTT LPSSLMNNLP NVTVTLKHIN VLLDLSRTSV ALLLLINLVFL IRKYILKPCI VGYFCVIFLL FAWGPVNVTF ERNGVSFSVQ  41    CTGAAGAAGT TTACTTTAAG CCTTCAATGC ATGACTCAGA CCTACAGA CCTACAGA CTACAGCAGA	51   PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPNP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVTG LPAQMMALTF LDSWIALYKM VGWGVPAVVV NVSMFIVVLV MYLFAIFNTL NGDVCLHDFT  51   TTTACTGACG CCTGGAAGAA CAGTTTTGCC CTTCAGGCGTC ATTTTTTAGA ACATATAACG GCTCAACAAA GGCCCAAAGG	60 120 180 240 300 360 420 600 600 720 780 840 900 120 180 240 360 420 420 480 540
50 55 60 65 70	CTCAGAAGGA  Seq ID NO: Protein Acci      WYFSVRQCGH VTLSLLPSNE LSLSELKRSE IRPMEHCCCS SQVPKATSFA OTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFNFFETPAL VFWDLGRNGG ITTIGCGLSS QGLCISVAVF TILLTISPDN OLCRIKKKKQ QGPFIFIFYC GKQBMFNEKB Seq ID NO: Nucleic Ac: Coding seq 1     ATGGTTTTCT TTCAAGATAT GATACTGATA CCCTCCTCAT ATGGCACCT AATGGCACA AATGGCACCT ACCCTGCAAA	CTTCAAAGCG  18 Protein lession #: 1 11   VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EPPDYSPVTH VKASFSSPTV WKASFSSPTV WKNOVSRLLH NTTTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFILVSFT YGLGSYGKPP JGAGRKTSIQ VAKENVRKQW DSCNGKGRMA  19 DNA seq id Accessio ence: 13 11   CTGTCAGGCA TCCTTGTCAT ATTCCAGTTT ATGAGGTTTCA ATTCCAGTTT ATGAGGTTCA CAGAAAAAAAC GAAATATCTG TGTTTCAATGA TAACTGGAGT CCCTAAGGAT CCCTAAGAT CCCTAAGGAT CCCTA	GGGAAGCTTA  sequence Eos sequence 21   FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKIQCDLQ NVPSPIGEIQ SAPANVNITS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAFEKIRRDY MMGLEAFHMY NGSPDDFCWI LRSTSAGLTF RRYLCCGKLR LRRTSKRGSL UENCE ##: EOS SE 045 21   GTGTGGCCAT GTTACCTT GTCACCACCA AACAACAAGC TAAAATCACT CAATTTGTCAT	CACTITATIG  31    HVVLVISLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVI APENSIGTIT ANLITVRNLTR CTCSHLISFG PSKILIQLCA LALVKVFNTY NNNAVFYITV LIGITWGFAF LAENSGNAST HFIEQM  31    GTTGGCAGAA CATGTCGTTC CCTGCTAAAT CTCAATGATAAAA TCTATTTGCA AGCACTGTTC AGTGAATTAAA ATTATTGTG	41    DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSSQS ASSPAIDMPP TSSISDLEND GLQLNFSNTT LPSSLMNNLP NVTVTLKHIN VLLDLSRTSV ALLLLINLVFL IRKYILKPCI VGYFCVIFLL FAWGPVNVTF ERNGVSFSVQ  41    CTGAAGAAGT TTACTTTAAG CCTTCAATGC ATGACTCAGA CCTACAGA CCTACAGA CTACAGCAGA	51   PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL OSETISSPMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTF LDSWIALYKM VGWGVPAVVV NVSMFIVVLV MYLFAIFNTL NGDVCLHDFT  51   TTTACTGACG CCTGGAAGAA ACAGTTTTGCC CTTCAGGCGTC ATTTTTTAGG GCTCAACAAAA	60 120 180 300 360 420 540 600 720 780 840 900
50 55 60 65 70	CTCAGAAGGA  Seq ID NO: Protein Acci      WYFSVRQCGH VTLSLLPSNE LSLSELKRSE ERPMEHCCCS SQVPKATSFA OTHVSGTPPP GSLEPNLAGE AVIRVNASSF OFMFFETPAL VFWDLGRNGG ITTIGCGLSS QGLCISVAVF TILLTISPDN OLCRIKKKKQ QGFFIFIFYC GKQHMFNEKB Seq ID NO: Nucleic Ac: Coding sequil   ATGGTTTTCT TTCAAGATAT CCCTCCTCAA ACAACGAAA AAACCCCAGAA GGTGAGATCA AATGGCACTA ACCTCACTAA ACCTCACTAA	CTTCAAAGCG  18 Protein lession #: 1 11   VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EPPDYSPVTH VKASFSSPTV LHYFLLVSFT YGLGSYGKFP LGAQRKTSIQ VAKENVRKQN DSCNGKGRMA  19 DNA seq id Accessio Lence: 13 11   CTGTGGGCA TCCTGTCAGTA ATTCCAGTTT ATGAGATAATCTG TGTTTCAATA TAACTGGAGT TGTTTCAATA TAACTGGAGT CCCTAAGTGA GTACATTCAC	GGGAAGCTTA  sequence 20s sequence 21   FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SSPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI LISYVISSSV VKDRRLNETI LAFEKIRRDY WMGLEAFHMY NGSPDDFCWI LAFEKIRRDY EACHOLOGIC LERTSKRGSL UENCE 1 #: EOS SE 045 21   GTGTGGCCAT CATTTGTCTT GTCACCACCA AACAACAAGCT TAAAATCACT TCAATTTGTCAT CAATTTGTCAT CAATTTGTCAT CAATTTGTCAT CAATTTGTCAT CAATTTGTCAT CAATTTGTCAT CAATTTGTCAT CAATTTGTCAT CAATTTGTCAT CAATTACTTT CAATTTGTCAT CAATTTGTCAT CAATTTGTCAT CAATTTGTCAT CAATTTGTCAT CAATTTGTCAT CAATTTGTCAT CAATTTGTCAT CAATTACTTT CAATTACTTT CAATTACTTT CAATTACTTT CAATTACATTT CAATTACTTT CAATTACTTT CAATTACATT	CACTTTATTG  31  HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN APENSIGTIT ANLTVRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVFYITV NNNAVFYITV ANNAVFYITV MTNAVFYITV CTCSCTAAT LAENSGNAST HFIEQM  31  GTTGGCAGAA CATGTCGTTC CCTGCTAAT CTCAATGATG ATAGTAAAA ATAATGTGTG AATAATACAA	AGCAAATGTG  41    DTDNSSLSPP DKESTVPQNQ IKLINITMNAC RGPPPSSQS ASSPAIDMPP TSSISDLENQ GLQLINFSNTT LPSSLMNILP NVTVTLKHIN VILDLSRTSV ALILLINLVPL IRKYILKPCI VGYFCVIFIL FAWGPVVTF ERNGVSFSVQ  41    CTGAAGAAGT TTACTTTAAG TTACTTTAAG CCTTCAATGC ATGACTCAGC CCCAGAATCA AACGCTCAGA CTACAGCAGA TGAATGCATG	51   PEVETTSLND HITNGTLIGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTF LDSWIALYKM VGWGVPAVVV NVSMFIVVLV NVSMFIVVLN NGDVCLHDFT  51   TITACTGACG CCTGGAAGAA CAGTTTTGCC CTTTACTCCCT TTCAGGCGTC ATTTTTTAGA ACATATAACG GCTCAACAAAA GGCCCAAAGC TGCTGCAATA	60 120 180 300 360 420 480 540 660 720 780 900 620 120 180 240 300 420 480 540
50 55 60 65 70	CTCAGAAGGA  Seq ID NO: Protein Acci    WYFSVRQCGH VTLSLLPSNE LSLSELKRSE LSLSELKRSE SQUPKATSFA OTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFNFFETPAL VFWDLGRNGG ITYIGCGLSS QGLCISVAVF TILLTISPDN QLCRIKKKD QGFFIFIFYC GKQHMFNEKB  Seq ID NO: Nucleic Ac. Coding sequ 1   ATGGTTTCT TTCAAGATAT TGTAACGATAA CCCTCCAA AAACCCCAGA AGTGAGATCA AATGGCACCT ACCCTGCAAA ACATTAAATTA GCCGCTTTGG	CTTCAAAGCG  18 Protein ression #: 1  11    VGRTEEVLLT TGVKPQRNIC LNRTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV MINQVSRLLH MINQVSRLLH MINQVSRLLH MINGVSRLLH LGAGRENONGCS IPLSVTLVTY LHYFLLVSFT YGLGSYGKFP LGAGRKTSIQ DSCNGKGRMA  19 DNA seq id Accessio cence: 13  11    CTGTCAGGCA TCTTCAGGTTA ATGAGGTTGA CGAAAAAAAC GAAATATCTG GAAATATCTG GTACTTCAATTA TAACTGGAGT TGTTCTCATTA TAACTGGAGT CCTAAGTGAG AAAGAGTAAA	GGGAAGCTTA  Sequence 20 sequence 21   FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKORRINETI IAFEKIRRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF REVLCCGKLR LRRTSKRGSL  LRRTSKRGSL  UENCE 1 #: EOS Se 045 21 GTGTGGCCAT CATTTGTCTT GTCACCACCA AACAACAAGC TAAAAATCACT CAATTTGTCT TGATAAAGAA CCTGTCTCTA AGACTTACTT AATAAAACTG AGATTAGTCT TAATAAAACTG AGATTAGTCT AATAAAACTG AGATTAGTCT TAATAAAACTG AGATTAGTCT AATAAAACTG	CACTTTATTG  31  HVVLVTSLEE FFRGEIMPQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRLLKVVDDI ANITVRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAST HFIEQM  31  GTTGGCAGAA CATGTCGTTC CCTGCTAAAT CTCAATGATG ATAATCAA ATGAACACTTC AGGCACTGTTC AGGCACTGTTC AGGCACTGTTC AGGCACTGTTC AGGCACTGTTC AGGCACTGTTC AGGCACTGTTC AGGCACTGTTC AGGCACACTGTTC AGGCACACCTGTTC AGGCACACCTGTC AGGCACCTGTC AGGCACACCTGTC AGGCACCTGTC AGGCACACCTGTC AGGCACCTGTC AGGCACACCTGTC AGGCACACCTGTC AGGCACACCTGTC AGGCACACCTGTC AGGCACACCTGTC AGGCACACCTGTC AGGCACACCTGTC AGGCACACCTGTC AGGCACACCTGCTC AGGCACACCTGTC AGGCACACCTGCTC AGGCACACCTGCTC AGGCACCTGTC AGGCACCTGTC AGGCACACCTGTC AGGCACCTGTC AGGCACCTGTC AGGCACCTGTC AGGC	AGCAAATGTG  41  DTDNSSLSPP DKESTVPQNQ IKLINITMIAC RGPPFSSQS ASSPAIDMPP TSSISDLENQ GLQLINFSNTT LPSSLMNILP NVTVTLKHIN VILIDLSRTSV IRKYILKPCI VGYFCVIFIL FAWGPVNVTF ERNGVSFSVQ  41    CTGAAGAAGT TGGTAACATC TATCTGTTGT TTACTTTAAG CCTTCAATGC CCCAGAATCA AACGCTCAGA TGAATGCATG ATGAATGCATG GCTGCTGTTCC GCTGCTGTTCC GCTGCTGTTCC GCTGCTGTTCC GCTGCTGTTCC GCTGCTGTTCC	51   PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTF LDSWIALYKM VGWGVPAVVV NVSMFIVVLV MYLPAIPNTL NGDVCLHDFT  51   TTTACTGACG CCTGGACGAC ATTTTTTAGA ACATATAACG GCTCAACAAA GGCCCAAAGC TGCTGCAATA TGTCAGGATA	60 120 180 360 420 540 600 720 780 840 900 60 120 300 360 420 420 480 540 660
50 55 60 65 70	CTCAGAAGGA  Seq ID NO: Protein Acc  I   WYFSVRQCGH VTLSLLPSNE LSLSELKRSE SQVPKATSFA OTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFNFFETPAL VFMDLGRINGG ITYIGCGLSS QGLCISVAVF TILLTISPDN QLCRIKKKKQ QGFFIFIFYC GKQBMFNEKB  Seq ID NO: Nucleic Ac: Coding seq I   ATGGTTTTCT TTCAAGATAT GATACTGATA GATACTGATA CCCTCCCACA TCAAACGAAA AAACCCCAGA AATGGCACCTI ACCCTGCAAA ACTTAAATT GCCCTTTTGCCCTTTGCCCCTTTTCCCCTTTTCCCCTTTTCCCCTTTCCCCTTTCCCC	CTTCAAAGCG  18 Protein Pession #: 1  11    VGRTEEVLLT TGVKPQRNIC LNRTLQTLSE VRIPCPSSPE EPPDYSEVTH VKASFSSPTV MINQVSKLLH MINGVSKLLH MINGVSKLLH LHYFLLVSFT YGLGSYGKPP LGAGRKTSIQ VAKENVRQW DSCKGKGRMA  19 DNA seq id Accessio Lence: 13  11    CTGTCAGGCA TCTTGTCAT ATTCCAGTTT ATTCAGTTT ATTCAGTTT ATTCAGTTT TGATTCAGTA TGATTCAATCA CAAAAAATATCTG TAACTGGAGT CCCTAAGTGA CCCCAGAGTAAA CCTCCCCCAGA	GGGAAGCTTA  Sequence 20 sequence 21   FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRINETI IAFEKIRRDY MMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL  UENCE 1 #: EOS Se 045 21 GTGTGGCCAT GTGTGCCACC AACAACAAGC TAAAATCACT CAATTTGTCTT GTCACCACCAC TAAAATCACT CAATTTGTCA AGACTTACTTT AATAAAACTA GGTTTGTCTT AATAAAACTA GGTTTGTCTT AATAAAACTA GGATTTGTCA AGAGTTGGCACA AGAGTTGGCGA AGAGTTGGCGA AGAGTTGGCGA	CACTTATTG  31  HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRLLKVVDDI ANENSIGTIT ANLTVRNLTR CTCSHLISFG PSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAF LAENSGNAST HFIEQM  QUENCE 31  GTTGGCAGAA CATGTCGTTC CCTGCTAAAT CTCAATGATG ATAGTAAAAA TCTTATTTGCA AGCACTGTTC AGTGAATTAA ATGAAATACAA ATGAAATCAGT ATAATGATG ATAATACAGT ATAATACAGT ATAATACAGT ATAATACAGT ATAGAACACT AAGCTTCAGT	AGCAAATGTG  41    DTDNSSLSPP DKESTVPQNQ IKLINITMIAC RGPPFSSQS ASSPAIDMPP TSSISDLENQ GLQLINFSNIT LPSSLMNILP NVIVTLKHIN VILLDLSRTSV ALLLLINLVPL IRKYILKPCI VGYFCVIFLL FAWGPVNVTF ERNGVSFSVQ  41    CTGAAGAAGT TGGTAACATC TATCTGTTGT TTACTTTAAG CCTTCAATGC ATGACTCAGA ACCGTCAGA CTACAGCAGAA TGAATCATGG GTGACTTCG GTGACCTCCAC GTGACCTCCCA	51   PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTF LDSWIALYKM VGWGVPAVVV NVSMFIVVLV MYLFAIRNTL NGDVCLHDPT  51   TTTACTGACG CCTGGAAGAA CAGTTTTGCC CTTACTCCCT TTCAGGCGTC ATTTTTTTAGA ACATATAACG GCTCAACAAA GGCCCAAAGC TGCTGCAATAT TGTCAGGATA GGATCCCATT	60 120 180 240 360 420 540 600 720 780 840 900 60 120 120 1240 300 360 420 540 600 600 720 720 720 720 720 720 720 720 720 7
50 55 60 65 70	CTCAGAAGGA  Seq ID NO: Protein Acci      WYFSVRQCGH VTLSLLPSNE LSLSELKRSE IRPMEHCCCS SQVPKATSFA OTHVSGTPPP GSLEPNLAGE AVIRVNASSF OFMFFETPAL VFWDLGRNGG ITVIGCGLSS QGLCISVAVF TILLTISPDN DLCRIKKKKQ QGFFIFIFYC GKQHMFNEKB Seq ID NO: Nucleic Acc Coding sequil     ATGGTTTTCT TTCAAGATAT GCTTCTCTCAAA AAACCCAGAA GGTGAGATCA AATGCACTT ACCTCTCAAA ACATTAAATT GCCGCTTTGG CCCTGCCCTTTGG CCCTGCCCTTTGG CCCTGCCCTTTGG CCCTGCCCTTTGG CCCTGCTCTTGG CCCTGCTCTTGG CCCTGCTCTTTGG CCCTGCTCTTTGG CCCTGCTCTTTGG CCCTGCTCTTTGG CCCTGCTCTTTGG CCTGCTCTTTGG CTCTGTCTTTGG CTCTGTTTTGT CTCTGTCTTTGG CTCTGTCTTTGG CTCTGTCTTTGG CTCTGTCTTTGG CTCTGTCTTTGG CTCTGTCTTTGG CTCTTTTGG CTCTTTTGG CTCTTTTGG CTCTTTTGT CTCTTTTGT CTCTTTTGT CTCTTTTGT CTCTTTTGT CTCTTTTGT CTCTTTTGT CTCTTTTTGT CTCTTTTTTT CTCTTTTTTTT	CTTCAAAGCG  18 Protein Pession #: 1 11   VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EPPDYSPVTH VKASFSSPTV VKASFSSPTV WKASFSSPTV WKASFSSPTV VKASFSSPTV LHYFLLVSPT YGLGSYGKFP OVAKENVRKQN DSCNGKGRMA  19 DNA seq id Accessio Lence: 13 11   CTGTCAGGCA TCCTTGTCAT ATTCAGTTT ATGAGATTAA CGAAAAAAAC CGAAAAAAAC CGAAAAAAAC CGAAAAAAC CGAAAAAAC CGAAAAAAC CAAAAGGTAAA GTACATCAC AAAGGTAAA CCTCCCCAGG CCTCACCATCC CCTCACCATCC CCTCACCATCC CCTCACCATCC CCTCACCATCC CCTCACCATCC CCTCACCATCC CCTCACCATCC CCTCACCATCC CCTCCCCACG CTCACCATCC	GGGAAGCTTA  sequence 20s sequence 21   FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SSPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI LIAFEKIRRDY WMGLEAFHMY NGSPDDFCWI LIAFEKIRRDY ERYLCCGKLR LRRTSKRGSL UENCE 1	CACTITATIG  31   HVVLVISLEE FFRGEIMFQY AQSTLNCTFI DPIVCLADHP PLSPQPSAPI APPVQTDIVN APPVQTDIVN APENSIGTIT ANLITERIT CTCSHLISFG FSKILIQLCA LALVKVFNTY NNNAVFYITV NNNAVFYITV LIGITWGFAF LAENSGNAST HFIEQM  31   GTTGGCAGAA CATGTCGTTC CCTGCTAAAT CTCAATGATG ATAGTAAAAA ATAATGTGG AATAATACAA ATAATGTGTG AATGATCAGT AAGCTTCAGT AGCTTCAGT CCCATTTTCTT	AGCAAATGTG  41    DTDNSSLSPP DKESTVPQNQ IKLINITMNAC RGPPPSSSQS ASSPAIDMPP TSSISDLENQ GLQLINFSNTT LPSSLMNNLP NVTVTLKHIN VILDLSRTSV ALLLLINLVFL IRKYILKPCI VGYFCVIFILL FAWGPVVTF ERNGVSFSVQ  41    CTGAAGAAGT TTACTTTGT TTACTTTGT TTACTTTCATTGT TTACTTCATGC CCCAGAATCA AACGCTCAGA CTACAGCAGA CTACAGCAGA CTGACTGAGC GTGACTTGC GTGCTGTTCC GTGACTTCC CCAGCCAATCC CCAGCCAATCC CCAGCCAATCC CCAGCCAATCC	51   PEVETTSLND HITNGTLIGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTF LDSWIALYKM VGWGVPAVVV NVSMFIVVLV MYLFAIRNTL NGDVCLHDFT  51   TTTACTGACG CCTGGAAGAA CAGTTTTGCC CTTTACTCCCT TTCAGGCGTC ATTTTTAGA ACATATAACG GCTCAACAAG GCCCCAAAGC TGCTGCAATA TGTCAGGATA TGTCAGGATA CGGATCCCATT CATCCCATG	60 120 180 300 360 420 480 540 660 720 780 900 60 120 180 240 300 420 480 540 600 720 780
50 55 60 65 70 75	CTCAGAAGGA  Seq ID NO: Protein Acci      WYFSVRQCGH VTLSLLPSNE LSLSELKRSE IRPMEHCCCS SQVPKATSFA OTHVSGTPPP GSLEPNLAGE AVIRVNASSF OFMFFETPAL VFWDLGRNGG ITVIGCGLSS QGLCISVAVF TILLTISPDN DLCRIKKKKQ QGFFIFIFYC GKQHMFNEKB Seq ID NO: Nucleic Acc Coding sequil     ATGGTTTTCT TTCAAGATAT GCTTCTCTCAAA AAACCCAGAA GGTGAGATCA AATGCACTT ACCTCTCAAA ACATTAAATT GCCGCTTTGG CCCTGCCCTTTGG CCCTGCCCTTTGG CCCTGCCCTTTGG CCCTGCCCTTTGG CCCTGCTCTTGG CCCTGCTCTTGG CCCTGCTCTTTGG CCCTGCTCTTTGG CCCTGCTCTTTGG CCCTGCTCTTTGG CCCTGCTCTTTGG CCTGCTCTTTGG CTCTGTCTTTGG CTCTGTTTTGT CTCTGTCTTTGG CTCTGTCTTTGG CTCTGTCTTTGG CTCTGTCTTTGG CTCTGTCTTTGG CTCTGTCTTTGG CTCTTTTGG CTCTTTTGG CTCTTTTGG CTCTTTTGT CTCTTTTGT CTCTTTTGT CTCTTTTGT CTCTTTTGT CTCTTTTGT CTCTTTTGT CTCTTTTTGT CTCTTTTTTT CTCTTTTTTTT	CTTCAAAGCG  18 Protein Pession #: 1 11   VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EPPDYSPVTH VKASFSSPTV VKASFSSPTV WKASFSSPTV WKASFSSPTV VKASFSSPTV LHYFLLVSPT YGLGSYGKFP OVAKENVRKQN DSCNGKGRMA  19 DNA seq id Accessio Lence: 13 11   CTGTCAGGCA TCCTTGTCAT ATTCAGTTT ATGAGATTAA CGAAAAAAAC CGAAAAAAAC CGAAAAAAAC CGAAAAAAC CGAAAAAAC CGAAAAAAC CAAAAGGTAAA GTACATCAC AAAGGTAAA CCTCCCCAGG CCTCACCATCC CCTCACCATCC CCTCACCATCC CCTCACCATCC CCTCACCATCC CCTCACCATCC CCTCACCATCC CCTCACCATCC CCTCACCATCC CCTCCCCACG CTCACCATCC	GGGAAGCTTA  sequence 20s sequence 21   FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SSPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI LIAFEKIRRDY WMGLEAFHMY NGSPDDFCWI LIAFEKIRRDY EARTHOLEST GREENCE 1	CACTITATIG  31    HVVLVISLEE FFRGEIMFQY AQSTLNCTFI DPIVCLADHP PLSPQPSAPI APPVQTDIVN APPVQTDIVN APENSIGTIT ANLITERIT CTCSHLISFG FSKILIQLCA LALVKVFNTY NNNAVFYITA LAENSGNAST HFIEQM  31    GTTGGCAGAA CATGTGGTC CCTGCTAAAT CTCAATGATG ATAGTAAAA ATAATGTGG AATAATACAA ATAATGTGT AAGCTTCAGT AAGCTTCAGT AGCTTCATGTC AGGTTCATTAGTA ATAGTACAA ATAATGTGTG AATAATACAA ATAGTGTGT CCCATTTTCTT AAGCTTCAGT	AGCAAATGTG  41    DTDNSSLSPP DKESTVPQNQ IKLINITMNAC RGPPPSSSQS ASSPAIDMPP TSSISDLENQ GLQLINFSNTT LPSSLMNNLP NVTVTLKHIN VILDLSRTSV ALLLLINLVFL IRKYILKPCI VGYFCVIFILL FAWGPVVTF ERNGVSFSVQ  41    CTGAAGAAGT TTACTTTGT TTACTTTGT TTACTTTCATTGT TTACTTCATGC CCCAGAATCA AACGCTCAGA CTACAGCAGA CTACAGCAGA CTGACTGAGC GTGACTTGC GTGCTGTTCC GTGACTTCC CCAGCCAATCC CCAGCCAATCC CCAGCCAATCC CCAGCCAATCC	51   PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTF LDSWIALYKM VGWGVPAVVV NVSMFIVVLV MYLFAIRNTL NGDVCLHDPT  51   TTTACTGACG CCTGGAAGAA CAGTTTTGCC CTTACTCCCT TTCAGGCGTC ATTTTTTTAGA ACATATAACG GCTCAACAAA GGCCCAAAGC TGCTGCAATAT TGTCAGGATA GGATCCCATT	60 120 180 300 360 420 480 540 660 720 780 900 60 120 180 240 300 420 480 540 600 720 780
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-	CAACMON CON	C) COCCOOC	TTCCCCGCCT	CACAMOONO	COCCECTECE	TCAAACATTC	1260
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	CTGAAAGTAG	TGGATGACAT	TGGCCTACAG	CTGAACTTTT	CAAACACGAC	TATAAGTCTA	1320
			GGCTGTGATC	ACROMON NEC	CCS CTS CTPT	CARCACAACE	1380
	ACCTCCCCTT	CITIGGCICI	COCTOTONIC	MUMUIGHAIG	CCMGIMGIII	CHACACAMCI	
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	ATAACTTGGG	GCTTTGCCTT	CTTTGCCTGG	GGACCAGTTA	ACGTGACCTT	CATGTATCTG	2580
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			SNETEKTKIT				120
	GEIMFOYDKE	STVPONOHIT	NGTLTGVLSL	SELKRSELNK	TLOTLSETYF	IMCATAEAQS	180
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40	TENCTITIES	NNIMNACAAI	AALERVKIRP	MEHCCCSVRI	PCPSSPERIG	KINGCDINGDEX	240
	VCT.ADHDDGD	PESSSOSTPU	VPRATVLSQV	PKATSPAEPP	DYSPVTHNVP	SPIGEIOPLS	300
			TISSPMPQTH				360
	MOTOTOMEC	TODI-ENOVITO	MEKALSLGSL	EDMI.ACEMIN	OUGDI.I.UGDD	DMT.APT.AORT.	420
	LKVVDDIGLO	LNFSNTTISL	TSPSLALAVI	RVNASSFNTT	TFVAQDPANL	QVSLETQAPE	480
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	SHLTSFGVLL	DLSRTSVLPA	QMMALTFITY	IGCGLSSIFL	SVTLVTYIAF	EKIRRDYPSK	660
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	SHLTSFGVLL	DLSRTSVLPA LLNLVFLLDS	QMMALTFITY WIALYKMQGL	IGCGLSSIFL CISVAVFLHY	SVTLVTYIAF FLLVSFTWMG	LEAFHMYLAL	720
	SHLTSFGVLL	DLSRTSVLPA LLNLVFLLDS	QMMALTFITY WIALYKMQGL	IGCGLSSIFL CISVAVFLHY	SVTLVTYIAF FLLVSFTWMG	LEAFHMYLAL	
55	SHLTSFGVLL ILIQLCAALL VKVFNTYIRK	DLSRTSVLPA LLNLVFLLDS YILKFCIVGW	QMMALTFITY WIALYKMQGL GVPAVVVTII	IGCGLSSIFL CISVAVFLHY LTISPDNYGL	SVTLVTYIAF FLLVSFTWMG GSYGKFPNGS	LEAFHMYLAL PDDFCWINNN	720 780
55	SHLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY	DLSRTSVLPA LLNLVFLLDS YILKFCIVGW FCVIFLLNVS	QMMALTFITY WIALYKMQGL GVPAVVVTII MFIVVLVQLC	IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA	SVTLVTYIAF FLLVSFTWMG GSYGKFPNGS QRKTSIQDLR	LEAFHMYLAL PDDFCWINNN SIAGLTFLLG	720 780 840
55	SHLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY	DLSRTSVLPA LLNLVFLLDS YILKFCIVGW FCVIFLLNVS	QMMALTFITY WIALYKMQGL GVPAVVVTII MFIVVLVQLC	IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA	SVTLVTYIAF FLLVSFTWMG GSYGKFPNGS QRKTSIQDLR	LEAFHMYLAL PDDFCWINNN SIAGLTFLLG	720 780 840
55	SHLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW	DLSRTSVLPA LLNLVFLLDS YILKFCIVGW FCVIFLLNVS GPVNVTFMYL	QMMALTFITY WIALYKMQGL GVPAVVVTII MFIVVLVQLC PAIFNTLQGF	IGCGLSSIPL CISVAVPLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK	SVTLVTYIAP FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY	LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRLAE	720 780 840 900
55	SHLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW	DLSRTSVLPA LLNLVFLLDS YILKFCIVGW FCVIFLLNVS GPVNVTFMYL	QMMALTFITY WIALYKMQGL GVPAVVVTII MFIVVLVQLC	IGCGLSSIPL CISVAVPLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK	SVTLVTYIAP FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY	LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRLAE	720 780 840
55	SHLTSPGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN	DLSRTSVLPA LLNLVFLLDS YILKFCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG	QMMALTFITY WIALYKMQGL GVPAVVVTII MFIVVLVQLC PAIFNTLQGF VSSSSNSLQS	IGCGLSSIFL CISVAVPLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL	SVTLVTYIAP FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA	LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRLAE SGNGNASTER	720 780 840 900
55	SHLTSPGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN	DLSRTSVLPA LLNLVFLLDS YILKFCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG	QMMALTFITY WIALYKMQGL GVPAVVVTII MFIVVLVQLC PAIFNTLQGF	IGCGLSSIFL CISVAVPLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL	SVTLVTYIAP FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA	LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRLAE SGNGNASTER	720 780 840 900
	SHLTSPGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN	DLSRTSVLPA LLNLVFLLDS YILKFCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG	QMMALTFITY WIALYKMQGL GVPAVVVTII MFIVVLVQLC PAIFNTLQGF VSSSSNSLQS	IGCGLSSIFL CISVAVPLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL	SVTLVTYIAP FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA	LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRLAE SGNGNASTER	720 780 840 900
	SHLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG	DLSRTSVLPA LLNLVFLLDS YILKFCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK	QMMALTFITY WIALYKMQGL GVPAVVVTII MFIVVLVQLC PAIFNTLQGF VSSSNSLQS QHMFNEKEDS	IGCGLSSIFL CISVAVPLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL	SVTLVTYIAP FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA	LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRLAE SGNGNASTER	720 780 840 900
55 60	SHLTSFGVLL ILIQLCAALL VKVENTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO:	DLSRTSVLPA LLNLVFLLDS YILKFCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq	QMMALTFITY WIALYKMQGL GVPAVVVTII MFIVVLVQLC PAIFNTLQGC VSSSSNSLQS QHMFNEKEDS uence	IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA PIFIFYCVA SSNSTNSTTL CNGKGRMALR	SVTLVTYIAP FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA	LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRLAE SGNGNASTER	720 780 840 900
	SHLTSFGVLL ILIQLCAALL VKVENTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO:	DLSRTSVLPA LLNLVFLLDS YILKFCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq	QMMALTFITY WIALYKMQGL GVPAVVVTII MFIVVLVQLC PAIFNTLQGF VSSSNSLQS QHMFNEKEDS	IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA PIFIFYCVA SSNSTNSTTL CNGKGRMALR	SVTLVTYIAP FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA	LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRLAE SGNGNASTER	720 780 840 900
	SHLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac:	DLSRTSVLPA LIMIVFILIDS YILKFCIVGW FCVIFILINVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accessio	QMMALTFITY WIALYKMOGL GVPAVVVTII MFIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS Uence n #: NM_005	IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA PIFIFYCVA SSNSTNSTTL CNGKGRMALR	SVTLVTYIAP FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA	LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRLAE SGNGNASTER	720 780 840 900
	SHLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding seq	DLSRTSVLPA LLMINFILDS YILKFCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA sequid Accession	QMMALTFITY WIALYKMQGE GVPAVVVTII MFIVVLVQLC FAIFNTLQGF VSSSSNSLQS QHMFNEKEDS uence n #: NM_005 3117	IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR	SVTLVTY1AP FILIVSFTWMG GSYGKPPNGS GRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHP	LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRLAE SGNGNASTER IEQM	720 780 840 900
	SHLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac:	DLSRTSVLPA LIMIVFILIDS YILKFCIVGW FCVIFILINVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accessio	QMMALTFITY WIALYKMOGL GVPAVVVTII MFIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS Uence n #: NM_005	IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA PIFIFYCVA SSNSTNSTTL CNGKGRMALR	SVTLVTYIAP FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA	LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRLAE SGNGNASTER	720 780 840 900
60	SHLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding seq	DLSRTSVLPA LLMINFILDS YILKFCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA sequid Accession	QMMALTFITY WIALYKMQGE GVPAVVVTII MFIVVLVQLC FAIFNTLQGF VSSSSNSLQS QHMFNEKEDS uence n #: NM_005 3117	IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR	SVTLVTY1AP FILIVSFTWMG GSYGKPPNGS GRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHP	LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRLAE SGNGNASTER IEQM	720 780 840 900
60	SHLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding sequence	DLSRTSVLPA LIMINFILIDS YILKFCIVGW FCVIFILINVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession Lence: 37	QMMALTFITY WIALYKMQGL GVPAVVVTII MFIVVLVQLC PAIFNTLQGF VSSSNSLQS QHMFNEKEDS Uence n #: NM_005 3117 21	IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA PIFIFYCVAK SSNSTNSTTL CNGKGRMALR 756.1	SVTLVTYIAP FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHP	LEAFHMYLAL PDDFCWINNN SIAGLIFILG LCCGKLRLAE SGNGNASTER IEQM 51	720 780 840 900 960
	SHLTSFGVLL ILIQLCAALL VKVENTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding sequence 1 AGCCAGCCCG	DLSRTSVLPA LLNLVFLLDS YILKPCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession Lence: 37 11 AGGACGCGAG	QMMALTFITY WIALLYKMGGI GUPAVVVTII MFIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS UEDCE n #: NM_005 3117 21   CGGCAGGTGT	IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR 756.1 31   GCACAGAGGT	SVTLVTYIAP FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHP	LEAFHMYLAL PDDFCWINNN SIAGLIFLIG LCCGKLRLAE SGNGNASTER IEQM  51   GTTTTCTGAA	720 780 840 900 960
60	SHLTSFGVLL ILIQLCAALL VKVENTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding sequence 1 AGCCAGCCCG	DLSRTSVLPA LLNLVFLLDS YILKPCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession Lence: 37 11 AGGACGCGAG	QMMALTFITY WIALLYKMGGI GUPAVVVTII MFIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS UEDCE n #: NM_005 3117 21   CGGCAGGTGT	IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR 756.1 31   GCACAGAGGT	SVTLVTYIAP FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHP	LEAFHMYLAL PDDFCWINNN SIAGLIFLIG LCCGKLRLAE SGNGNASTER IEQM  51   GTTTTCTGAA	720 780 840 900 960
60	SHLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac. Coding seq 1   AGCCAGCCCG CTCGCGGTCA	DLSRTSVLPA LLNLVFLLDS YILKPCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession Lence: 37 11   AGGACGCGAG GGATGGTTTT	QMMALTFITY WIALIYKMQGL GVPAVVVTII MFIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS uence n #: NM_005 3117 21   CGGCAGGTGT CTCTGTCAGG	IGGGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR 756.1 31   GCACAGAGGT CAGTGTGGCC	SVTLVTYIAP FLLVSFTMPF GSYGKPPMGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHP 41   TCTCCACTTT ATGTTGGCAG	LEAFHMYLAL PDDFCWINNN SIAGLIFILG LCCGKLRLAE SGNGNASTER IEQM  51   GTTTTCTGAA AACTGAAGAA	720 780 840 900 960
60	SHLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding seq 1   AGCCAGCCCG CTCGCGGTCA GTTTTACTGA	DLSRTSVLPA LIMILVFLIDS YILKFCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession Lence: 37 11   AGGACGCGAG GGATGGTTTT CGTTCAAGAT	QMMALTFITY WIALIYKMQGL GVPAVVVTII MPIVVLVQLC PAIFNTLQGF VSSSNSLQS QHMFNEKEDS uence n #: NM_005 3117 21   CGGCAGGTGT CTCTGTCAGG ATTCCTTGTC	IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR  756.1  31   GCACAGAGGT CAGTGTGGCC ATCATTTGTC	SVTLVTYIAP FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHP  41   TCTCCACTIT ATGTTGGCAG TTCATGTCGT	LEAFHMYLAL PDDFCWINNN SIAGLIFILG LCCGKLRLAE SGNGNASTER IEQM  51   GTTTTCTGAA AACTGAAGAA TCTGGTAACA	720 780 840 900 960 60 120 180
60	SHLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding seq 1   AGCCAGCCCG CTCGCGGTCA GTTTTACTGA	DLSRTSVLPA LIMILVFLIDS YILKFCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession Lence: 37 11   AGGACGCGAG GGATGGTTTT CGTTCAAGAT	QMMALTFITY WIALIYKMQGL GVPAVVVTII MPIVVLVQLC PAIFNTLQGF VSSSNSLQS QHMFNEKEDS uence n #: NM_005 3117 21   CGGCAGGTGT CTCTGTCAGG ATTCCTTGTC	IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR  756.1  31   GCACAGAGGT CAGTGTGGCC ATCATTTGTC	SVTLVTYIAP FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHP  41   TCTCCACTIT ATGTTGGCAG TTCATGTCGT	LEAFHMYLAL PDDFCWINNN SIAGLIFILG LCCGKLRLAE SGNGNASTER IEQM  51   GTTTTCTGAA AACTGAAGAA TCTGGTAACA	720 780 840 900 960 60 120 180
60	SHLTSFGVLL ILIQLCAALL VKVENTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding seq 1   AGCCAGCCCG CTCGCGGTCA GTTTTACTGA TCCCTGGAAG	DLSRTSVLPA LLNLVFLLDS LLNLVFLLDS FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK  21 DNA sequid Accession Lence: 37 11   AGGACGCGAG GGATGGTTTT CGTTCAAGAT AAGATACTGA	QMMALTFITY WIALLYKMGGI GUPAVVVTII MPIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS  UEENCE  #: NM_005 3117 21   CGGCAGGTGT CTCTCTCAGG ATTCCTTGTC TAATTCCAGT	IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR  756.1  31   GCACAGAGGT CAGTGTGGCC TTGTCACCAC	SYTLVTYIAP FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHP  41   TCTCCACTTT ATGTTGGCAG TTCATGTGGTGT CACCTGCTAA	LEAFHMYLAL PDDFCWINNN SIAGLIFILG LCCGKLRLAE SGNGNASTER IEQM  51   GTTTTCTGAA AACTGAAGAA TCTGGTAACA ATTATCTGTT	720 780 840 900 960 60 120 180 240
60 65	SHLTSFGVLL ILIQLCAALL VKVENTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding seq 1   AGCCAGCCCG CTCGCGGTCA GTTTTACTGAA TCCCTGGAAG GTCAGTTTTG	DLSRTSVLPA LLNLVFLLDS YILKPCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession tence: 37 11   AGGACGCGAG GGATGGTTTT CGTTCAAGAT AAGATACTGA CCCCCTCCTC	QMMALTFITY WIALYKMGGL GVPAVVTII MFIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS uence n #: NM_005 3117 21   CGGCAGGTGT CTCTGTCAGG ATTCCTTGTC TAATTCCAGT CAATGAGGTT	IGGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR 756.1  31   GCACAGAGGT CAGTGTGGCC ATCATTGTC TTGTCACCAC GGAACACAA	SVTLVTYIAP FILVSFTMMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHP  41   TCTCCACTTT ATGTTGGCAG TTCATGTCGT CACCTGCTAA GCCTCAATGA	LEAFHMYLAL PDDFCWINNN SIAGLIFILG LCCGKLRLAE SGNGNASTER IEQM  51   GTTTTCTGAA AACTGAAGAA TCTGGTAACA ATTATCTGTT TGTTACTTTA	720 780 840 900 960 60 120 180 240 300
60 65	SHLTSFGVLL ILIQLCAALL VKVENTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding seq 1   AGCCAGCCCG CTCGCGGTCA GTTTTACTGAA TCCCTGGAAG GTCAGTTTTG	DLSRTSVLPA LLNLVFLLDS YILKPCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession tence: 37 11   AGGACGCGAG GGATGGTTTT CGTTCAAGAT AAGATACTGA CCCCCTCCTC	QMMALTFITY WIALYKMGGL GVPAVVTII MFIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS uence n #: NM_005 3117 21   CGGCAGGTGT CTCTGTCAGG ATTCCTTGTC TAATTCCAGT CAATGAGGTT	IGGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR 756.1  31   GCACAGAGGT CAGTGTGGCC ATCATTGTC TTGTCACCAC GGAACACAA	SVTLVTYIAP FILVSFTMMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHP  41   TCTCCACTTT ATGTTGGCAG TTCATGTCGT CACCTGCTAA GCCTCAATGA	LEAFHMYLAL PDDFCWINNN SIAGLIFILG LCCGKLRLAE SGNGNASTER IEQM  51   GTTTTCTGAA AACTGAAGAA TCTGGTAACA ATTATCTGTT TGTTACTTTA	720 780 840 900 960 60 120 180 240 300
60	SHLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Accoding seq 1   AGCCAGCCCG CTCGCGGTCA GTTTTACTGA TCCCTGGAAG GTCAGTTTTG AGCTTACTCC	DLSRTSVLPA LIMILVFLIDS YILKPCIVGW YCLIFLIAVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accessio. 11   AGGACGCGAG GGATGGTTTT CGTTCAAGAT AAGATACTGA ACCCCTCCTC CTTCAAACGA	QMMALTFITY WIALYKMQGL GVPAVVVTII MFIVULVQLC FAIFNTLQGF VSSSSNSLQS QHMFNEKEDS  uence #: NM_005 3117 21   CGGCAGGTGT CTGTCAGG ATTCCTTGTC TAATTCCAGT CAATGAGGTT AACAGAAAA	IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR  756.1  31   GCACAGAGGT CAGTGTGGCC ATCATTTGTC TTGTCACCAC GAAACAACAA ACTAAAATCA	SVTLVTYIAP FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHP  41   TCTCCACTTT ATGTTCGCT TCATGTCGT CACCTGCTAA GCCTCAATGA CTATAGTAAA	LEAFHMYLAL PDDFCWINNN SIAGLIFILIG LCCGKLRLAE SGNGNASTER IEQM  51   GTTTTCTGAA AACTGAAGAA TCTGGTAACA ATTATCTGTT TGTTACTTTA AACCTTCAAT	720 780 840 900 960 60 120 180 240 360
60 65	SHLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Accoding seq 1   AGCCAGCCCG CTCGCGGTCA GTTTTACTGA TCCCTGGAAG GTCAGTTTTG AGCTTACTCC	DLSRTSVLPA LIMILVFLIDS YILKPCIVGW YCLIFLIAVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accessio. 11   AGGACGCGAG GGATGGTTTT CGTTCAAGAT AAGATACTGA ACCCCTCCTC CTTCAAACGA	QMMALTFITY WIALYKMQGL GVPAVVVTII MFIVULVQLC FAIFNTLQGF VSSSSNSLQS QHMFNEKEDS  uence #: NM_005 3117 21   CGGCAGGTGT CTGTCAGG ATTCCTTGTC TAATTCCAGT CAATGAGGTT AACAGAAAA	IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR  756.1  31   GCACAGAGGT CAGTGTGGCC ATCATTTGTC TTGTCACCAC GAAACAACAA ACTAAAATCA	SVTLVTYIAP FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHP  41   TCTCCACTTT ATGTTCGCT TCATGTCGT CACCTGCTAA GCCTCAATGA CTATAGTAAA	LEAFHMYLAL PDDFCWINNN SIAGLIFILG LCCGKLRLAE SGNGNASTER IEQM  51   GTTTTCTGAA AACTGAAGAA TCTGGTAACA ATTATCTGTT TGTTACTTTA	720 780 840 900 960 60 120 180 240 360
60 65	SHLTSFGVLL ILIQLCAALL VKVENTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding seq 1   AGCCAGCCCG CTCGCGGTCA AGCTTAACTGA TCCCTGGAAG GTCAGTTTTA AGCTTACTCC GGCTTCAGGCCG GCTTCAGGCCG	DLSRTSVLPA LLNLVFLLDS LLNLVFLLDS GYVNTFMYL GLKKQTVNQG DVCLHDFTGK  21 DNA seq id Accessio. Lence: 37 11   AGGACGCGAG GGATGGTTTT CGTTCAAGAT AAGATACTGA CCCCTCCTCA TCAAACCCCA	QMMALTFITY WIALLYKMGGI GUPAVVVTII MPIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS  1 #: NM_005 3117 21   CGGCAGGTGT CTCTCTCAGG ATTCCTTGTC TAATTCCAGT CAATGAGGTAT AACAGAAATAA GAGAAATATC	IGCGLSSIFL CISVAVFLHY LTISPDHYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR  756.1  31   GCACAGAGGT CAGTGTGGCC ATCATTGTC TTGTCACCAC GAAACACAA ACTAAAATCA	SYTLVTYIAP FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHP  41   TCTCCACTTT ATGTTGGCAG TTCATGTGGTGT CACCTGCTAA GCCTCAATGA CCTTATTTG	LEAFHMYLAL PDDFCWINNN SIAGLIFILG LCCGKLRLAE SGNGNASTER IEQM  51   GTTTTCTGAA AACTGAAGAA TCTGGTAACA ATTATCTGTT TGTTACTTTA CAATGACTCAAT CAATGACTCAAT	720 780 840 900 960 60 120 180 240 300 360 420
60 65	SHLTSFGVLL ILIQLCAALL VKVENTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding seq 1   AGCCAGCCCG CTCGCGGTCA GTTTTACTCG GCTTCAGCCG GCATTTTTTA	DLSRTSVLPA LLNLVFLLDS YILLKPCIVGW PCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK  21 DNA seq id Accession Lence: 37 11   AGGACGCGAG GGATGGTTTT CGTTCAAGGTA CCCCTCCTC CTTCAAACCAC GAGGTGAGAGT	QMMALTFITY WIALLYKMGGI GUPAVVVTII MPIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS uence n #: NM_005 3117 21   CGGCAGGTGT CTCTGTCAGG ATTCCTTGTC TAATTCCTGGT CAATGAGGTT AACAGAAAAAA GAGAAAATATC CATGTTTCAA	IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR 756.1 31   GCACAGAGGT CAGTGTGGCC ATCATTTGTC TTGTCACCAC GAACAACAA ACTAAAATCA ACTAAAATCA TGCAATTTGT TATGATAAAG	SYTLVTYIAP FILVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHF  41   TCTCCACTIT ATGTTGGCAG TTCATGTCGT CACCTGCTAA GCCTCAATGA CTATAGTAAA CATCTATTG AAAGCACTGT	LEAFHMYLAL PDDFCWINNN SIAGLIFILG LCCGKLRLAE SGNGNASTER IEQM  51   GTTTTCTGAA AACTGAAGAA ACTGGTAACA ATTATCTGTT TGTTACTTTA AACCTTCAAT CAATGACTCA TCACCAGAAT	720 780 840 900 960 120 180 240 300 420 480
60 65	SHLTSFGVLL ILIQLCAALL VKVENTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding seq 1   AGCCAGCCCG CTCGCGGTCA GTTTTACTCG GCTTCAGCCG GCATTTTTTA	DLSRTSVLPA LLNLVFLLDS YILLKPCIVGW PCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK  21 DNA seq id Accession Lence: 37 11   AGGACGCGAG GGATGGTTTT CGTTCAAGGTA CCCCTCCTC CTTCAAACCAC GAGGTGAGAGT	QMMALTFITY WIALLYKMGGI GUPAVVVTII MPIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS uence n #: NM_005 3117 21   CGGCAGGTGT CTCTGTCAGG ATTCCTTGTC TAATTCCTGGT CAATGAGGTT AACAGAAAAAA GAGAAAATATC CATGTTTCAA	IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR 756.1 31   GCACAGAGGT CAGTGTGGCC ATCATTTGTC TTGTCACCAC GAACAACAA ACTAAAATCA ACTAAAATCA TGCAATTTGT TATGATAAAG	SYTLVTYIAP FILVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHF  41   TCTCCACTIT ATGTTGGCAG TTCATGTCGT CACCTGCTAA GCCTCAATGA CTATAGTAAA CATCTATTG AAAGCACTGT	LEAFHMYLAL PDDFCWINNN SIAGLIFILG LCCGKLRLAE SGNGNASTER IEQM  51   GTTTTCTGAA AACTGAAGAA ACTGGTAACA ATTATCTGTT TGTTACTTTA AACCTTCAAT CAATGACTCA TCACCAGAAT	720 780 840 900 960 120 180 240 300 420 480
60 65	SHLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding seq 1 AGCCAGCCCG CTCGCGGTCA GTTTTACTGA TCCCTGGAAG GTCAGTTTTG AGCTTACTCC GCTTCAGGCG GCATTTTTG CAACATATAA	DLSRTSVLPA LLNLVFLIDS YILKPCIVGW FCVIFILNVS GPVNVTFMYL GLKKQTVNGG DVCLHDFTGK 21 DNA seq id Accession HENCE: 37 11   AGGACGCGAG GGATGGTTTT CGTTCAAGAT AGATACTGA CCCCCTCCTC CTTCAAACGA TCAAACCCCA GGATGGTAGAT CGAATGGCAC	QMMALTFITY WIALYKMQGL GVPAVVTII MFIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS UMENCE H * NM_005 3117 21   CGGCAGGTGT CTCTGTCAGG ATTCCTTGTC TAATTCCAGT CAATGAGGTT AACAGAAAAA GAGAAATATC CATGTTTCAG CTTAACTGGA	IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR  756.1  31   GCACAGAGGT CAGTGTGGCC ATCATTTGTC TTGTCACCAC GGAACAACAA ACTAAAATCA TGCAATTTGT TATGAATTAGG GTCCTGTCTC	SVTLVTYIAP FILVSFTMMF GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA  41    TCTCCACTTT ATGTTGGCAG TTCATGTCGT TCACTGCTAA GCCTCAATGA CTATAGTAAA CATCTATTTG TAAGTGAAT TAAGTGAATT	LEAFHMYLAL PDDFCWINNN SIAGLIFILG LCCGKLRLAE SGNGNASTER IEQM  51   GTTTTCTGAA AACTGAAGAA TCTGGTAACA ATTATCTGTT TGTTACTTTA AACCTTCAAT CAATGACTCA ATCCCCAGAAT AAACGCTCA	720 780 840 900 960 120 180 360 420 420 540
60 65 70	SHLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVUGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding seq 1   AGCCAGCCCG CTCGCGGTCA GTTTTACTGA TCCCTGGAAG GTCAGTTTCC GCTTCAGGCG GCATTTTTTA CAACATATAA GAGCTCAACA	DLSRTSVLPA LIMILVFLIDS YILKFCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK  21 DNA seq id Accessio. 11   AGGACGCGAG GGATGGTTTT CGTTCAAGAT AAGATACTGA TCAAACCCCA CCTCCTAA CCGCTCCTC CGTCAACGA TCAAACCCCA AAACCCCAA AAACCCCACA AAACCCCTCCAC	QMMALTFITY WIALYKMQGL GVPAVVVTII MFIVVLVQLC PAIFNTLQGF VSSSNSLQS QHMFNEKEDS UENCE n #: NM_005 3117 21   CGGCAGGTGT CTCTGTCAGG ATTCCTTGTC TAATTCCAGT AACAGAAAA GAGAAATATC CATGTTTCAA CTTAACTGGA ACCTTAACTG	IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR  756.1  31   GCACAGAGGT CAGTGTGGCC ATCATTTGTC TTGTCACCAC GAAACAACAA ACTAAAATCA TGCAATTTGT TATGATAAAG GTCCTGTCTC GAGACTTACT	SVTLVTYIAP FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHP  41   TCTCCACTTT ATGTTGGCAG TTCATGTCGT CACCTGCTAA GCCTCCAATGA CCTATATTG AAAGCACTGT TAAGTAAAT TTATAATGTG	LEAFHMYLAL PDDFCWINNN SIAGLIFILIG LCCGKLRLAE SGNGNASTER IEQM  51   GTTTTCTGAA AACTGAGAGA TCTGGTAACA ATTATCTGTT TGTTACTTTA TAGATGATCA TCCCCAGAAT AAAACGCTCA TCCCCAGAAT AAAACGCTCA	720 780 840 900 960 120 180 240 300 420 480 540
60 65 70	SHLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVUGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding seq 1   AGCCAGCCCG CTCGCGGTCA GTTTTACTGA TCCCTGGAAG GTCAGTTTCC GCTTCAGGCG GCATTTTTTA CAACATATAA GAGCTCAACA	DLSRTSVLPA LIMILVFLIDS YILKFCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK  21 DNA seq id Accessio. 11   AGGACGCGAG GGATGGTTTT CGTTCAAGAT AAGATACTGA TCAAACCCCA CCTCCTAA CCGCTCCTC CGTCAACGA TCAAACCCCA AAACCCCAA AAACCCCACA AAACCCCTCCAC	QMMALTFITY WIALYKMQGL GVPAVVVTII MFIVVLVQLC PAIFNTLQGF VSSSNSLQS QHMFNEKEDS UENCE n #: NM_005 3117 21   CGGCAGGTGT CTCTGTCAGG ATTCCTTGTC TAATTCCAGT AACAGAAAA GAGAAATATC CATGTTTCAA CTTAACTGGA ACCTTAACTG	IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR  756.1  31   GCACAGAGGT CAGTGTGGCC ATCATTTGTC TTGTCACCAC GAAACAACAA ACTAAAATCA TGCAATTTGT TATGATAAAG GTCCTGTCTC GAGACTTACT	SVTLVTYIAP FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHP  41   TCTCCACTTT ATGTTGGCAG TTCATGTCGT CACCTGCTAA GCCTCCAATGA CCTATATTG AAAGCACTGT TAAGTAAAT TTATAATGTG	LEAFHMYLAL PDDFCWINNN SIAGLIFILIG LCCGKLRLAE SGNGNASTER IEQM  51   GTTTTCTGAA AACTGAGAGAA TCTGGTAACA ATTATCTGTT TGTTACTTTA TAGATGATCA TCCCCAGAAT AAAACGCTCA TCCCCAGAAT AAAACGCTCA	720 780 840 900 960 120 180 240 300 420 480 540
60 65	SHLTSFGVLL ILIQLCABLI ILIQLCABLI VKVENTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding seq 1   AGCCAGCCCG CTCGCGGTCA GTTTTACTGA GTCAGTTTTG AGCTTACTCC GCTTCAGCG GCATTTTTTA CAACATATAA GAGCTCAACA GAGGCCCAAA	DLSRTSVLPA LLNIVFILIDS YILKPCIVGW PCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK  21 DNA seq id Accession Lence: 37 11   AGGACGCGAG GGATGGTTTT CGTTCAAGGA CCCCTCCTC CTTCAACGA TCAAACCAC GAGGTGAGAT CGAATGGAC AAACCCTGA AAACCCTGA AAACCCTGA AAACCCTTCAACGA AAACCCTGA GCACATTAAA	QMMALTFITY WIALLYKMGGI GUPAVVVTII MPIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS uence n #: NM_005 3117 21   CGGCAGGTGT CTCTGTCAGG ATTCCTTGTC TAATTCCAGT CAATGAGGTT AACAGAAAAA GGGAAAAAT CATGTTTCAA CTTAACTGGA AACCCTAAGT TTGTACATTC	IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR  756.1  31   GCACAGAGGT CAGTGTGGCC ATCATTTGTC TTGTCACCAC GAAACAACAA ACTAAAATCA TGCAATTTGT TATGATTAAAG CGCACTTCTC GAGACTTACT ACAATAAAAC	SYTLVTYIAP FILVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHF  41   TCTCCACTTT ATGTTGGCAG TTCATGTCGT CACCTGCTAA GCCTCAATGA CTATAGTAAA GCTCTATTTG AAAGCACTGT TAAATGAATT TTATAAATGTG TGAATAATACT	LEAFHMYLAL PDDFCWINNN SIAGLIFILG LCCGKLRLAE SGNGNASTER IEQM  51   GTTTTCTGAA AACTGAAGAA ACTGGAAGAA ACTGGTAACA ATTATCTGTT TGTTACTTTA AACCTTCAAT TCAATGACTCA TCCCCAGAAT AAAACGCTCA TGCTACAGCA AATGAATGCA	720 780 840 900 960 120 180 240 300 360 420 480 540 660
60 65 70	SHLTSFGVLL ILIQLCAALL VKVENTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding seq 1   AGCCAGCCCG CTCGCGGTCA GTTTTACTGA TCCCTGGAAG GTCAGTTTTG AGCTTACTCC GCTTCAGCCG GCATTTTTTTA CAACATATAA GAGGCCCAAA TGTGCTGCAAA	DLSRTSVLPA LLNIVFLIDS YILKPCIVGW FCVIFILNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession HENCE: 37 11   AGGACGCGAG GGATGGTTT CGTTCAAGAT AAGATACTGA CCCCCTCCTC CTTCAAACGA TCAAACCCCA GAGGTGAGAT GGATGGAGAT CGAATGCAC AAACCCTGCA AAACCCCTGCA AAACCCCTGCA AAACCCCTGCA AAACCCCTGCA AAACCCCTGCA AAACCCCCCTTT	QMMALTFITY WIALYKMGIL GYPAVVOTI MFIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS  UENCE #: NM_005 3117 21   CGGCAGGTGT CTCTGTCAGG ATTCCTTGTC TAATTCCAGT AACAGAAAAA GAGAAATATC CATGTTTCAA CTTAACTGGA AACCTTAAGTT TTGTACATT GGGAAAGAGTA	IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR  756.1  31   GCACAGAGGT CAGTGTGGCC ATCATTTGTC CAGAACAACAA ACTAAAATCA IGCAATTTGT TATGATTAAAG GTCCTGTCTC GAGACTTACT ACAATAAACA ACTAAAATCA	SVTLVTYIAP FILVSFTMMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHP  41   TCTCCACTIT ATGTTGGCAG TTCATGTCGT TCACTGCTAA GCCTCAATGA CATTAGTAAA CATCTATTTG TAAGCACTGT TAAGTGAATT TTATAATGG CAATAGAACA CAATGGAACA	LEAFHMYLAL PDDFCWINNN SIAGLIFILIG LCCGKLRLAE SGNGNASTER IEQM  51   GTTTTCTGAA AACTGAAGAA TCTGGTAACA ATTATCTGTT TGTTACTTTA AACCTTCAAT CAATGACTCA TCCCCAGAAT AAAACGCTCA TGCTACAGCA AATGAATGCA CTGCTGCTGT	720 780 900 960 60 120 180 240 360 420 480 540 600 600
60 65 70	SHLTSFGVLL ILIQLCAALL VKVENTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding seq 1   AGCCAGCCCG CTCGCGGTCA GTTTTACTGA TCCCTGGAAG GTCAGTTTTG AGCTTACTCC GCTTCAGCCG GCATTTTTTTA CAACATATAA GAGGCCCAAA TGTGCTGCAAA	DLSRTSVLPA LLNIVFLIDS YILKPCIVGW FCVIFILNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession HENCE: 37 11   AGGACGCGAG GGATGGTTT CGTTCAAGAT AAGATACTGA CCCCCTCCTC CTTCAAACGA TCAAACCCCA GAGGTGAGAT GGATGGAGAT CGAATGCAC AAACCCTGCA AAACCCCTGCA AAACCCCTGCA AAACCCCTGCA AAACCCCTGCA AAACCCCTGCA AAACCCCCCTTT	QMMALTFITY WIALYKMGGL GYPAVVTII MFIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS UENCE n #: NM_005 3117 21   CGGCAGGTGT CTCTGTCAGG ATTCCTTGTC TAATTCCAGT AACAGAAAAA GAGAAATATC CATGTTTCAA CTTAACTGGA AACCTTAAGTT TTGTACATT GGGAAAGAGTA	IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR  756.1  31   GCACAGAGGT CAGTGTGGCC ATCATTTGTC CAGAACAACAA ACTAAAATCA IGCAATTTGT TATGATTAAAG GTCCTGTCTC GAGACTTACT ACAATAAACA ACTAAAATCA	SVTLVTYIAP FILVSFTMMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHP  41   TCTCCACTIT ATGTTGGCAG TTCATGTCGT TCACTGCTAA GCCTCAATGA CATTAGTAAA CATCTATTTG TAAGCACTGT TAAGTGAATT TTATAATGG CAATAGAACA CAATGGAACA	LEAFHMYLAL PDDFCWINNN SIAGLIFILIG LCCGKLRLAE SGNGNASTER IEQM  51   GTTTTCTGAA AACTGAAGAA TCTGGTAACA ATTATCTGTT TGTTACTTTA AACCTTCAAT CAATGACTCA TCCCCAGAAT AAAACGCTCA TGCTACAGCA AATGAATGCA CTGCTGCTGT	720 780 900 960 60 120 180 240 360 420 480 540 600 600 720
60 65 70	SHLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATIN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding seq AGCCAGCCCG CTCGCGGTCA GTTTTACTGA GCTTGCAGTG GCTTCAGCCG GCATTTTTG CAACATATAA GAGCTCAACA GAGGCCCAAA TGTGCTGCAG TCTGCAGAA TGTGCTGCAG TCTGCTCAGGAA TGTGCTGCAG TCTGCTGCAGA TCTGTCAGGAA TGTGCTGCAA TCTGTCAGGAA TCTGTCAGGAA TCTGTCAGGAA TCTGTCAGGAA	DLSRTSVLPA LINIVFLIDS YILKPCIVGW FCVIFILINVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accessio. 11   AGGACGCGAG GGATGGTTTT CGTTCAAGAT AAGATACTGA TCAAACCCCA GAGGTGAGAT TCAAACCCCA GAGGTGAGAT TCAAACCTGCA AACCTTCA AACCTTCA AACCTTCA AACCTTCA AACCTTCA TCAACCA AACCTTCA AACCTTCA TCAACCA TTAACA TAGCACTTTT TACCCTTCCCC	QMMALTFITY WIALYKMQGL GVPAVVVTII MFIVULVQLC FAIFNTLQGF VSSSSNSLQS QHMFNEKEDS  LUENCE #: NM_005 3117 21   CGGCAGGTGT CTGTCAGG ATTCCTTGTC TAATTCCAGT CAATGAGGTT CAATGAGGTT CAATGAGGTT CAATGAGGTT CAATGAGTT AACAGAAAAA CGTAACTGGA CTTAACTGGA TGTTTCAGT TGTACATTC GGAAAGAGTA CTTGTACATTC GGGAAAGAGTA TTCTTCCCCA	IGGGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR  756.1  31   GCACAGAGGT CAGTGTGGCC ATCATTGTC TTGTCACCAC GAACAACAA ACTAAAATCA ACTAAAATCA TGGAATTGT TATGATAAAG GTCCTGTCTC GAGACTTACT ACAATAAAAC AAGATAAAAC AAGATAAAAC AAGATAAAAC AAGATTAGAC AAGATTAGAC AAGATTGGAC GAGAGTTGGC GAGAGTTGGC GAGAGTTGGC	SVTLVTYIAP FLLVSFTWMG GSYGKPPMGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHP  41   TCTCCACTTT ATGTTGGCAG TTCATGTGTT CACCTGCTAA GCCTCAATGA CATCTATTTG AAAGCACTGT TAAGTGAATT TTATAATGTG TGAATAATATAC CAATGGAACA GAAAGCTTCA	LEAFHMYLAL PDDFCWINNN SIAGLTFILIG LCCGKLRLAE SGNGNASTER IEQM  51   GTTTTCTGAA AACTGAAGAA TCTGGTAACA ATTATCTGTT TGTTACTTTA AACCTTCAAT CAATGACTCA TCCCCAGAAT TCCCCAGCA AATGAATGCA TGCTACAGCA AATGAATGCA TGCTACAGCA AATGAATGCA TGCTACAGCA	720 780 900 960 60 120 180 240 300 420 480 560 720 780
60 65 70	SHLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATIN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding seq AGCCAGCCCG CTCGCGGTCA GTTTTACTGA GCTTGCAGTG GCTTCAGCCG GCATTTTTG CAACATATAA GAGCTCAACA GAGGCCCAAA TGTGCTGCAG TCTGCAGAA TGTGCTGCAG TCTGCTCAGGAA TGTGCTGCAG TCTGCTGCAGA TCTGTCAGGAA TGTGCTGCAA TCTGTCAGGAA TCTGTCAGGAA TCTGTCAGGAA TCTGTCAGGAA	DLSRTSVLPA LINIVFLIDS YILKPCIVGW FCVIFILINVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accessio. 11   AGGACGCGAG GGATGGTTTT CGTTCAAGAT AAGATACTGA TCAAACCCCA GAGGTGAGAT TCAAACCCCA GAGGTGAGAT TCAAACCTGCA AACCTTCA AACCTTCA AACCTTCA AACCTTCA AACCTTCA TCAACCA AACCTTCA AACCTTCA TCAACCA TTAACA TAGCACTTTT TACCCTTCCCC	QMMALTFITY WIALYKMQGL GVPAVVVTII MFIVULVQLC FAIFNTLQGF VSSSSNSLQS QHMFNEKEDS  LUENCE #: NM_005 3117 21   CGGCAGGTGT CTGTCAGG ATTCCTTGTC TAATTCCAGT CAATGAGGTT CAATGAGGTT CAATGAGGTT CAATGAGGTT CAATGAGTT AACAGAAAAA CGTAACTGGA CTTAACTGGA TGTTTCAGT TGTACATTC GGAAAGAGTA CTTGTACATTC GGGAAAGAGTA TTCTTCCCCA	IGGGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR  756.1  31   GCACAGAGGT CAGTGTGGCC ATCATTGTC TTGTCACCAC GAACAACAA ACTAAAATCA ACTAAAATCA TGGAATTGT TATGATAAAG GTCCTGTCTC GAGACTTACT ACAATAAAAC AAGATAAAAC AAGATAAAAC AAGATTAGAC AAGATTGGC GAGAGTTGGC GAGAGTTGGC	SVTLVTYIAP FLLVSFTWMG GSYGKPPMGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHP  41   TCTCCACTTT ATGTTGGCAG TTCATGTGTT CACCTGCTAA GCCTCAATGA CATCTATTTG AAAGCACTGT TAAGTGAATT TTATAATGTG TGAATAATATAC CAATGGAACA GAAAGCTTCA	LEAFHMYLAL PDDFCWINNN SIAGLIFILIG LCCGKLRLAE SGNGNASTER IEQM  51   GTTTTCTGAA AACTGAAGAA TCTGGTAACA ATTATCTGTT TGTTACTTTA AACCTTCAAT CAATGACTCA TCCCCAGAAT AAAACGCTCA TGCTACAGCA AATGAATGCA CTGCTGCTGT	720 780 900 960 60 120 180 240 300 420 480 560 720 780
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60 65 70 75	SHLTSFGVLL ILIQLCABLL ILIQLCASLI ILIQLCASIL ILIQLCASIL ILIQLCASIC ILIQLCASIC INVESTATON INGUSERSTATON Seq ID NO: Nucleic Ac: Coding sequence I AGCCAGCCCG CTCGCGGTCA GTITTACTGA TCCCTGGAAG GTCAGTTTTG AGCTTACTCC GCTTCAGGCA GGCTTCAGCC GCATTTTTTA CAACATATAA GAGGTCCAAC TGTGCTGCAAA TGTGCTGCAAA TGTGCTCAGCA AGGGTCCAAC TCCATCCCAG CCGCTCCCAG CCGCTCCCAG CCGCTCCCAG CCGCTCCCAG CCGCTCCCAG CCCCATCCCCAG CCCCATCCCCAG TCCATCCCAG	DLSRTSVLPA LLNLVFLLDS YILLKPLIVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK  21 DNA seq id Accession Lence: 37 11 AGGACGCGAG GGATGGTTTT CGTTCAAGGA CCCCTCCTC CTTCAAACCA AAACCCTGA GGATGGGAG GGATGGGAG TCAAACCCA AGGGTGAGAT TAGCATGAA TAGCCGCTT TACCTTGCCTT TAGCTGCTCT TTGGTGCTTCGTTCT	QMMALTFITY WIALLYKMGGI GUPAVVVTII MFIVVLVQLC FAIFNTLQGF VSSSSNSLQS QHMFNEKEDS  UENCE n #: NM_005 3117 21   CGGCAGGTGT CTCTGTCAGG ATTCCTTGT CAATGAGGTT AACAGAAAAA GAGAAATATC CATGTTTCAA CATGATGTTCAA TGTTACATGG TTGTACATTC GGAAAGAGTA TTGTACATTC GGAAAGAGTA TTGTACATTC GGAAAGAGTA TTCCTCCCCA TTCCTCCCCA TTCCTCCCCA TGCTGACCAT GGCCACTGTG	IGGLSSIFL CISVAVFLHY CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR  756.1  31    GCACAGAGGT CAGTGGCC ATCATTGTC TTGTCACCAC GAACAACAA ACTAAAATCA ACTAAAATCA CTGCAATTTGT TATGATAAAG GTCCTCTC GAGACTTACT ACAATTAGAC ACAATAAAC ACAATAAAC CGAGACTTCC ACAATAAAAC ACAATAAAC CGAGACTTCGC CGAGACTTCGC CGAGACTTCGC CCACGTGGCC CCTTCCCAGG	SVTLVTYIAP FILVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHP  41   TCTCCACTIT ATGTTGGCAG TTCATGTCGT CACCTGCTAA GCCTCAATGA CTATAGTAAA GCTTCAATTG AAAGCACTGT TAAATGGATT TTATAATGT TGAATTAATGT GTGAATTATT TTATAATGT CAATGGAACA CAATGGAACA CACCATTTC TCCCCAAAGC	LEAFHMYLAL PDDFCWINNN SIAGLIFILG LCCGKLRLAE SGNGNASTER IEQM  51   GTTTTCTGAA AACTGAAGAA TCTGGTAACA ATTATCTGTT TGTTACTTTA AACCTTCAAT AAACGCTCA TCCCCAGAAT AAAACGCTCA TCCTCAGGCAA TACTGCTGCTGT GTTGACCTG TTCCAGCAA TACTGCTGCTGT TTCCTGCTGTTACCTTTT	720 780 840 900 960 120 120 240 300 360 420 480 540 600 720 780 840 900
60 65 70	SHLTSFGVLL ILIQLCABLL ILIQLCASLI ILIQLCASIL ILIQLCASIL ILIQLCASIL ILIQLCASIL IVEVITY IRK AVFYITVVGY ITMGFAFFAW NSDWSKTATN NGVSFSVONG Seq ID NO: Nucleic Ac: Coding sequit I AGCCAGCCCG CTCGCGGTCA GTTTTACTGA TCCGGGTCAGCTCAGGAG GCATTTTTA GAGCTCAACA GAGGTCCAAA TGTGCTGCAAA TGTGCTGCAAA TGTGCTCAGGA CAGGATCCCAA TCCATCCCAG CCATCCCAG TCCATCCCAG	DLSRTSVLPA LLNLVFLLDS YILLKPLIVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK  21 DNA seq id Accession Lence: 37 11 AGGACGCGAG GGATGGTTTT CGTTCAAGGA CCCCTCCTC CTTCAAACCA AAACCCTGA GGATGGGAG GGATGGGAG TCAAACCCA AGGGTGAGAT TAGCATGAA TAGCCGCTT TACCTTGCCTT TAGCTGCTCT TTGGTGCTTCGTTCT	QMMALTFITY WIALLYKMGGI GUPAVVVTII MFIVVLVQLC FAIFNTLQGF VSSSSNSLQS QHMFNEKEDS  UENCE n #: NM_005 3117 21   CGGCAGGTGT CTCTGTCAGG ATTCCTTGT CAATGAGGTT AACAGAAAAA GAGAAATATC CATGTTTCAA CATGATGTTCAA TGTTACATGG TTGTACATTC GGAAAGAGTA TTGTACATTC GGAAAGAGTA TTGTACATTC GGAAAGAGTA TTCCTCCCCA TTCCTCCCCA TTCCTCCCCA TGCTGACCAT GGCCACTGTG	IGGLSSIFL CISVAVFLHY CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR  756.1  31    GCACAGAGGT CAGTGGCC ATCATTGTC TTGTCACCAC GAACAACAA ACTAAAATCA ACTAAAATCA CTGCAATTTGT TATGATAAAG GTCCTCTC GAGACTTACT ACAATTAGAC ACAATAAAC ACAATAAAC CGAGACTTCC ACAATAAAAC ACAATAAAC CGAGACTTCGC CGAGACTTCGC CGAGACTTCGC CCACGTGGCC CCTTCCCAGG	SVTLVTYIAP FILVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHP  41   TCTCCACTIT ATGTTGGCAG TTCATGTCGT CACCTGCTAA GCCTCAATGA CTATAGTAAA GCTTCAATTG AAAGCACTGT TAAATGGATT TTATAATGT TGAATTAATGT GTGAATTATT TTATAATGT CAATGGAACA CAATGGAACA CACCATTTC TCCCCAAAGC	LEAFHMYLAL PDDFCWINNN SIAGLIFILG LCCGKLRLAE SGNGNASTER IEQM  51   GTTTTCTGAA AACTGAAGAA TCTGGTAACA ATTATCTGTT TGTTACTTTA AACCTTCAAT AAACGCTCA TCCCCAGAAT AAAACGCTCA TCCTCAGGCAA TACTGCTGCTGT GTTGACCTG TTCCAGCAA TACTGCTGCTGT TTCCTGCTGTTACCTTTT	720 780 840 900 960 120 120 240 300 360 420 480 540 600 720 780 840 900
60 65 70 75	SHLTSFGVLL ILIQLCAALL VKVPNTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding seq I AGCCAGCOCG CTCGCGGTCA GTTTTACTGA AGCTTACTCC GCTTCAGGCG GCATTTTTA CAACATATAA GAGCTCAACA GAGGCCCAAC TCGTGCAGC	DLSRTSVLPA LINIVFLIDS YILKPCIVGW FCVIFILINVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession Hence: 37 11   AGGACSCGAG GGATGGTTTT CGTTCAAGAT AGATACTGA CCCCCTCCTC CTTCAAACGA TCAAACCCCA GAGGTGAGAT CGAATGCAC GAATGCAC GCACATTAA TAGCCGCTT TACCCTGCCC TTGTCTCTCT TTGTCTCTCT TGGTGCCCCC CGAGTTGTCTCCCT CGAGTGCCCCCCCCCC	QMMALTFITY WIALLYKMGEI GYPAVVVTII MFIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS UENCE #: NM_005 3117 21   CGGCAGGTGT CTCTGTCAGG ATTCCTTGTC CTAATTCCAGT CAATGAGGTT AACAGAAAAA CAGAAAAAA CAGAAAAAA CATAACTGGA CTTAACTGGA ACCTTAAGT TTGTACATTC GGGAAAGAGTA TTCCTCCCCA TTCCTCCCCA TGCTGACCAT GGCCACTGTG	IGGGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTIL CNGKGRMALR  756.1  31   GCACAGAGGT CAGTGTGGCC ATCATTTGTC TTGTCACCAC GGAACAACAA ACTAAAATCA TGCAATTTGTC TATGATAAAG GTCCTGTCTC GAGACTTACT ACAATAAAC AAGATTCGAC AAGATTCGAC CAAGAGGTTGG CCACAGTGGCG CTTTCCCACG	SVTLVTYIAP FILVSFTMM GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA  41    TCTCCACTTT ATGTTGGCAG TTCATGTCGT TCACTGCTAA GCCTCAATGA CATCTATTTG TAAGTGAAT TTATAATGT TAATATGT TGAATAATAC CAATGGAACA GAAAGCTTCA CACCATTTCC CACCATTTCC CACCCCAATGC CCCCCAATGC CCCCCCAATGC CCCCCCAATGC CCCCCCAATGC CCCCCCAATGC CCCCCCAATGC CCCCCTACCC	LEAFHMYLAL PDDFCWINNN SIAGLIFILIG LCCGKLRLAE SGNGNASTER IEQM  51   GTTTTCTGAA AACTGAAGAA TCTGGTAACA ATTATCTGTT TGTTACTTTA AACCTTCAAT CAATGACTCA TCCCAGAAT AAAAGGCTCA TGCTACAGCA AATGAATGCA CTGCTGCTGT GTGTGCCCAGCAAA ATGAATGCA TTCCAGCCAAA TACCCTCTTT AGGGGAGATT AGGGGAGATT	720 780 900 960 960 120 180 240 360 420 480 600 650 780 840 900 960
60 65 70 75	SHLTSFGVLL ILIQLCAALL ILIQLCAALL VKVENTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding seq 1 AGCCAGCCCG CTCGCGGTCA GTTTTACTGA GCTTCACCG GCTTCACGG GCATTTTTA AGCTTACTGC GCTTCACACA GAGGCCCAAA TGTGCTCACA TGTGCTGGAA TCTGTCAGGA CAGGGTCCCA CCACCCTTT CAACCCTTT	DLSRTSVLPA LLNIVFILIDS LLNIVFILIDS FVIILKPCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK  21 DNA sequid Accession Lence: 37 11   AGGACGCGAG GGATGGTTTT CGTTCAAACGA TCAAACCTA GAGTGAGAT TCAACCTGCA GAATGCACC GAATGCACT TACCCTGCA GCACTTCAAC GCACTTCAACGAT TAGCCGCTTT TACCCTGCA TAGCCGCTTT TACCCTGCCC TTGTTCTTCTT TGGTGCCTCC CACCCCAGCC	QMMALTFITY WIALLYKMGEI GUPAVVVTII MPIVVLVQLC FAIFNTLQGF VSSSSNSLQS QHMFNEKEDS  UENCE  n #: NM_005 3117 21   CGGCAGGTGT CTCTGTCAGG ATTCCTTGTC TAATTCCAGT CAATGAGGTT AACAGAAAA CCTTAACTGGA ATTCTAGT TTGTCTCCCCA TTGTCTAAGT GGAAAGAGTA TTCTTCCCCCA TGCTGACCAT GGCCACTGGC ACCTGTACCAT GGCCACTGGC ACCTGTACCAT CACCTGTACCAT GGCCACTGGC CACCTGTACCAT TCTGCTCCCC TTCAGGTCCCC	IGCGLSSIFL CISVAVFLHY CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR  756.1  31  GCACAGAGGT CAGTTTGGCC ATCATTGTC TTGTCACCAC GAAACACAA ACTAAAATCA CGACATTGTC TATGATAAAG CGACATTGTC CAGACTTACT CAGAGATTGGCC CAGAGCTTACT CACAATTTGC CAGAGCTTACT CACAATTTGC CACACTGGCC CACAATCTTCC CATAGCTTCCAGG CACAATCTCCAGG CACAATCTCCA	SYTLVTYIAP FILLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHF  41   TCTCCACTTT ATGTTGGCAG TTCATGTGGTAG GCCTCAATGA GCCTCAATGA AAGCACTGT TAAGTAAAT CAATGAATT TTATAATGTG TGAATAATGC TGAATGAATC CAATGAACT CCCCAAAGC CCCCCCCAAGC CCCCCCCAAGC	LEAFHMYLAL PDDFCWINNN SIAGLIFILIG LCCGKLRLAE SGNGNASTER IEQM  51   GTTTTCTGAA AACTGAAGAA TCTGGTAACA ATTATCTGTT TGTTACTTTA AACCTCTAAT AAACGCTCA ATGAAGCA CTCCCAGAAT AGAAGCTCA CTCCCAGAAT AGAAGCTCA TCCTACAGCA AATGAATGCA TGTTACAGCA AATGAATGCA TGTGTGACCTG TTCCAGCCAA TACCTCTTTT AGGGGGAGATT TGACATGCCC	720 780 840 900 960 120 180 240 300 420 480 540 600 660 720 780 900 900 900
60 65 70 75	SHLTSFGVLL ILIQLCAALL ILIQLCAALL VKVENTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding seq 1 AGCCAGCCCG CTCGCGGTCA GTTTTACTGA GCTTCACCG GCTTCACGG GCATTTTTA AGCTTACTGC GCTTCACACA GAGGCCCAAA TGTGCTCACA TGTGCTGGAA TCTGTCAGGA CAGGGTCCCA CCACCCTTT CAACCCTTT	DLSRTSVLPA LLNIVFILIDS LLNIVFILIDS FVIILKPCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK  21 DNA sequid Accession Lence: 37 11   AGGACGCGAG GGATGGTTTT CGTTCAAACGA TCAAACCTA GAGTGAGAT TCAACCTGCA GAATGCACC GAATGCACT TACCCTGCA GCACTTCAAC GCACTTCAACGAT TAGCCGCTTT TACCCTGCA TAGCCGCTTT TACCCTGCCC TTGTTCTTCTT TGGTGCCTCC CACCCCAGCC	QMMALTFITY WIALLYKMGEI GUPAVVVTII MPIVVLVQLC FAIFNTLQGF VSSSSNSLQS QHMFNEKEDS  UENCE  n #: NM_005 3117 21   CGGCAGGTGT CTCTGTCAGG ATTCCTTGTC TAATTCCAGT CAATGAGGTT AACAGAAAA CCTTAACTGGA ATTCTAGT TTGTCTCCCCA TTGTCTAAGT GGAAAGAGTA TTCTTCCCCCA TGCTGACCAT GGCCACTGGC ACCTGTACCAT GGCCACTGGC ACCTGTACCAT CACCTGTACCAT GGCCACTGGC CACCTGTACCAT TCTGCTCCCC TTCAGGTCCCC	IGCGLSSIFL CISVAVFLHY CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR  756.1  31  GCACAGAGGT CAGTTTGGCC ATCATTGTC TTGTCACCAC GAAACACAA ACTAAAATCA CGACATTGTC TATGATAAAG CGACATTGTC CAGACTTACT CAGAGATTGGCC CAGAGCTTACT CACAATTTGC CAGAGCTTACT CACAATTTGC CACACTGGCC CACAATCTTCC CATAGCTTCCAGG CACAATCTCCAGG CACAATCTCCA	SYTLVTYIAP FILLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHF  41   TCTCCACTTT ATGTTGGCAG TTCATGTGGTAG GCCTCAATGA GCCTCAATGA AAGCACTGT TAAGTAAAT CAATGAATT TTATAATGTG TGAATAATGC TGAATGAATC CAATGAACT CCCCAAAGC CCCCCCCAAGC CCCCCCCAAGC	LEAFHMYLAL PDDFCWINNN SIAGLIFILIG LCCGKLRLAE SGNGNASTER IEQM  51   GTTTTCTGAA AACTGAAGAA TCTGGTAACA ATTATCTGTT TGTTACTTTA AACCTCTAAT AAACGCTCA ATGAAGCA CTCCCAGAAT AGAAGCTCA CTCCCAGAAT AGAAGCTCA TCCTACAGCA AATGAATGCA TGTTACAGCA AATGAATGCA TGTGTGACCTG TTCCAGCCAA TACCTCTTTT AGGGGGAGATT TGACATGCCC	720 780 840 900 960 120 180 240 300 420 480 540 600 660 720 780 900 900 900
60 65 70 75	SHLTSFGVLL ILIQLCABLI ILIQLCABLI ILIQLCABLI VKVENTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding seq 1   AGCCAGCCCG CTCGCGGTCA GTTTTACTCC GCTTCAGGAG GCATTTTTA GAGCTCAACA GAGGCCCAAA TGTGCTGCAA TGTGCTGCAA TGTGCTCAGGA CAGGATCCCAA CAGGGCCCAAA TCCATCCCAG GCTGAGCCTC CAACCCCTTT CCACAGTCTG CAACCCCTTT CCACAGTCTG CCACCCTTT CCACAGTCTG CAACCCCTTT CCACAGTCTG CACCAGTCTG CACACCCTTT CCACAGTCTG CACACCTTT CCACAGTCTG CACACCCTTT CCACAGTCTG CACACCCTT CCACACCCTTT CCACAGTCTG CACACCCTTT CCACAGTCTCACACCCTTT CCACAGTCTCT CCACACCCTTT CCACAGTCTCACACCCTTT CCACACCCTTT CCACACCCTTT CCACACACCCTTT CCACACCCTTT CCACACCCTTT CCACACCCTTT CCACACCCTTT CCACACCT CACACCCTTT CCACACCCTTT CCACACCT CACACCCT CACACCCT CACACCT CACACCCT CACACCCT CACACCC CACACC CACACCC CACACCC CACACC C	DLSRTSVLPA LLNLVFLLDS YILLKPLIVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK  21 DNA seq id Accessio uence: 37 11   AGGACGCGAG GGATGGTTTT CGTTCAAGGAT CCCCTCCTC CTTCAAACCAA CCCCCTCCTC CTTCAAACCAA ACCCTCAC GAGGTGAGAT TAGCATTAAA TAGCCGCTTT TACCTTGCCT TGCTCTCTCTCTCTCTCTCTCTCTCTCTCTC	QMMALTFITY WIALLYKMGGI GUPAVVVTII MFIVVLVQLC FAIFNTLQGF VSSSSNSLQS QHMFNEKEDS  uence n #: NM_005 3117 21   CGGCAGGTGT CTCTGTCAGG ATTCCTTGTCAGG ATTCCTTGTCAGG CAATGAGGTT AACAGAAAAA CGAAAAAA CATTACTGGA TTGTACATTC GGAAGAGTA ACCCTAAGT TTGTACATTC GGAAGAGTA TTGTACATTC GGAAGAGTA TTCCTCCCCA TGCTGACCC TTCAGCTCCC	IGGLSSIFL CISVAVFLHY CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR  756.1  31    GCACAGAGGT CAGTGTGGCC ATCATTTGTC TTGTCACCAC GAACAACAA ACTAAAATCA ACTAAAATCA CGAGACTTACT ACAATTAGTC CAGAGCTTACT CACAGTGGCC CCACGTGGCC CCACAGTGGCC CCACAGTGGCC CATAGCTTCCAGG CCACAGTGGCC CATAGCTTCCAGG CACACTTGGC CATAGCTTCCAGG CACACATGTTCC ATAGCTTCCAGG CCACAAACCC	SYTLVTYIAP FILVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHF  41   TCTCCACTIT ATGTTGGCAG TTCATGTCGT CACCTGCTAA GCCTCAATGA CTATAGTAAA GCTCTAATTG AAAGCACTGT TAAATGGATT TTATAATGTG TGAATAATAC CAAAGCACTCTC TCCCCAAAGC CCCCTCTCCAAT GCCCTGCCAT ATGTCTCCGG	LEAFHMYLAL PDDFCWINNN SIAGLIFILIG LCOGKLRLAE SGNGNASTER IEQM  51   GTTTTCTGAA AACTGAAGAA TCTGGTAACA ATTATCTTTA AACCTTCAAT TCAATGACTCA TCCCCAGAAT AAAACGCTCA TGCTACAGCA AATGAATGCA TGCTGCTGT GTTGCCTGT GTTGCCTGT TTCCAGCAA TACATCCCC CACCCCACCC	720 780 840 900 960 120 180 240 300 420 480 540 600 720 780 960 1020 1080
60 65 70 75	SHLTSFGVLL ILIQLCAALL ILIQLCAALL ILIQLCAALL VKVENTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATN NGVSFSVONG Seq ID NO: Nucleic Ac. Coding seq 1   AGCCAGCCCG CTCGCGGTCA GTTTTACTGA AGCTACTCC GCTTCAGGC GCATTTTGA GAGCTCAACA ATGTGCTGCAA TCTGTCAGGA TCTGTCAGGA TCTGTCAGGA TCTGTCAGGA CCAGGTCCCA CCACCCTTT CCACAGCTCT CCACAGCTCT CCACGCTTT CCTGTGAAAG	DLSRTSVLPA LLNIVFILIDS LLNIVFILIDS GPVNTFMYL GLKKQTVNQG DVCLHDFTGK  21 DNA seq id Accessio uence: 37 11   AGGACGCGAG GGATGGTTTT CGTTCAAGAT AAGATACTGA CCCCTCCTC CTTCAAACGAT TCAAACCCAT CGAATGCAC AAACCCTGCA TCACCTGCCTTC TTGCTGTCT TTGCTGTCT TGGTGCCTTC CAGATTTTC CACCCCAGCC CAAACGATCTCC CAAACGATCTCC CAAACGATCTCC CAAACCAGCC CAAACGATCTCC CACCATTTTCC CCCCAGTCT CCCCAGTCTCC CACACCTAGTCTCC CACACCAGCCC CAAACGATCTCC CCCCAGTCTCC CCCCATTTTCC CCCCAGTCTCC CCCCATTTTCC CCCCATTTCC CCCCATTTCC CCCCATTTTCC CCCCATTTCC CCCCATTCC CCCCATTTCC CCCCCATTTCC CCCCATTTCC CCCCATTTCC CCCCATTTCC CCCCATTCC CCCCATTTCC CCCCATTTCC CCCCATTTCC CCCCATTTCC CCCCATTTCC CCCCATTCC CCCCATTTCC	QMMALTFITY WIALYKMGGL GYPAVVTII MFIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS UENCE #: NM_005 3117 21   CGGCAGGTGT CTCTGTCAGG ATTCCTTGTC TAATTCCAGT CAATCAGGTT AACAGAAAAA CCTAACTGGA CATGTTCAA CTTAACTGGA AACCTAAGT TTGTACATT GGAAACAGTA CTTACTGGACC TTCCTCCCCA GGCACTGTGACC TTCCTCCCACC TTCCCCACC	IGGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR  756.1  31    GCACAGAGGT CAGTGTGGCC ATCATTTGTC CAGACACAA ACTAAAATCA TAGAATTGTC TATGATAAAG GTCCTGTCTC GAGACTTACTC CAAGAGTTGGC CACAGGGC CCTTTCCCAGG CCACAGGCC CCTTTCCCAGG CCACATGCC CTTTCCCAGG CCACATGCC CACAATGTTC ATAGCTTCCC CATAGCT CACAATGTCC CTTTCCCAGG CCCCAAACCC CCCCAAACCC CGTGTCTCCCC	SVTLVTYIAP FILVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHP  41   TCTCCACTITI ATGTTGGCAG TTCATGTCGT TACGTCGTAA GCCTCAATGA CATCTATTTG TAAGTGAATT TTATAATGTAG GAAAGCTTCA GAAAGCTTCA CACTGTTTCC TCCCCAAAGC CCTCTCCAAT GCCCTCCAATG CCTCTCCAAT GCCTTCCAAT GCCCTGCCAT ATGTCTCCGG CTTCTCCAAT GCCCTGCCAT TATGTCTCCGG CTGCCAATGT	LEAFHMYLAL PDDFCWINNN SIAGLIFILIG LCCGKLRLAE SGNGNASTER IEQM  51   GTTTTCTGAA AACTGAAGAA TCTGGTAACAA ATTATCTGTT TGTTACTTTA AACCTTCAAT AAACGTCA TCCCCAGAAT AAAAGGCTCA TGCTACAGCA AATGAATGCA CTGCTGTGTGTGTGTGTGCTGT TCCAGCCAA AATGAATGCA TCCCAGCAGT TAGGGGAGATT TGACATGCCC CACCCCACCT CAACACTACC	720 780 900 960 60 120 180 240 360 420 480 600 660 720 780 840 960 1020 1020
60 65 70 75	SHLTSFGVLL ILIQLCAALL ILIQLCAALL ILIQLCAALL VKVENTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATN NGVSFSVONG Seq ID NO: Nucleic Ac. Coding seq 1   AGCCAGCCCG CTCGCGGTCA GTTTTACTGA AGCTACTCC GCTTCAGGC GCATTTTGA GAGCTCAACA ATGTGCTGCAA TCTGTCAGGA TCTGTCAGGA TCTGTCAGGA TCTGTCAGGA CCAGGTCCCA CCACCCTTT CCACAGCTCT CCACAGCTCT CCACGCTTT CCTGTGAAAG	DLSRTSVLPA LLNIVFILIDS LLNIVFILIDS GPVNTFMYL GLKKQTVNQG DVCLHDFTGK  21 DNA seq id Accessio uence: 37 11   AGGACGCGAG GGATGGTTTT CGTTCAAGAT AAGATACTGA CCCCTCCTC CTTCAAACGAT TCAAACCCAT CGAATGCAC AAACCCTGCA TCACCTGCCTTC TTGCTGTCT TTGCTGTCT TGGTGCCTTC CAGATTTTC CACCCCAGCC CAAACGATCTCC CAAACGATCTCC CAAACGATCTCC CAAACCAGCC CAAACGATCTCC CACCATTTTCC CCCCAGTCT CCCCAGTCTCC CACACCTAGTCTCC CACACCAGCCC CAAACGATCTCC CCCCAGTCTCC CCCCATTTTCC CCCCAGTCTCC CCCCATTTTCC CCCCATTTCC CCCCATTTCC CCCCATTTTCC CCCCATTTCC CCCCATTCC CCCCATTTCC CCCCCATTTCC CCCCATTTCC CCCCATTTCC CCCCATTTCC CCCCATTCC CCCCATTTCC CCCCATTTCC CCCCATTTCC CCCCATTTCC CCCCATTTCC CCCCATTCC CCCCATTTCC	QMMALTFITY WIALYKMGGL GYPAVVTII MFIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS UENCE #: NM_005 3117 21   CGGCAGGTGT CTCTGTCAGG ATTCCTTGTC TAATTCCAGT CAATCAGGTT AACAGAAAAA CCTAACTGGA CATGTTCAA CTTAACTGGA AACCTAAGT TTGTACATT GGAAACAGTA CTTACTGGACC TTCCTCCCACC TTCCCCTATG CTTCCCCCACC CTTCCCCACC	IGGGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR  756.1  31    GCACAGAGGT CAGTGTGGCC ATCATTTGTC CAGACACACA ACTANANTCA IGCAATTTGTC CAGACTTACC CAGACTTACC CAGACTTACC CAGAGGTTTGC CACATGGCC CTTTCCCAGG CCACATGCC CTTTCCCAGG CCACATGCC CACATGCC CACATGCC CACAATGTC CACAATGTC CACAATGTC CACAACCC CCCCAAACCC CGTGTCTCCCC CGTGTCTCCCCC CGTGTCTCCCCC CGTGTCTCCCCC CGTGTCTCCCCCC CGTGTCTCCCCC	SVTLVTYIAP FILVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHP  41   TCTCCACTITI ATGTTGGCAG TTCATGTCGT TACGTCGTAA GCCTCAATGA CATCTATTTG TAAGTGAATT TTATAATGTAG GAAAGCTTCA GAAAGCTTCA CACTGTTTCC TCCCCAAAGC CCTCTCCAAT GCCCTCCAATG CCTCTCCAAT GCCTTCCAAT GCCCTGCCAT ATGTCTCCGG CTTCTCCAAT GCCCTGCCAT TATGTCTCCGG CTGCCAATGT	LEAFHMYLAL PDDFCWINNN SIAGLIFILIG LCCGKLRLAE SGNGNASTER IEQM  51   GTTTTCTGAA AACTGAAGAA TCTGGTAACAA ATTATCTGTT TGTTACTTTA AACCTTCAAT AAACGTCA TCCCCAGAAT AAAAGGCTCA TGCTACAGCA AATGAATGCA CTGCTGTGTGTGTGTGTGCTGT TCCAGCCAA AATGAATGCA TCCCAGCAGT TAGGGGAGATT TGACATGCCC CACCCCACCT CAACACTACC	720 780 900 960 60 120 180 240 360 420 480 600 660 720 780 840 960 1020 1020
60 65 70 75 80	SHLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATIN NGVSFSVQNG Seq ID NO: Nucleic Ac. Coding seq I AGCCAGCOCG CTCGCGGTCA GTTTTACTGA AGCTTACTCC GCTTCAGGCG GCATTTTTA CAACATATAA GAGCCCAAA TCTGTCAGCAG CAGGATCCCAC CAGGATCCCCAC CCATCCCCCCCCCC	DLSRTSVLPA LINIVFLIDS YILKPCIVGW FCVIFILINVS GPVNVTFMYL GLKKQTVNGG DVCLHDFTGK 21 DNA seq id Accession lence: 37 11   AGGACGCGAG GGATGGTTTT CGTTCAAGAT AAGATACTGA CCCCCTCTC CTTCAAACGA TCAAACCCTGCA GCACATTAAA GAGGTGAGAT CGAATGGCAC TGAACCCTGCA GCACATTAAC CGATTTTT TACCCTGCCC TTGTCTTGTT TGGTGCCTCG CAGAGTTATTC CACCCCAGCC AAACGATTTTC CCTCTCATTTTC CTCTCATTTTC CCTCTCTCATTTTC CCCCCCAGCC CCCCCAGACC CCCCCCAGCC CCCCCCCAGCC CCCCCCAGCC CCCCCCCAGCC CCCCCCCC	QMMALTFITY WIALLYKMGEI GVPAVVVTII MFIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS  UENCE #: NM_005 3117 21   CGGCAGGTGT CTCTGTCAGG ATTCCTTGTC TAATTCCAGT CAATGAGGTT AACAGAAAAA CAGAAAAAA CAGAAAAAA CAGAAAAAA CTTAACTGGA ATCCTTAGG TTCCTCAGG TTCCTCCCCA TGCTGACCAT GGCACCATG GGCACCTGT ACCTTGTCCCCA TTCCCCTATG CTTCCCCCACC TTCCCCCACC AGACATCTTCCCCACC AGACATCTCCCCACC AGACATCTCCCCACC AGACATCTCCCCACC AGACATCTCCCCACC AGACATCTCCCCACC AGACATCTCTCCCACC	IGGGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR  756.1  31   GCACAGAGGT CAGTGTGGCC ATCATTTGTC TTGTCACCAC GGAACAACAA ACTAAAATCA TGCAATTTGTC GAGACTTACT ACAATAAAAC AGAATAACA AGAATAACA CACAGAGGT CCACTGGCCC CACAGTGGCC CCCCAAACCCC CGTGTCTCC CGTGTCTCC CATAGCTTCCAC CGTGTCTCC CATAGCTTCCAC CCCAAACCCC CAACACCACCC	SVTLVTYIAP FLLVSFTMME GSYGKPPMGS GRKTSIQDLR ENVRKQWRRY LVNNDCSVHA  41    TCTCCACTTT ATGTTGGCAG TTCATGTGGT CACCTGCTAA GCCTCAATGA CATCTATTTG AAAGCACTGT TAATGTAAA CATCTATTG CACATGTAATTTG CAATGGAACA GAAAGCTTCA CACCATTTCC CACCTGCCAAT GCCCCAATG CCTCCCAATG GCCTTCCCAAT GCCCTGCCAT ATGTCTCCGG CTGCCAT CTGCGAATGT CTGCGGAATGT GTATTTCTGA	LEAFHMYLAL PDDFCWINNN SIAGLIFILIG LCCGKLRLAE SGNGNASTER IEQM  51   GTTTTCTGAA AACTGAAGAA TCTGGTAACAA TCTGGTAACTAA TCAATGACTCA TCCCCAGAAT AAACGCTCA TCCCAGCAA AATGAATGCA TCCCGGCGAA TCCCGCGCGTG TTCCAGCCAA TACCTCTTTT AGGGGAGATT TGACATGCCC CACCCCACCT CAACCTACCC CACCCCACCT CACACTACC TCTTGAGAAC	720 780 900 960 60 120 180 240 300 420 420 480 660 720 900 1020 1080 1180 1200
60 65 70 75	SHLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATIN NGVSFSVQNG Seq ID NO: Nucleic Ac. Coding seq I AGCCAGCOCG CTCGCGGTCA GTTTTACTGA AGCTTACTCC GCTTCAGGCG GCATTTTTA CAACATATAA GAGCCCAAA TCTGTCAGCAG CAGGATCCCAC CAGGATCCCCAC CCATCCCCCCCCCC	DLSRTSVLPA LINIVFLIDS YILKPCIVGW FCVIFILINVS GPVNVTFMYL GLKKQTVNGG DVCLHDFTGK 21 DNA seq id Accession lence: 37 11   AGGACGCGAG GGATGGTTTT CGTTCAAGAT AAGATACTGA CCCCCTCTC CTTCAAACGA TCAAACCCTGCA GCACATTAAA GAGGTGAGAT CGAATGGCAC TGAACCCTGCA GCACATTAAC CGATTTTT TACCCTGCCC TTGTCTTGTT TGGTGCCTCG CAGAGTTATTC CACCCCAGCC AAACGATTTTC CCTCTCATTTTC CTCTCATTTTC CCTCTCTCATTTTC CCCCCCAGCC CCCCCAGACC CCCCCCAGCC CCCCCCCAGCC CCCCCCAGCC CCCCCCCAGCC CCCCCCCC	QMMALTFITY WIALLYKMGEI GVPAVVVTII MFIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS  UENCE #: NM_005 3117 21   CGGCAGGTGT CTCTGTCAGG ATTCCTTGTC TAATTCCAGT CAATGAGGTT AACAGAAAAA CAGAAAAAA CAGAAAAAA CAGAAAAAA CTTAACTGGA ATCCTTAGG TTCCTCAGG TTCCTCCCCA TGCTGACCAT GGCACCATG GGCACCTGT ACCTTGTCCCCA TTCCCCTATG CTTCCCCCACC TTCCCCCACC AGACATCTTCCCCACC AGACATCTCCCCACC AGACATCTCCCCACC AGACATCTCCCCACC AGACATCTCCCCACC AGACATCTCCCCACC AGACATCTCTCCCACC	IGGGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR  756.1  31   GCACAGAGGT CAGTGTGGCC ATCATTTGTC TTGTCACCAC GGAACAACAA ACTAAAATCA TGCAATTTGTC GAGACTTACT ACAATAAAAC AGAATAACA AGAATAACA CACAGAGGT CCACTGGCCC CACAGTGGCC CCCCAAACCCC CGTGTCTCC CGTGTCTCC CATAGCTTCCAC CGTGTCTCC CATAGCTTCCAC CCCAAACCCC CAACACCACCC	SVTLVTYIAP FLLVSFTMME GSYGKPPMGS GRKTSIQDLR ENVRKQWRRY LVNNDCSVHA  41    TCTCCACTTT ATGTTGGCAG TTCATGTGGT CACCTGCTAA GCCTCAATGA CATCTATTTG AAAGCACTGT TAATGTAAA CATCTATTG CACATGTAATTTG CAATGGAACA GAAAGCTTCA CACCATTTCC CACCTGCCAAT GCCCCAATG CCTCCCAATG GCCTTCCCAAT GCCCTGCCAT ATGTCTCCGG CTGCCAT CTGCGAATGT CTGCGGAATGT GTATTTCTGA	LEAFHMYLAL PDDFCWINNN SIAGLIFILIG LCCGKLRLAE SGNGNASTER IEQM  51   GTTTTCTGAA AACTGAAGAA TCTGGTAACAA ATTATCTGTT TGTTACTTTA AACCTTCAAT AAACGTCA TCCCCAGAAT AAAAGGCTCA TGCTACAGCA AATGAATGCA CTGCTGTGTGTGTGTGTGCTGT TCCAGCCAA AATGAATGCA TCCCAGCAGT TAGCATGCCC CACCCCACCT CAACACTACC	720 780 900 960 60 120 180 240 300 420 420 480 660 720 900 1020 1080 1180 1200

	CABATCATCA	A COTA A COTO A G	CAGACTCCTT	CATTOCCCC	CHGACATGCT	GGCCCCTTTTTG	1320
			AGTGGATGAC				1380
			TTCTTTGGCT				1440
			GGCCCAAGAC				1500
5			TGGCACAATT				1560
,			AGCTTCCAGG				1620
			GGAGAACCTC				1680
			GAACTTGACA				1740
	NACCOCACCC	ACCATCACTT	AACAGTGAGA	TETETATTT	CCCACTTCCC	CAGAAATGGT	1800
10	CCCACACCAC	AGGAIGAGI I	CAATGGCTGC	TCTCTCDAAG	ACAGGAGATT	GAATGAAACC	1860
10	GGCHOHGGAG	GC1GG1CAGA	AACAAGCTTC	CCCCITCAAAG	TEGACCTATC	TACCACATCT	1920
			GGCTCTGACG				1980
	GIGCIGCCIG	CICAAAIGAI	TCTTGTAACC	TACATACOTT	TTCDARACAT	CCCCACCCAT	2040
	TCAATTITIC	TGTCAGTGAC	CCAGCTGTGT	TACATAGCTT	TTOTOTOTO	CCGCAGGGAI	2100
15	TACCCTTCCA	WWICCICKI	TCTGTATAAG	ATTOCARCOC	TICIOCIONA	ACTICICATE	2160
13	CICCIGGACI	CGIGGATIGC	GGTCTCATTC	ACATOCATOCC	CCCTAGAACC	ATTCCATATC	2220
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			AGCTGTGGTT				2340
			TGGGAAATTC				2400
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	CIGAACGICA	GCATGITCAT	TGTGGTCCTG	GIICAGCICI	GICGAMIIAM	MANGANGANG	2580
			AACCAGTATT				
			GGGCTTTGCC				2640 2700
25	TTCATGTATC	TGTTTGCCAT	CTTTAATACC	TTACAAGGAT	TTTTCATATT	CATCITITAC	
25	TGTGTGGCCA	AAGAAAATGT	CAGGAAGCAA	TGGAGGCGGT	ATCTTTGTTG	TGGAAAGTTA	2760
	CGGCTGGCTG	AAAATTCTGA	CTGGAGTAAA	ACTGCTACTA	ATGGTTTAAA	GAAGCAGACI	2820
			CTCTTCAAAT				2880
	TCCACCACAC	TGCTAGTGAA	TAATGATTGC	TCAGTACACG	CAAGCGGGAA	TOGAMATGCT	2940 3000
30	TCTACAGAGA	GGAATGGGGT	CTCTTTTAGT	DAGGAATG	CAUATGIGIG	CANACCOCCE	3060
30	TTCACTGGAA	AACAGCACAT	GTTTAACGAG	AAGGAAGATT	CCTGCAATGG	A MODEL COLLEGE	
			AAAGCGGGGA				3120
	CTTTCTTCTA	AAATCAAAGC	ATGATGCTTG	ACAGTGTGAA	ATGTCCAATT	TTACCTTTTA	3180
			AATCAACTCA				3240
25			TTATTATTAC				3300
35	TTTAGACATT	TCTGATTTGG	TTTCTTATCT	TTCATTTTAT	AAGAAGGTTG	GTTTTAAACA	3360
	ATACACTAAG	AATGACTCCT	ATAAAGAAAA	CAAAAAAAGG	TAGTGAACIT	TCAGCTACCT	3420
	TTTAAAGAGG	CTAAGTTATC	TTTGATAACA	TCATATAAAG	CAACTGTTGA	CITCAGCCIG	3480
			TGCCTTTGTT				3540
40			ATTTTTTTGT				3600
40			TGTCTCACGT				3660
			GAGATGATAT				3720
			CCAGACTGAG				3780
			AGTTAGGAAA				3840
4.5	TGGGTCATGG	TTTGACAAAC	AGAGTGAGAG	ACCATATTTT	AGCCCCACTC	ACCCTCTTGG	3900
45	GTGCACGACC	TGTACAGCCA	AACACAGCAT	CCAATATGAA	TACCCATCCC	CTGACCGCAT	3960
	CCCCAGTAGT	CAGATTATAG	AATCTGCACC	AAGATGTTTA	GCTTTATACC	TTGGCCACAG	4020
	AGAGGGATGA	ACTGTCATCC	AGACCATGTG	TCAGGAAAAT	TGTGAACGTA	GATGAGGTAC	4080
	ATACACTGCC	GCTTCTCAAA	TCCCCAGAGC	CTTTAGGAAC	AGGAGAGTAG	ACTAGGATTC	4140
50	CTTCTCTTAA	AAAGGTACAT	ATATATGGAA	AAAAATCATA	TTGCCGTTCT	TTAAAAGGCA	4200
50	ACTGCATGGT	ACATTGTTGA	TTGTTATGAC	TGGTACACTC	TGGCCCAGCC	AGAGCTATAA	4260
	TTGTTTTTTA	AATGTGTCTT	GAAGAATGCA	CAGTGACAAG	GGGAGTAGCT	ATTGGGAACA	4320
	GGGAACTGTC	CTACACTGCT	ATTGTTGCTA	CATGTATCGA	GCCTTGATTG	CTCCTAGTTA	4380
	TATACAGGGT	CTATCTTGCT	TCCTACCTAC	ATCTGCTTGA	GCAGTGCCTC	AAGTACATCC	4440
c c			CCCTTTTAGT				4500
55			CTCAGACTAA				4560
			TTCTTTTCTG			TTTATATGTT	4620
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15	PSSNEVETTS	LNDVTLSLLP	SNETGVKPQR	NICNLSSICN	DSAFFRGEIM	FQYDKESTVP	120
65 ·	QNQHITNGTL	TGVLSLSELK	RSELNKTLQT	LSETYFIMCA	TAEAQSTLNC	TPTIKLNNTM	180
			CCSVRIPCPS				240
			SFAEPPDYSP				300
			PPPVKASFSS				360
<b>7</b> 0			AGEMINOVSR				420
70			SSFNTTTFVA				480
	NLPAHDMELA	SRVOFNFFET	PALFQDPSLE	NLSLISYVIS	SSVANLTVRN	LTRNVTVTLK	540
						SFGVLLDLSR	600
	TSVLPAQMMA	LTFITYIGCG	LSSIFLSVTL	VTYLAFEKIR	RDYPSKILIQ	LCAALLLLINL	660
75	VFLLDSWIAL	YKMQGLCISV	AVFLHYPLLV	SPTWMGLEAF	HMYLALVKVF	NTYIRKYILK	720
75	FCIVGWGVPA	VVVTIILTIS	PDNYGLGSYG	KPPNGSPDDF	CWINNNAVFY	ITVVGYFCVI	780
						PAFFAWGPVN	840
						SKTATNGLKK	900
						PSVQNGDVCL	960
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	GAGACATTCC	TCAATTGCTT	AGACATATTC	TGAGCCTACA	GCAGAGGAAC	CTCCAGTCTC	60
	AGCACCATGA	ATCAAACTGC	GATTCTGATT	TGCTGCCTTA	TCTTTCTGAC	TCTAAGTGGC	120
	ATTCARGGAG	TACTOTOTOTO	TAGAACCGTA	CGCTGTACCT	CCATCACCAT	TAGTAATCAA	180
	CONCERN A TO		202222222000	GAAATTATTC	OTTO DE COCA	V-CANALACACACA	240
5	CCIGITAAIC	CAAGGICTTT	AGMAMACII	GARATIATIC	CIGCAAGCCA	ATTTTOTCO	
5	CGTGTTGAGA	TCATTGCTAC	AATGAAAAAG	AAGGGTGAGA	AGAGATGTCT	GAATCCAGAA	300
	TCGAAGGCCA	TCAAGAATTT	ACTGAAAGCA	GTTAGCAAGG	Aaatgtctaa	AAGATCTCCT	360
	TAAAACCAGA	GGGGAGCAAA	ATCGATGCAG	TGCTTCCAAG	GATGGACCAC	ACAGAGGCTG	420
				ATGTCAAGCC			480
				CCAAATCAGC			540
10	GTTACACTAA	AAGGTGACCA	AIGAIGGICA	CCAAAICAGC	IGCIACIACI	CCIGIAGGAA	
10	GGTTAATGTT	CATCATCCTA	AGCTATTCAG	TAATAACTCT	ACCCTGGCAC	TATAATGTAA	600
	GCTCTACTGA	GGTGCTATGT	TCTTAGTGGA	TGTTCTGACC	CTGCTTCAAA	TATTTCCCTC	660
	ACCTTTCCCA	TCTTCCAAGG	GTACTAAGGA	ATCTTTCTGC	TTTGGGGTTT	ATCAGAATTC	720
				ATCAAATCTG			780
1.5				AGGGGCCCAA			840
15				GAAATATCTG			900
	CTTATTTAAT	GAAAGACTGT	ACAAAGTATA	AGTCTTAGAT	GTATATATTT	CCTATATTGT	960
				AGTACTATGT			1020
				CATGTTACAT			1080
					MONIMANIG	IGCIGNAIGG	1080
00	TTTTCAAATA	AAAATGAGGT	ACTOTOCTGG	AAATATTAAG			
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25				TCISISNQPV	NPRSLEKLEI	IPASQFCPRV	60
	EIIATMKKKG	EKRCLNPESK	AIKNLLKAVS	KEMSKRSP			
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20			1 #: XM_0305	22			
30	Coding sequ	lence: 111	119				
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	A THOU A COCOCO	COCNOCCCO	occorrector.	AGOGGCTGCC	TOCOCOACTAT	GCAGCTGAAG	60
25				TCGCTGGAAA			120
35	GAGGAGTTTT	ATGGATTACT	ACAACATGTT	CATAAGATCC	CCAATGTTGA	CGTTTTGGTA	180
	GGCTATGCAG	ACATCCATGG	AGACTTACTA	CCTATAAATA	ATGATGATAA	TTATCACAAA	240
				ATATTTATAC			300
							360
	TACAGTGCCT	TIGGTACAGA	CACGCTAATA	AAGAAGAAGA	AIGITITAAC	CAACGIAIIG	
40				ATAGTCATTA			420
40	CCTGTGTCTT	CTATTATAGA	CGTGGATATT	CTCCCAGAAA	CGCATCGTAG	GGTACGTCTT	480
				TTCTACATCC			540
	CENTOCOCOC	A THE COMPACA	AAACCTTCCA	GGGATCTTTA	TATCCACCCT	TCTCCCACCA	600
	GIMACACCAC	AIGGCIIAGA	AAAGGIICCA	GGGAICIIIA	INICCAGGCI	101CCCNOCA	
				GTTAATGATG			660
	ATAGAAGTTT	CAGGGAAGAG	CCTTGATCAA	GTAACAGACA	TGATGATTGC	AAATAGCCGT	720
45	AACCTCATCA	TAACAGTGAG	ACCGGCAAAC	CAGAGGAATA	ATGTTGTGAG	GAACAGTCGG	780
				AACAGCCTTC			840
							900
				AGCGAAGAAG			
				GTTCCTAATA			960
	ACACAGATAG	AGCTAAGCTT	TGAGTCTGGA	CAGAATGGCT	TTATTCCCTC	TAATGAAGTG	1020
50	AGCTTAGCAG	CCATAGCAAG	CAGCTCAAAC	ACGGAATTTG	AAACACATGC	TCCAGATCAA	1080
			AACAATCATA				
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				SLERSKPGKF			
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<b>CO</b>				LPETHRRVRL			180
60	VTPHGLEKVP	GIFISRLVPG	GLAOSTGLLA	VNDEVLEVNG	IEVSGKSLDQ	VTDMMIANSR	240
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70	1	1	I	I	I	1	
70						GCTGGCGACC	60
	GGGGGCAGCT	CTCCCAGGTC	TGGTGTGTTG	CTGAGGGGCT	GCCCCACACA	CTGTCATTGC	120
						CTCGGAGCTG	
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75						TGCGGGAAAC	
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85	ACTGGAACTC	CANACCTGG	GAGTCTGACT	TTAACTGGAG	CACAGATCTO	ATCTCTTCCT	960

	CAAACCGTCT	GCAATCAGTT	ACCTAATCTC	CAAGTGCTAG	ATCTGTCTTA	CAACCTATTA	1020
	GAAGATTTAC	CCAGTTTTTC	AGTCTGCCAA	AAGCTTCAGA	AAATTGACCT	AAGACATAAT	1080
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_	TTGGCTTGGA	ACAAAATTGC	TATTATTCAC	CCCAATGCAT	TTTCCACTTT	GCCATCCCTA	
5	ATAAAGCTGG	ACCTATOGTO	CAACCTCCTG	TCGTCTTTTC	CTATAACTGG	GTTACATGGT	1260`
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	TTTCCAGAAC	TCAAGGITAT	AGAAATGCCT	TATGUTTACC	AGIGCIGIGC	ATTIGGAGIG	1380
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10	TTCCTGCTTG	ACTTTGAGGA	AGACCTGAAA	GCCCTTCATT	CAGTGCAGTG	TTCACCTTCC	1560
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	TGGACCATAG	CAGTTCIGGC	ACTTACTTGT	AATGCTTTGG	IGHCIICAAC	AGIIII CAGA	
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15	CICACGGAG	TCTCCAGTGC	C010C100C1	0010100010	* BOBON GEOGRA		1860
15	GCACGACATG	GTGCCTGGTG	GGAGAATGGG	GTIGGTIGCC	AIGICATIGG	TITITIGICC	
	ATTTTTGCTT	CAGAATCATC	TGTTTTCCTG	CTTACTCTGG	CAGCCCTGGA	GCGTGGGTTC	1920
	monomon a a a m	Ammomoca	ATTTGAAACG	AAACCTCCAT	بلمان لا بالمان المانية	CABACTBATC	1980
	ATTTTGCTCT	GTGCCCTGCT	GGCCTTGACC	ATGGCCGCAG	TTCCCCTGCT	GGGTGGCAGC	2040
	BACTATECES	CCTCCCCTCT	CTGCCTGCCT	TTGCCTTTTG	GGGAGCCCAG	CACCATGGGC	2100
20		OTTO COLUMN	GCTCAATTCC	COMMODITATION OF	TOTATOTOTO	CATTCCCTAC	2160
20	TACATGGTCG	CTCTCATCTT	GCTCAATTCC	CITIGCTICC	ICAIGAIGAC	CHIIGCCIMC	
	ACCAAGCTCT	ACTGCAATTT	GGACAAGGGA	GACCTGGAGA	ATATTTGGGA	CIGCICTATG	2220
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	TTGTCCTTCT	CCTCTTTAAT	AAACCTTACA	TTTATCAGTC	CIGAAGIAAI	IMMGITIMIC	
	CTTCTCGTGG	TAGTCCCACT	TCCTGCATGT	CTCAATCCCC	TTCTCTACAT	CTTGTTCAAT	2400
25	COMOR CHIMER	ACCACCATOT	GGTGAGCCTG	ACANACCAAA	CCLFCACALCAC	GACAAGATCA	2460
20	CCICACITIA	MUUMUUMICI	COLONGECTIO			OMORON CEC	
	AAACACCCAA	GCTTGATGTC	AATTAACTCT	GATGATGTCG	AAAAACAGTC	CIGIGACTCA	2520
	ACTCA ACCCT	TEGTAACCTT	TACCAGCTCC	AGCATCACTT	ATGACCTGCC	TCCCAGTTCC	2580
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			AGTGACTGAG	MOCIOCIAIC			
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35	MDTSRLGVLL	SLPVLLOLAT	GGSSPRSGVL	LRGCPTHCHC	EPDGRMLLRV	DCSDLGLSEL	60
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	PONDOVETOI	TOTOLEMATON	DUCKEBESEK	CLEMBERS	THE PART OF T	DATA E MISTINGS	
	LQNNQLRHVP	TEALQNLRSL	QSLRLDANHI	SYVPPSCFSG	PHSPKHFMPD	DNALTEIPVQ	180
	AFRSLSALOA	MTLALNKIHH	IPDYAFGNLS	SLVVLHLHNN	RIHSLGKKCF	DGLHSLETLD	240
	TANDAU DEED	TO TOTT CALLY	ELHFYDNPIQ	EVED CA FOHT.	DELETITING	ASOITEFPDL	300
40	PHINNPDELL	INTKIDONDY	POULIDIALIO	FVGRSAFQIID			
40	TGTANLESLT	LTGAQISSLP	QTVCNQLPNL	QVLDLSYNLL	EDLPSFSVCQ	KTÖKTDPKHM	360
	ETYETKVDTF	OOLLSLRSLN	LAWNKIAIIH	PNAFSTLPSL	IKLDLSSNLL	SSFPITGLHG	420
		AT OOT TOOM	PPELKVIEMP	VAVOCCARCU	CENTAVETONO	WINCOMESMD	480
	LINDRUTGINH	ALOSE122EM	PERTINATEME	INICCALGA	CEMMINISMS	MATOCATO COLOR	
	DLHKKDAGMF	QAQDERDLED	FLLDFEEDLK	ALHSVQCSPS	PGPFKPCEHL	LDGWLIRIGV	540
	WTTAMEAT.TC	MALATSTVER	SPLYISPIKL	I.TGVTAAVNM	LTGVSSAVLA	GVDAFTFGSF	600
45							660
43			IFASESSVFL				
	TLLCALLALT	MAAVPLLGGS	KYGASPLCLP	LPFGEPSTMG	YMVALILLNS	LCFLMMTIAY	720
			VKHIALLLFT				780
	LLVVVPLPAC	LNPLLYILFN	PHFKEDLVSL	RKQTYVWTRS	KHPSLMSINS	DDAEKOSCDS	840
	TOALVTFTSS	SITYDLPPSS	VPSPAYPVTE	SCHLSSVAFV	PCL		
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55	Coding sequence of the control of th	uence: 135.  11	.1472 21   GTCAGTGCTG CGCACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG	CTCGGGGGCT GCGCAACCTG AGGACTATGA GGAGGAAGAG AAGCTGAGAA	TCTCCATCCA CGTGAGGCAG AGTGTTGTAC TGATGGCAAG ACAGATGCTT	GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTGAAG	120 180 240 300
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	Coding sequence of the control of th	uence: 135. 11	.1472 21 GTCAGTGCTG GCACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA	CTCGGGGGCT GCGCAACCTG AGGACTATGA GGAGGAAGAG AAGCTGAGAA ACATCGTTCG	TCTCCATCCA CGTGAGGCAG AGTGTTGTAC TGATGGCAAG ACAGATGCTT TTACTATGAT	GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTGAAG CGGATTATTG	120 180 240 300 360
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60	Coding sequence of the control of th	uence: 135.  11	.1472 21 GTCAGTGCTG GGCACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAA AACATCCAA AACATTCTAA AAGGAAAGGC GCCCTGAAGG	CTCGGGGGCT GCGCAACCTG GCGCACTATGA GGAGGAAGAG AAGCTGAGAA ACATCGTTCG TGGAATATTG AATACTTAGA AATGCCACAG	TCTCCATCCA CCTGAGGCAG CGTGTTGTAC TCATGGCAAG ACAGATGCTT TTACTATGAT TGAAGGAGGTT TGAAGAGGTT ACGAAGTGAT	GGTCCCTGGA GGGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTGAAG CGGATTATTG GATCTGCCAG GGTCTTCCAG GGTGGTCATA	120 180 240 300 360 420 480 540
	Coding sequence of the control of th	uence: 135.  11	.1472 21     GTCAGTGCTG GGCACTTGGC TCCCGGGCTG CAGAAGATC TCCATGACAG AAACATCCAA TACATTGTAA AAGGAAAAGGC GCCCTGAAGG AAACCAGCCA	CTCGGGGGCT GCGCAACCTG AGGACTATGA GGAGGAAGAG AACCTGAGAA ACATCGTTCG TGGAATATTG AATACTTAGA AATGCCACAG ATGTTTTCCT	TCTCCATCCA CCTGAGGCAG AGTGTTGTAC TCATGGCAAG ACAGATGCTT TTACTATGAT TGAAGGAGGG TGAAGAGTTT ACGAAGTGAT GGATGCCAAG	GGTCCCTGGA GGCGACTCTG ACCATTGGCA ATATTAGFTT GTTTCTGAAG CGGATTATTG GATCTGGCTA GTTCTTCGAG GGTGGTCATA CAAAACGTCA	120 180 240 300 360 420 480 540
60	Coding sequilibrium sequilibriu	uence: 135.  11  GGGGTGGCGG CCTGGAGCTC GGCCATGCCT CGGCCGCTGC TGACTATGGC TGACTATGGC TACAACACTG AAAGGGAACC GTTGACTCTT CCTTTGGGCTA	.1472 21 GTCAGTGCTG GGCACTTGGC TCCCGGGCTG TCCATGACAG AAACATCCAAA TACATTGTAA AAGGAAAGGC GCCCTGAAGG AAACCAGCA GCTAGAGATAT	CTCGGGGGCT GCGCAACCTG AGGACTATGA GGAGGAAGAG AACATCGTTCG TGGAATATTG AATACTTAGA AATGCCACAG ATGTTTCCT TAAACCATGA	TCTCCATCCA CGTGAGGCAG AGTGTTGTAC TGATGGCAAG ACAGATGCTT TTACTATGAT TGAAGGAGGG TGAAGAGTGTA ACGAAGTGAAT GGATGGCAAG CACGAGTTTT	GGTCCCTGGA GGGGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTGAAG CGGATTATTG GATCTGGCTA GATCTTCGAG GGTGGTCATA CAAAACGTCA GCAAAACAT	120 180 240 300 360 420 480 540 600 660
60	Coding sequilibrium sequilibriu	uence: 135.  11  GGGGTGGCGG CCTGGAGCTC GGCCATGCCT CGGCCGCTGC TGACTATGGC TGACTATGGC TACAACACTG AAAGGGAACC GTTGACTCTT CCTTTGGGCTA	.1472 21 GTCAGTGCTG GGCACTTGGC TCCCGGGCTG TCCATGACAG AAACATCCAAA TACATTGTAA AAGGAAAGGC GCCCTGAAGG AAACCAGCA GCTAGAGATAT	CTCGGGGGCT GCGCAACCTG AGGACTATGA GGAGGAAGAG AACATCGTTCG TGGAATATTG AATACTTAGA AATGCCACAG ATGTTTCCT TAAACCATGA	TCTCCATCCA CGTGAGGCAG AGTGTTGTAC TGATGGCAAG ACAGATGCTT TTACTATGAT TGAAGGAGGG TGAAGAGTGTA ACGAAGTGAAT GGATGGCAAG CACGAGTTTT	GGTCCCTGGA GGGGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTGAAG CGGATTATTG GATCTGGCTA GATCTTCGAG GGTGGTCATA CAAAACGTCA GCAAAACAT	120 180 240 300 360 420 480 540
60	Coding sequence of the control of th	uence: 135.  11  GGGGTGGCGG CCTGGAGCTC GGCCATGCCT TGACTATGGC TGACTATGGC TCGTGAACTG AAAGGGAACCG GTTGACTCTG TCGGGATCTT CCTTTGGGCATCTT	.1472 21 GTCAGTGCTG GGCACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA TACATTGTAA AAGGAAAGGC GCCCTGAAGG AAACACAGCA GCTAGAATAT ATGTCTCCTG	CTCGGGGGCT GCGCAACCTG GCGCAACCTG AGGACTATGA GGAGGAAGAG AAGCTGAGAA ACATCGTTCG AATACTTAGA AATGCCACAG ATGTTTTCCT TAAACCATGA AACAAATGAA	TCTCCATCCA CCTGAGGCAG ACTGTTGTAC TGATGGCAAG ACAGATGCTT TTACTATGAT TGAAGAGGG TGAAGAGTTT ACGAAGTGAT CCACAGGTTTT TCGCATGTCC	GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTGAAG CGGATTATTG GATCTTGGCTA GTTCTTCGAG GGTGGTCATA CAAAAACGTCA GCAAAAACAT TACAATGAGA	120 180 240 300 360 420 480 540 600 660 720
60	Coding sequilibrium sequilibriu	uence: 135.  11	.1472 21	CTCGGGGGCT GCGCAACCTG AGGACTATGA GGAGGAAGAG AACCTGAGA ACATCGTTCG TGGAATATTG AATACTTAGA AATGCCACAG ATGTTTCCT TAAACCATGA AACAAATGAA TGTATGAGTT	TCTCCATCCA CCTCAGGCAG ACTGTTGTAC TGATGCCAG ACAGATGCT TTACTATGAT TGAAGGAGGG TGAAGAGTTT ACGAAGTGAT GGATGCCAAG CACGAGTTTT TCGCATGTCC ATGTGCATTA	GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTCAGAG GGTGTCATTCTCGAG GGTGGTCATA CAAAACGTCA GCAAAAACAT TACAATGAGA	120 180 240 300 360 420 480 540 600 660 720 780
60	Coding sequilibrium control co	uence: 135.  11  GGGGTGGCGG CCTGGAGCTC CGGCCGCTGC TGACTATGGC TGACAACACTG AAAGGGAACCC GTTGACTCTC CTTTGGGCTAT CTTTGGGCTA ACCTTATTAC ACCTTATTAC TTGGCCAAA	1472 21 GTCAGTGCTG GGCACTTGGC TCCAGGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA AAGGAAAGGC GCCCTGAAGG AAACCAGCA GCTAGAATAT ATGCTTCCTG GGCTGCTTGC GAACTCGCTG	CTCGGGGGCT CGCAACCTG AGGACTATGA GGAGGAAGAG AAGCTGAGAA ACATCGTTCG TATACTTAGA AATGCCACAG ATGTTTTCCT TAAACCATGA ACAAATGAA TGTATCAGTT GGAAAATCAG	TCTCCATCCA CGTGAGGCAG AGTGTTGTAC TGATGGCAAG ACAGATGCTT TTACTATGAT TGAAGGAGGG TGAAGAGTTT ACGAAGTGAT TGGATGGCAAG CACGAGTTTT TCGCATGCCAAA ATGTGCATAT AGAAGGCAAA	GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTCAGAG GGAGTTATG GATCTTGGCTA GTTCTTCGAG GGTGGTCAT CAAAACGTCA GCAAAAACAT TACAATGAGA ATGCCTCCAT	120 180 240 300 360 420 480 540 600 660 720 780 840
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60 65 70 75	Coding sequilibrium control co	uence: 135.  11  GGGGTGGCGG CCTGGAGCTC GGCCATGCCT CGGCCATGCCT CGGCATGCCT TGACTATGGC TACACACTG AAAGGGAACC GTTGACTCT CCTTTGGGCTA CCTTTGTGATCT TACGCAGAAA TTACTCTGA ACCATGAAACA CTTCTAAAGCA ACCTTCTAAAGCA ACCTTCTAAAGCA ACCTTCTAAAGCA ACTTACAGAAA CAGCACCTAAAGCA ACTAGCAGAAA ATTACAGAAA ATTCTGAAAGAA ATTCTGAAAGCT ACGAACGAAAA ATTCTGAAAGCT CGGAACGAAAA ATTCTGAAAGCT CTCTCAAAGCT CTCTCACAGCT CTCTCCAAGCT CTCTCCAAGCT CTCTCCAAGCT CTCCCAAGCT CTCCCCAAGCT CTCCCCAAGCT CTCCCCAAC CTCTCTCAAAGCT CTCTCCCAAGCT CTCTCCCAAGCT CTCCCCAAC CTCTCTCACAC CTCTCTCACAC CTCTCTCT	1472 21 21 GTCAGTGCTG GGCACTTGGC TCCAGGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA TACATTGTAA AAGGAAAGGC GCCCTGAAGG AAACCAGCAA GGTAGAATAT TATGTTCCTG GAATTGAATAT GAAGAAAATTGAATGAATGAATGAA	CTCGGGGGCT GCGCAACCTG AGGACTATGA GGAGGAAGAG AAGCTGAGAA ACATCGTTCG TGGAATATTG AATACTTAGA AATGCCACAG AACAAATGAA ACAACATGAA ACAACATGA AACAAATGAA TGTATAGATTAC TTGAGAACCA GAGGGCAACA GATTGGGACAC TGGAACTGAAC TGAACCAGA TGCAAGTAA CTAGGCAGA TTGGCAAGTAA CTAGTCGGGGC TTGAGTCCAA	TCTCCATCCA CGTGAGGCAG AGTGTTGTAC TGATGGCAAG ACACATGCTT TTACTATGAT TGAAGGAGGG TGAAGAGTTT ACGAAGTGAT ACGAAGTGAT TGCGATGCCAAG CACGAGTTTT TCGCATGCCAAG CACGAGTTTT AGAAGGCAAA AGAAGGCAAA AGAAGGCAAA AGAAGACACA ATTAGGAAGAG AAATTCAG AAATTCAGAACTT AAGTAAAGAG TCCAGAACTT AAGTAAAGAG ATTAGGAACAC TTCAGGAACTT AAGTAAAGAG TTCCAGGAACTT AAGTAAAGAG TTCCAGGAACTT AAGTAAAGAG TTTCAGGAACAC TTTTGAGGAAGA	GGTCCCTGGA CGGGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTCAGG GGATTATTG GATCTGGCTA GTTCTTCGAG GGATAAACATCA GCAAAACATCA ACCATCAGAAAACATCA CGAAAAACATCATTCGAGG GATTTGGTGAA AACTTAAAGG GATTTGGTG CCAGAAAAAT TTACAGGAGC GAGCTTTGGT GAGCATATCCATCA CTTAATCTC AACATCATGA AACATCATGA	120 180 240 300 360 420 600 650 720 780 840 900 1020 1080 1140 1260 1320 1380 1340
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5	TGTCATGTCT CCAGTTAGAT TCTGTAGTTC	AGATTTAAAT GCAATTTGGT AAATCTGTTA TTTAACAGAA	TTTAAGTCTG CATTAATACC GCTTTGTGAA	TTTTAAATGA AGATTTTAAA ATGACATCTT AATTCATCAC CTGTCATTTA	TGTTTTTGAG GCTTATAAAT TGTGATGTTT	CTTAGAAAAC ATTCCATTGC	1860 1920 1980 2040 2100
10	Seq ID NO: Protein Acc	ession #: 1 11 	IP_002488.1 21	31 GKILVWKELD	. 41 VGSMTELEKO	51     MINSEUNILE	60
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25	Coding sequ	ence: 65 11	1057 21	31	41	51	
22	ī	1	1	1-2	1	1	
	CGCCATGCGG	AGGCCGAGCG	TGCGCGCGGC	TTGGGACCGC CGGGCTGGTC	CTGTGCACCC	TGTGTTACCT	60 120
••	GCTGGTGGGC	GCTGCTGTCT	TCGACGCGCT	CGAGTCCGAG	GCGGAAAGCG	GCCGCCAGCG	180
30	ACTGCTGGTC	CAGAAGCGGG	GOGCTCTCCG	GAGGAAGTTC TGAGCCCCAC	GGCTTCTCGG	CCGAGGACTA	240 300
	GTTCCCCGGC	TCCTTCTACT	TOGCCATCAC	CGTCATCACT	ACCATCGGGT	ACGGCCACGC	360
	CGCGCCGGGT	ACGGACTCCG	GCAAGGTCTT	CTGCATGTTC	TACGCGCTCC	TGGGCATCCC	420
35	GCTGACGCTG	GTCACTTTCC	AGAGCCTGGG	CGAACGGCTG GCGGTGGACG	AACGCGGTGG	CGGAGAACCT	480 540
55	GGTGGTGGCC	GCCTGCTGG	CGTGTGCCGC	CACCCTGGCC	CTCGGGGCCG	TCGCCTTCTC	600
	GCACTTCGAG	GGCTGGACCT	TCTTCCACGC	CTACTACTAC	TGCTTCATCA	CCCTCACCAC	660
	CATCGGCTTC	GGCGACTTCG	TGGCACTGCA	GAGCGGCGAG CCTGGGGCTC	GCGCTGCAGA ACGCTCATTG	GCGCCTTCCT	720 780
40	CAACCTGGTG	GTCCTGCGCT	TCCTCGTTGC	CAGCGCCGAC	TGGCCCGAGC	GCGCTGCCCG	840
	CCCCCCCAGC	CCGCGCCCCC	CGGGGGCGCC	CGAGAGCCGT	GGCCTCTGGC	TGCCCCGCCG	900
	CCCGGCCCGC	TCCGTGGGCT	CCGCCTCTGT	CTTCTGCCAC CTCGAGCCCG	GIGCACAAGC	GTGGCGGGCA	960 1020
. 2	GGCTCCCAGG	CCTGGGGCCC	GGTGGAAGTC	CATCTGACAA	CCCCACCCAG	GCCAGGGTCG	1080
45	AATCTGGAAT	GGGAGGGTCT	GGCTTCAGCT	ATCAGGGCAC	CCTCCCCAGG	GATTGGAAAC	1140
	GGATGACGGG	CCTCTAGGCG	GTCTTCTGCC	ACGAGCAGTT TACAGTCACA	CCATAAAAAA	AAAAAAAAA	1200 1260
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55	MRRPSVRAAG RIJERIJALOAE	PHRAGROWKE	PGSFYFAITV	SEAESGRORL ITTIGYGHAA	PGTDSGKVFC	MFYALLGIPL	120
	TLVTFOSLGE	RLNAVVRRLL	LAAKCCLGLR	WICVSTENLV	VAGLLACAAT	LALGAVAFSH	180
	FEGWTFFHAY	YYCFITLTTI	GFGDFVALQS	GEALQRKLPY	VAFSFLYILL	GLTVIGAFLN	240 300
•			PSPRPPGAPE PRPGARWKSI	SRGLWLPRRP	ARSVGSASVE	CHVHADERCA	300
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05	GGAAACATGA	TOCAGOTGAS	I GGACTGATTY	CAGGAAAACT	TGGCAGCTCC	CCAACCTTGG	60
	TGGCCCAGGG	AGTGTGAGGC	TGCAGCCTC	GAAGGTGTGA	GCAGTGGCC	CGAGAGGCAG	120
	GCTGGCTGGG	ACATGAGGTT	GGCAGAGGG	AGGCAAGCTC	GCCCTTGGTC	GGCCTCGCCC	180 240
70	GCCCTCCTCC	GAGGCACTCC	CCCCACACT	CTGGCACAGO	GAGAAGCCAG	GGTCCAGCAG GAGGAGCCGA	300
, 0	AACACCACCA	GGCCCGCTCT	CCTGAGGCTC	TCGGATTACC	: TTTTGACCA	CTACAGGAAG	360
	GGTGTGCGCC	CCGTGAGGG	CTGGAGGAAG	CCAACCACCC	TATCCATTG	CGTCATTGTC	420 480
	CAGTACTGG	: TUAACGTGG!	TGAGAAGAA TCTCCAGTG	AACCCTGAGG	ACTITICACA	CTGGTACCGG CATCACCAAG	540
·75	TTGTCCATCC	CCACGGACAC	CATCTGGGT	CCGGACATTC	: TCATCAATG	A GTTCGTGGAT	600
	GTGGGGAAG7	CTCCAAATA	CCCGTACGT	TATATTCGG	: ATCAAGGCG	A AGTTCAGAAC	660 720
	CTCYACAAC	CCTCGCTGA	CTTCACCAG	r TGGCTGCAC	A CCATCCAGG	CCCCTTCGAT CATCAACATC	780
	TOTAL CALCAC	CCTTGCCAG	AAAGGTGAA	A TCCGACAGG	GTGTCTTCA	r gaaccagga	840
80	CACTCCCAC	r TGCTGGGGG	r GCTGCCCTA	C TTTCGGGAG	r TCAGCATGG	A AAGCAGTAAC	900
	TACTATGCA	AAATGAAGT	r CTATGTGGT	C ATCOGCOGG	A TOGTGGGCT	CTATGTGGTC CTACCTGCCC	960 1020
	CCCDACACT	ROCCAGAGGGG	T CTCTTTCAA	G ATTACACTO	C TCCTGGGCT	A CTCGGTCTTC	1080
05	CTCATCATC	C TTTCTGACA	C GCTGCCGGC	C ACTGCCATO	G GCACTCCTC	T CATTEGIGIC	1140
85	TACTTTGTG	G TGTGCATGG	C TCTGCTGGT	G ATAAGTTIG	AUDAUAUCA	T CITCATTGIG	1200

	CCCCTCCTCC	ACAAGCAAGA	CCTGCAGCAG	CCCGTGCCTG	CTTGGCTGCG	TCACCTGGTT	1260
				ACCCA CCACM	CA P CALLOCOCA	C1C0000001	1320
	CIGGAGAGAA	TCGCCTGGCT	ACTITGCCTG	MGGGWGCWG1	CHACTICCCH	GAUGCCCCCA	
	GCCACCTCCC	AAGCCACCAA	GACTGATGAC	TGCTCAGCCA	TGGGAAACCA	CTGCAGCCAC	1380
	ATTOGGAGGAG	CCCACCA CTT	CGAGAAGAGC	CYCACGGACA	GATGTAGCCC	TOTOTOTOTO	1440
5	aroomounc	CCCAGGACII		~~~~~		Cl Tecco	
<i>3</i>	CCTCGGGAGG	CCTCGCTGGC	GGTGTGTGGG	CIGCIGCAGG	AGCIGIOCIC	CATCCGGCAA	1500
	TTCCTGGAAA	AGCGGGATGA	GATCCGAGAG	GTGGCCCGAG	ACTGGCTGCG	CGTGGGCTCC	1560
	GTGCTGGACA	A COTO OTA TO	CCACATTAC	CTCCTACCCC	ALCALCCIACALY.	CAGCATCACC	1620
	GIGCIGGACA	MCIGCIAII	CONCRETE				
	CTGGTTATGC	TCTGGTCCAT	CTGGCAGTAC	GCTTGAGTGG	GTACAGCCCA	GTGGAGGAGG	1680
	GGGTACAGTC	CHESTABLEST	CCCCACAGAG	CATTTCTCCT	TAGGCCCCTC	AGGACCCAGG	1740
10	GGGIACAGIC	CIGGIINGGI	GGGGACAGAG		71100000000	7100722000	
10	GAATGCCAGG	GACATTTTCA	AGACACAGAC	AAAGTCCCGT	GCCCTGTTTC	CAATGCCAAT	1800
	TCATCTCAGC	AATCACAAGC	CAAGGTCTGA	ACCCTTCCAC	CAAAAACTGG	GTGTTCAAGG	1860
				max aan maaa	WWW. 0.0.0.00	COROMONNAC	
			CCCCAGCAGC				1920
	ATCAGGAGAA	ACTCGGGCAC	TCCCTAAGTC	CACTCTAGTT	GTGGACTTTT	CCCCATTGAC	1980
			TTGGAATTCT				2040
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15	GAAGGCAAAA	CCAACTCTCT	ACTACACAGG	CCTGATAACT	CTGTACGAGG	CTTCTCTAAC	2100
			TCACCTCACT				2160
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	TIQDINISLW	RLPEKVKSDR	SVFMNQGEWE	PPGAPALKE	F5ME55NIIA	EWINT I A A TRIK	
	RPLFYVVSLL	LPSTPLMVMD	IVGPYLPPNS	GERVSFKITL	LLGYSVFLII	VSDTLPATAI	300
			AETIFIVRLV				360
	GIATICALLA	ACLIMITY AT THE	WETTLIAKTA	TVÄNTVÄLAB	AMURALIVIER	THURSDAY.	
	STSQRPPATS	QATKTDDCSA	MGNHCSHMGG	PODFEKSPRD	RCSPPPPPRE	ASLAVCGLLQ	420
30			DWLRVGSVLD				
50	PPRZETKÖLPE	KRDETKEVAK	DMPKAG2ATD	KUDERLIEUM	ATMISTITUM	THOTHÔIV	
	Seg TD NO.	45 DNA sequ	ience				
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	CCCCAGAGGA	COTTOCCO	GGCTAGCCAG	GGCGCCCCCA	GCCCCTCCCC	AGGCCGCGAG	60
			GCCTCCCCTC				120
	CCACTCCACC	CCACCACCCC	AGCGGCTGAG	GAGAGAGGAG	GCGGCGGCTT	AGCTGCTACG	180
40				**********	G110G1GG1G	00000000000	240
40			CGAGGGGGGC				
	ATGCCTCTGC	CCTGGAGCCT	TGCGCTCCCG	CTGCTGCTCT	CCTGGGTGGC	AGGTGGTTTC	300
			GCATCACGGG				360
			GGCCTGCTGC				420
	TGTGAAGCTA	CATGCGAACC	TGGATGTAAG	TTTGGTGAGT	GCGTGGGACC	AAACAAATGC	480
45					1 mama 1 man	CONCORDO A RICC	540
47	AGATGCTTTC	CAGGATACAC	CGGGAAAACC	TGCAGTCAAG	AIGIGAAIGA	GIGIGGAAIG	
	AAACCCCGGC	CATGCCAACA	CAGATGTGTG	AATACACACG	GAAGCTACAA	GTGCTTTTGC	600
	CHENCHE	A CATCCENCANT	GCCAGATGCT	A COTOTOTON	ACTOTACEAC	ATCTCCCATC	660
	CICMOIGGCC	MCMIGCICAL	GCCAGAIGCI	ACGIGIGIOA	ACTOINGGAC	770000110	
	ATAAACTGTC	AGTACAGCTG	TGAAGACACA	GAAGAAGGGC	CACAGTGCCT	GTGTCCATCC	720
	TCAGGACTCC	GOTTGGCCCC	AAATGGAAGA	GACTGTCTAG	ATATTGATGA	ATGTGCCTCT	780
50							840
J0			CAATCGAAGA				
	AAATGTCACA	TTGGTTTCGA	ACTGCAATAT	ATCAGTGGAC	GATATGACTG	TATAGATATA	900
			CCATACGTGC				960
	GGGTCCTTCA	AGTGTAAATG	CAAGCAGGGA	TATAAAGGCA	ATGGACTTCG	GIGITCIGCI	1020
	ATCCCTGAAA	ATTCTCTCAA	GGAAGTCCTC	AGAGCACCTG	GTACCATCAA	AGACAGAATC	1080
55							
JJ	AAGAAGTTGC	TIGCTCACAA	AAACAGCATG	малансалсс	CHAMMATTAA	WWIGITWCC	1140
	CCAGAACCCA	CCAGGACTCC	TACCCCTAAG	GTGAACTTGC	AGCCCTTCAA	CTATGAAGAG	1200
	Value Construction	CACCCCCC.	Chlancyman	CCTABBBBB	CCANTONNON	CAAAATCAAA	1260
	MINGITICCA	AADOCOGAA	CTCTCATGGA	Gummin	- CONTRACTOR		
	GAGGGGCTTG	AGGATGAGAA	AAGAGAAGAG	AAAGCCCTGA	AGAATGACAT	AGAGGAGCGA	1320
	ACCCTCCCAC	CACATYSTYSTE	TTTCCCTAAG	GTGAATGAAG	CAGGTGAATT	CGGCCTGATT	1380
60	CONTRACTOR OF THE PARTY OF THE		220000000	000011010	N N CONTINUES S.	U. J. U. California	1440
UU			AACTTCCAAA				
	GACTGCAGCT	TCAATCATGG	GATCTGTGAC	TGGAAACAGG	ATAGAGAAGA	TGATTTTGAC	1500
						GGCCTTGGCA	1560
	GGTCACAAGA	AAGACATTGG	CCGATTGAAA	CTTCTCCTAC	CIGACCITGCA	ACCCCAAAGC	1620
	AACTTCTGTT	TGCTCTTTGA	TTACCGGCTG	GCCGGAGACA	AAGTCGGGAA	ACTTCGAGTG	1680
65						GGATGAAAAG	
00							
	TGGAAGACAG	GGAAAATTCA	GITGTATCAA	GGAACTGATG	CTACCAAAAG	CATCATTTTT	1800
	GAAGCAGAAC	GTGGCAAGGG	CAAAACCGGC	GAAATCGCAG	TGGATGGCGT	CTTGCTTGTT	1860
						ATCTTTATAT	
	TTGACTTTGT	ATGTCAGTTC	CCTGGTTTTT	TTGATATTGC	ATCATAGGAC	CTCTGGCATT	1980
70						AAGATGCCTT	
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	TCTTGTATAA	GATATGCCAA	. TATTTGCTTT	<b>AAATATCATA</b>	TCACTGTATC	TTCTCAGTCA	2100
	The Windship Water	Jalah C. V. V. V. Jalah	מ ממדי מדים מדמ	ATATCCALAT	GTCACTTTAT	CTCCCCTCCT	2160
	TITCIGAMIC	LITCUACATT	WINTINIUM	MINIOUNNI			2220
	CAGTATATCT	GATTTGTATA	. AGTAAGTTGA	TGAGCTTCTC	TCTACAACAT	TTCTAGAAAA	2220
	TAGAAAAAA	ACCACACACA	AATCTTTAAC	Hellelate Vert	TTATCATACT	TCTTGGAAAC	2280
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00	1     MPLPWSLALP	   LLLSWVAGGE	   GNAASARHHO	   LLASARQPGV	CHYGTKLACO	   YGWRRNSKGV	60
	1     MPLPWSLALP	   LLLSWVAGGE	   GNAASARHHO	   LLASARQPGV	CHYGTKLACO		60 120
	1     MPLPWSLALF   CEATCEPGCK	LLLSWVAGGE FGECVGPNK	   GNAASARHHO   RCFPGYTGKT	   LLASARQPGV   CSQDVNEOGN	CHYGTKLACO KPRPCQHRCV	NTHGSYKCFC	120
	1     MPLPWSLALF   CEATCEPGCK   LSGHMLMPDA	LLLSWVAGGE FGECVGPNKC TCVNSRTCAN	   GNAASARHHO   RCFPGYTGKT   INCQYSCEDI	   LLASARQPGV   CSQDVNEOGN   EEGPQCLCPS	CHYGTKLACO KPRPCQHRCV SGLRLAPNGE	NTHGSYKCFC DCLDIDECAS	120 180
85	1     MPLPWSLALF   CEATCEPGCK   LSGHMLMPDA	LLLSWVAGGE FGECVGPNKC TCVNSRTCAN	   GNAASARHHO   RCFPGYTGKT   INCQYSCEDI	   LLASARQPGV   CSQDVNEOGN   EEGPQCLCPS	CHYGTKLACO KPRPCQHRCV SGLRLAPNGE	NTHGSYKCFC	120

5	PEPTRTPTPK SLRGDVFFPK WNPADRDNAI	VNLQPFNYEE VNEAGEFGLI GFYMAVPALA WEKTTSEDEK	IVSRGGNSHG LVQRKALTSK GHKKDIGRLK	RAPGTIKDRI GKKGNEEKMK LEHKDLNISV LLLPDLQPQS GTDATKSIIF	EGLEDEKREE DCSFNHGICD NFCLLFDYRL	KALKNDIEER WKQDREDDFD AGDKVGKLRV	300 360 420 480 540
		47 DNA sequid Accession		146			
10		ence: 167		31	41	51	
	Ī	1		CTCCTGCCCC		Ī	60
1.5	TTAGCCTTGG	AAACTGCAGG	AGAAGAAGCC	CAGGGTGACA	AGATTATTGA	TGGCGCCCCA	120
15	GGAGGCGTCC	TGGTCAATGA	GCGCTGGGTG	GCCCTGCTCA CTCACTGCCG	CCCACTGCAA	GATGAATGAG	180 240
	TACACCGTGC TCGAAGTCAT	ACCTGGGCAG TCCGCCACCC	TGATACGCTG	GGCGACAGGA ACACAGACCC	GAGCTCAGAG ATGTTAATGA	GATCAAGGCC CCTCATGCTC	300 360
20	GTGAAGCTCA	ATAGCCAGGC	CAGGCTGTCA	TCCATGGTGA GTCTCCGGCT	AGAAAGTCAG	GCTGCCCTCC	420 480
20	GATGTGACCT	TTCCCTCTGA	CCTCATGTGC	GTGGATGTCA	AGCTCATCTC	CCCCCAGGAC	540 600
	TCCAAGAAAA	ACGCCTGCAA	TGGTGACTCA	AATTCCATGC GGGGGACCGT	TGGTGTGCAG	AGGTACCCTG	660
25	CAAGGTCTGG ACTCAAGTGT	TGTCCTGGGG GCAAGTTCAC	AACTTTCCCT CAAGTGGATA	TGCGGCCAAC AATGACACCA	CCAATGACCC TGAAAAAGCA	AGGAGTCTAC TCGCTAACGC	720 780
	CACACTGAGT	TAATTAACTG	TGTGCTTCCA	AČAGAAAATG TTCCTCAAAG	CACAGGAGTG	AGGACGCCGA	840 900
	CTGTTGATAA	ACCAATCAAA	TTGGTAAAGA	CCTAAAACCA	AAACAAATAA	AGAAACACAA	960
30	AACCCTCAA						
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	1	11	21 	31 	41	51	
35				IDGAPCARGS QRIKASKSFR			60 120
	QARLSSMVKK	VRLPSRCEPP	GTTCTVSGWG	TTTSPDVTFP CRGTLQGLVS	SDLMCVDVKL	ISPODCTKVY	180 240
40	PTKWINDTMK		CNGDSGGFEV	CKGIDQUIVS	WOLLI COOLIN	21011141011	
40		49 DNA seq					
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45	1	11 	21 	31 	41	51 	
45	GAATTCGGCG	 ATGCCTCACA	21   ACTCCATCAG	 ATCTGGCCAT	 GGAGGGCTGA	ACCAGCTGGG	60 120
45	GAATTCGGCG AGGGGCCTTT GGCCCACCAG	 ATGCCTCACA GTGAATGGCA GGTGTAAGGC	21 ACTCCATCAG GACCTCTGCC CCTGCGACAT	ATCTGGCCAT GGAAGTGGTC CTCTCGCCAG	GGAGGGCTGA CGCCAGCGCA CTCCGCGTCA	ACCAGCTGGG TCGTAGACCT GCCATGGTTG	120 180
<b>45</b> <b>50</b>	GAATTCGGCG AGGGGCCTTT GGCCCACCAG CGTCAGCAAG GGGCTCCAAG	ATGCCTCACA GTGAATGGCA GGTGTAAGGC ATCCTTGGCA CCCAAGGTGG	21   ACTCCATCAG GACCTCTGCC CCTGCGACAT GGTACTACGA CCACCCCCAA	ATCTGGCCAT GGAAGTGGTC CTCTCGCCAG GACTGGCAGC GGTGGTGGAG	GGAGGGCTGA CGCCAGCGCA CTCCGCGTCA ATCCGGCCTG AAGATTGGGG	ACCAGCTGGG TCGTAGACCT GCCATGGTTG GAGTGATAGG ACTACAAACG	120 180 240 300
	GAATTCGGCG GAATTCGGCG AGGGGCCTTT GGCCCACCAG CGTCAGCAAG GGGCTCCAAG CCAGAACCCT TGACAATGAC	ATGCCTCACA GTGAATGGCA GGTGTAAGGC ATCCTTGGCA CCCAAGGTGG ACCATGTTTG ACTGTGCCCA	21 ACTCCATCAG GACCTCTGCC CCTGCGACAT GGTACTACGA CCACCCCCAA CCTGGGAGAT GTGTCAGCTC	ATCTGGCCAT GGAAGTGGTC CTCTCGCCAG GACTGGCAGC GGTGGTGGAG CCGAGACCGG CATTAATAGA	GGAGGGCTGA CGCCAGCGCA CTCCGCGTCA ATCCGGCCTG AAGATTGGGG CTCCTGGCTG ATCATCCGGA	ACCAGCTGGG TCGTAGACCT GCCATGGTTG GAGTGATAGG ACTACAAAACG AGGGCGTCTG CCAAAGTGCA	120 180 240 300 360 420
50	GAATTCGGCG AGGGGCCTTT GGCCCACCAG CGTCAGCAAG GGGCTCCAAG CCAGAACCCT TGACAATGAC GCAACCATTC CACGCTGATC	ATGCCTCACA GTGAATGGCA GGTGTAAGGC ATCCTTGGCA CCCAAGGTGG ACCATGTTTG ACTGTGCCCA AACCTCCCTA CCCAGCTCAG	21 ACTCCATCAG GACCTCTGCC CCTGCGACAT GGTACTACGA CCTGCGAGAT GTGTCAGCT TGGACAGCTG CTGTAACTCC	ATCTGGCCAT GGAAGTGGTC CTCTCGCCAG GACTGGCAGC GGTGGTGGAG CCGAGACCGG CATTAATAGA CGTGGCCACC CCCGGAGTCA	GGAGGGCTGA CGCCAGCCGC CTCCGCGTCA ATCCGGCCTG AAGATTGGG CTCCTGGCTG ATCATCCGG AAGATCCCTGA CCCCAGTCGG	ACCAGCTGGG TCGTAGACCT GCCATGGTTG GAGTGATAGG ACTACAAACG AGGGCGTCTG CCAAAGTGCA GTCCCGGACA ATTCCCTGGG	120 180 240 300 360
	GAATTCGGCG AGGGGCCTTT GGCCCACCAG GGGCTCCAAG GGGCTCCAAG CCAGAACCCT TGACAATGAC GCAACCATTC CACGCTGATC CTCACCTAC	ATGCCTCACA GTGAATGGCA GGTGTAAGGC ATCCTTGGCA CCCAAGGTGG ACCATGTTTG ACTGTGCCCA AACCTCCCTA CCCAGGCTCAG TCCATCAATG	21   ACTCCATCAG GACCTCTGCC CCTGCGACAT GGTACTACGA CCTGCGAGAGT GTGTCAGCTC TGGACAGCTC TGGACAGCTC GGCTCCTGGG	ATCTGGCCAT GGAAGTGGTC CTCTCGCCAG GACTGGCAGC GGTGGTGGAG CCGAGACCGG CATTAATAGA CCCGGAGTCA CATCGCTCAG	GGAGGGCTGA GGCCAGCGCA ATCCGGCCTG AAGATTGGG CTCCTGGCTG ATCATCCGGA AAGTCCCTGA ACCCCAGTCGGCAGCG CCTGGCAGCG	ACCAGCTGGG TCGTAGACCT GCCATGGTTG GAGTGATAGG ACTACAAACG AGGCCGTCTG CCAAAGTGCA GTCCCGGACA ATTCCCTGGG ACCAGAGGAA	120 180 240 300 360 420 480
50	GAATTCGGCG AGGGCCTTT GGCCCACCAG GGCTCCAAG GGGCTCCAAG CCAGAACCCT TGACAATGAC GCAACCATTC CACGCTGATC CTCACCTAC CATGGATGAC CAGGCCCGA	ATGCCTCACA GTGAATGGCA GGTGTAAGGC ATCCTTGGCA CCCAAGGTGG ACCATGTTG ACCTCCCTA CCCAGCTCAG TCCATCAATG TCCATCAATG AGTGATCAGG AAGCACCTTCC	21   ACTCCATCAG GACCTCTGCC CCTGCGACAT CCTGCGAGAT CCTGCGAGAT CTGGCAGCT CTGACAGCTG CTGTAACTCC GGCTCCTGGG ATAGCTGCCG GCACGGATGC	ATCTGGCCAT GGAAGTGGTC CTCTCGCCAG GACTGGCAGC GGTGGTGGAG CCGAGACCCG CATTAATAGA CCTGGCCACC CCCGGAGTCA CATCGCTCAG ACTAAGCATT CTTCAGCCAG	GGAGGGCTGA GGCAGCGCA CTCCGGGTCA ATCCGGCCTG AAGATTGGGG CTCCTGGCTG AAGTCCCTGA ACTCCCTGA CCCCAGTCGG GACTCACAGA CACCACCTCG	ACCAGCTGGG TCGTAGACCT GCCATGGTTG GAGTGATAGG ACTACAAACG AGGGCGTCTG CCAAAAGTGCA ATTCCCTGGG ACAAGAGGAA ACTCCCTGGACA ACCAGCAGAAAAGAGGAA ACCAGCAGCAGAAAAGAGAAAAGAGAAAAGAAAAAAAA	120 180 240 300 360 420 480 540 600 660 720
50 55	GAATTCGGCG AGGGGCCTTT GGCCACCAG GGTCAGCAAG CCAGAACCCT TGACAATGAC GCACCATTC CACGCTGATC AATGGATGAC GGACCCCTAC AATGGATGAC GTGCCCATTT CGAGCAGGGGG	ATGCCTCACA GTGAATGGCA GGTGTAAGGC ATCCTTGGCA CCCAAGGTGG ACCATGTTTG ACTGCCCA ACCTCCTA CCCAGCTCAG TCCATCAATG AGTGATCAGG AAGCACCTTC GAGCAGCC CTCTACCGGC	21 ACTCCATCAG GACCTCTGCC CCTGCGACAT GGTACTACGA CCTGCGAGAGT GTGTCAGCTC TGGACAGCTC GGCTCCTGGG ATAGCTCC GCACGCATGC ACTACCCAGA ACTCCCTGGG ACTACCCAGA TGCCCTTGCT	ATCTGGCCAT GGAAGTGGTC CTCTCGCCAG GACTGGCAGC GGTGGTGGAG CCGAGACCG CATTAATAGA CGTGGCCACC CCCGGAGTCA CATCGCTCAG ACTAAGCATT CTTCAGCCAG GGCCTATGCC CAACAGCACC	GAAGGGCTGA GGCAGGGCA ATCOGGCTG AAGATTGGGG CTCCTGGCA ATCCCGGA AAGTCCCTGA ACCCAGTCGG CCTGGCAGCG GACTCACAGA CACCACCTCG TCCCCCAGCG CTGGAGAGACG	ACCAGCTGGG TCGTAGACCT GCCATGGTTG GAGTGATAGG ACTACAAACG ACGCGCTCGG CCAAAGTGCA ATTCCCTGGG ACTACAGAGGAA GCAGCAGCAG AGCCGCTCGA AGCACCAAAGG GGAAGGCAC GGAAGGCAC	120 180 240 300 360 420 480 540 600 660 720 780 840
50	GAATTCGGCG AGGGGCCTTT GGCCCACCAG GGTCACAAG GCACCATGACATGA	ATGCCTCACA GTGAATGGCA GTGTAAGGC ATCCTTGGCA ACCATGTTTG ACTGTGCCA AACCTCCCTA ACCTCACTA AGTGATCAGG TCCATCAATG AGGACCTTC GAGCGGCAGC CTCTACCAGG CCTCACTCAC	21   ACTCCATCAG GACCTCTGCC CCTGCGACAT CCTGCGACAT CCTGGGAGAT CTGGGAGAT CTGGACAGCT CTGACTACCC GGCTCCTGGG ATACCTCCC GCACGGATGC ACTACCCAGA TGCCCTTGGCT CCTCGGCGC CCTTCGCCAT	ATCTGGCCAT GGAAGTGGTC GGATGGAGG GACTGGCAGC CCGGAGCCGG CATTAATAGA CCTCGCACC CACCTCAG ACTAGCACC CAACAGCACC CAACAGCACC AACAGCACC AAACAGCAGAA	GGAGGGCTGA GGCAGGGCTGA ATCCGGCTG AAGATTGGGG CTCCTGGCTG ATCATCCGGA AAGTCCCTGA CCCCAGTCGG GACTCACAGA CACCACCTCG TCCCCCAGCC CTGGACGACA ACTCACCAGA ACCCCCGAGGG	ACCAGCTGGG ACCAGCTTGGTTG GCGTGGTTG GAGTGATAGG AGGCGTCTG CCAAAGTGCA ATTCCCTGGG ACAGCAGCA ACAGCAGCAGCA ACAGCAGCAGCAG ACACCAAAGG GCAGCACCGT TGTCCAGTTC	120 180 240 300 360 420 480 540 600 720 780 840 900 960
50 55	GAATTCGGCG AGGGGCCTTT GGCCCACCAG GGTCACAAG GGGCTCCAAG GCAACCAT TGACAATGAC GCAACCATTC CACGCTGATC CTCCACCTAC AATGGATGAC GGACCCCTA GGACCCCTAC CGAGCACCATT CGAGCAGGGC CCTGACCCCT TGGTGGCAGCT TAGCTCCACCT	ATGCCTCACA GTGAATGGCA GTGAATGGCA GTGTAAGGC ATCCTTGGCA ACCTCCTTA ACCTCCCTA ACCTCCCTA ACCTCACTCA	21   ACTCCATCAG GACCTCTGCC CCTGCGACAT GGTACTACGA CCTGGGAGAT CTGGGAGAT CTGTCAGCT CGGCTCCTGGG ATAGCTCC GCCTCCCGA ACCCGATGC ACTACCCAGA TGCCCTTGCT CACTGGGGCCT CACTGGGGCAT TATCTAGCTCC	ATCTGGCCAT GGAAGTGGTC CTCTCGCCAG GACTGGCAGC GCTGGTGGAG CCTGAGCACC CCCGGAGTCA CATCGCTCAG ACTAGCATT CTTCAGCCAG GGCCTTATGCC CAACACCTCTCG AAAGCAGGA CGCCTTTTG	GAAGGGCTGA CGCAGCGCA ATCCGGCTG AAGATTGGGC CTCCTGGCTG ATCATCCGGA AAGTCCCTGA ACCCCAGTCGG GACTCACAGA CACCACCTGG CTCCCCAGCG CTGGACGAGA ACCCCCAGGG GATTCACCAGA ACCCCCAGGG GATTCACCAGA ACCCCCAGGG	ACCAGCTGGG TCGTAGACCT GCCATGGTTG GAGTGATAGG ACTACAAACG AGGCGTCTG CCAAAGTGCA ATTCCCGGACA ATTCCCTGGG ACAGAGGAA GCAGCAGCAG AGCCGCTCGA ACACCAAAGG GGAAGGCAC CCTACCCCGT TGTCCAGTTC AAGTCGGCTC	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50 55 60	GAATTCGGCG AGGGCCTTT GGCCACCAG CGTCAGAACC TGACAAG CCAGAACCATTC CACGTTATCAC CACGCTGATC CACGCTGATC CACGCTGATC CACGCTGATC CGACCCCGA GTGCCCATT CGACCACCT GGTGGCAGAT TAGCTCCACC CCGGGCCCCT CCACCCCCCCCCC	ATGCCTCACA GTGAATGGCA GTGAATGGCA GGTGTAAGGC ATCCTTGGCA ACCATGTTGG ACCATCATA ACCTCCCTA ACCTCCCTA ACCTCCCTA AGCACCTCAG AGGCGCAGCC CTCTACCCGC CCTCACTACC CCTTCACTACC CCTTCACTCAC CCTTCACTCAC	21   ACTCCATCAG GACCTCTGCC CCTGCGACAT CCTGCGAGAT CCTGCGAGAT CTGGCAGAT CTGAGCTC GGCTCCTGGG ATACTCCG GCACGATGC ACTACCCAGA TGCCCTTGCC CCTTCGCCAT TATCTAGCTC CCTTTCCCAT GAGAGATGGT	ATCTGGCCAT GGAAGTGGTC CTCTCGCCAG GACTGGCAGC GGTGGTGGAG CCGAGACCG CATTAATAGA CATGGCTCAG ACTAGCATCAG ACTAAGCATT CTTCAGCCAG GGCTATGCC CAACCTCTCG AAAGCAGGA CGCCTTTTTG TGCCTCCC GGGGCCCCACG	GGAGGGCTGA CGCCAGCGCA CTCCGGGCTG AAGATTGGGG CTCCTGGCTG ATCATCCGGA AAGTCCCTGA CCCCAGTCG GACTCACAGA CACCACCTCG ACTCACCAGCG GACTCACAGA ACCCCCAGCG GACTCACAGA CCCCCAGCG CTGGACGACG GATCTCCCGAGCG CTGGACGACG CTGCCCGAGCG GATCTCCCGAGCG CTGCCCGAGG	ACCAGCTGGG TCGTAGACCT GCCATGGTTG GAGTGATAGG ACTACAAACG AGGGCGTCTG CCAAAGTGCA ATTCCCTGGG ACAAGAGGAA ACACCAAAGG AGCGCTCGA AGCACCACCGT TGTCCAGTTC AAGTGCAGCA ACACCAAGG AGCACCAGCAG ACACCAAGG ACACCAGT TGTCCAGTTC AAGTGCAGCCA	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1080 1140
50 55	GAATTCGGCG AGGGGCCTTT GGCCACCAG GGTCACAAG GGGCTCCAAG GCACAATGAC CAGAACCATTC CACGCTGATC AATGATGAC GGACCCCTAC CAGGCACCATTT CGAGCAGGCCCCGA GTGCCCATTT CGAGCAGGGCCCCC CCAGGCCCCCAC CAGGCCCCCAC CAGGCCCCCAAGGCCCCAAAGTGAATACCAAAT	ATGCCTCACA GTGAATGGCA GTGAATGGCA GTGTAAGGC ATCCTTGGCA ACCTCCTCA ACCTCCCTA ACCTCCCTA ACCTCCCTA ACCTCCCTC	21   ACTCCATCAG GACCTCTGCC CCTGCGACAT GGTACTACGA CCTGGGAGAT CTGGGAGAT CTGGACAGCT CTGGACAGCT GGCTCCTGGG ATAGCTCCC GCTCCCAGA TGCCCTTGCT CACTGGGGCG TTTCCCCAT TATCTAGCTC CCTTTCCCCA GAGAGATGGT GCAGATGGT CCTTTCCCCA CCTTTCCCCCA CCTTTCCCCA CCTTTCCCCCA CCTTTCCCCCA CCTTTCCCCCA CCTTTCCCCA CCTTTCCCCA CCTTTCCCCCA CCTTTC	ATCTGGCCAT GGAAGTGGTC GGAGACCGG GCTGGCCAC CATCACACA ACTAACACAC ACTACCACAC ACACACAC	GGAGGGCTGA GGCAGGGCA ATCCGGCTG ATCCGGCTG ATCATCCGGA ATGATCCGGA AAGTCCCTGA ACCACCTCG GACTCACAGA CACCACCTCG CTGGACGAGCG GACTCACCAGCA CTCACCAGCA CTCCCCGACT TATCGCAGGCA TCCTCCCTACA	ACCAGCTGGG TCGTAGACCT GCCATGGTTG GAGTGATAGG ACTACAAACG AGGCGTCTG CCAAAGTGCA ATTCCCTGGG ACAGAGGAAA GCAGCAGCAG AGCCGCTCGA AGCACCATCCA AGTCCATACCGGT TGTCCAGTTC AGTTCACGGG ACCCACCCAC AGTCACCGGG ACCCACCCAG ACCCACCCAG TGTGCCAGG GCAGGCCTG GCGAGGCCTG GCGAGGCCTG	120 180 240 360 420 480 540 660 720 780 840 900 960 1020 1140 1200 1260
50 55 60	GAATTCGGCG AGGGCCTTT GGCCACCAG GGTCACAAG CCAGAACCCT TGACAATGAC GCACCATTC CACCTAC AATGATGAC GGACCCGA GTGCCCATTC CAGCACCCG GTGCCCATC CAGCACCCC CAGCCCCC CAGGCCCCC CAGGCCCCC CATCCCCACC CAGGCCCCC CATCCCCACC CATCCCCACC CAGGCCCCC CATCCCCACC CAGGCCCCC CAGGCCCCC CATCCCCACC CAGGCCCTC CATCCCCACC CAGGCCCTC CATCCCCACC CAGGCCCTC CATCCCCACC CAGGCCTTCCCCACC CAGGCCTTCCCCACC CAGGCCTTCCCCCC CAGGCCTTCCCCCCC CAGGCCTTCCCCCCC CAGGCCTTCCCCCCC CAGGCCTTCCCCCCCC CAGGCCTTCCCCCCCC CAGGCCTTCCCCCCCC CAGGCCTTCCCCCCCCC CAGGCCTTCCCCCCCCCC	ATGCCTCACA GTGAATGGCA GTGAATGGCA GTGTAAGGC ATCCTTGGCA CCCAAGGTGG ACCATGTTTG ACTGTGCCCA AACCTCCCTA CCCAGCTCAG AGCACCTTC GAGCACCTTC CTCTACCGC TCCAACACGC CCTCACTCACC CCTCTCACTCAC CCTTCCATCT CCCTTTCCTCTT CCCTTCAATG CTCTCAATG AGCGCAAGG CTCTCAATG CTCTCAATG CTCTCAATG CTCTCAATG AGCGCAACG AGCGAACAGG AGCGAACAGG ACTCGCAATG AACTCCAGCT	21  ACTCCATCAG  ACTCCATCAG  GACCTCTGCC  CTGGGAGAT  GTGACTACTAGA  CTGGGAGAT  GTGACAGCTG  GGCTCCTGGG  ACTACCCAGA  ATAGCTGCCG  ACTACCCAGA  TGCCCTTGGC  CCTTTCCCCA  GAGAGATGGT  GAGAGATGGT  GAGAGATGGT  CCTTTCCCCA  GAGAGATGGT  GCAGCTATGCC  CCTTTGCCAT  TATCTAGCTAGC  CCTTTCCCCA  GAGAGATGGT  GCAGCTATGCC  CCTTTGCCAT  TGCTGAGTTC	ATCTGGCCAT GGAAGTGGTC GGAGACCGG GCTGGCCAC CATCACACA ACTAACACAC ACTACCACAC ACACACAC	GAAGGGCTGA ACCAGCTGA ATCCGGCTG AAGATTGGGG ATCATCCGGA AAGTCCCTGA CCCCAGTCG GACTCACAGA CACCACCTGG TCCCCAGCG GACTCACAGA ACTCACCAGA ACTCACCAGG GACTCACAGA ACTCACCAGG ACTCACAGA ACCCCCAGGG GATTACCGGA ACTCACAGA ACCCCCAGGG TGTACCGGGC GTGTACCGGGC CTGCCCGGAT ATCGCAGGCA TCCTCCTACA	ACCAGCTGGG ACCAGCTGGG ACTACANACG ACGAGTATGC ACGAGTATGC ACGAGTATGC ACGAGTATGC ACTCCCGGACA ATTCCCTGGG ACAAGAGGAA ACACGAACA ACCACAAGG AGCACCACAAGG CGAACACCACACC CCTACCCCGT TGTCAGTTC AGTCGCTC AGTCGCCCA TCGTGGCACC ACTCACCCCA TCGTGGCACC ACTCACCCCA TCGTGGCACC ACTCACCCCA TCGTGGCACC ACTCACCCCA TCGTGGCACG ACCCACCCCA TCGTGGCACG ACTCACCCCA CGTACCCCCA TCGTGGCACG ACCCACCCCA TCGTGGCACG ACCCACCCCA CATCAAGGCCT CATCAAGGCC	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1080 1140 1200
50 55 60	GAATTCGGCG AGGGGCCTTT GGCCCACCAG GGTCAGAAG GGGTCCAAG GCAGAACCAT TGACAATGAC GCAACCATTC CACGCTGATC AATGATGAC GGACCCCT GGAGCCCCT GGGGCCCAT GGTGCAGCCCT GGTGGCAGAC CCGAGCCCCT GAGCACCAC CAGGCCTCAC CAGGCCTCAC CAGGCCCCAC CAGGCCCCC CAGGCCCCCC CAGCCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCC CAGCCCCCCC CAGCCCCCCC CAGCCCCCCCC	ATGCCTCACA GTGAATGGCA GTGAATGGCA GTGTAAGGC ATCCTTGGCA CCCAAGGTGG ACCATGTTTG ACTGTGCCCA AACCTCCCTA CCCAGCTCAG AGCACCTTC GAGCACCTTC CTCTACCGC TCCAACACGC CCTCACTCACC CCTCTCACTCAC CCTTCCATCT CCCTTTCCTCTT CCCTTCAATG CTCTCAATG AGCGCAAGG CTCTCAATG CTCTCAATG CTCTCAATG CTCTCAATG AGCGCAACG AGCGAACAGG AGCGAACAGG ACTCGCAATG AACTCCAGCT	21   ACTCCATCAG GACCTCTGCC CCTGCGACAT GGTACTACGA CCTGCGAGAT CCTGGGAGAT CTGGGAGAT CTGGACAGCT CTGGACAGCT GGCTCCTGGG ACTACCCCAGA TGCCCTTGCC ACTACCCAGA TGCCTTGCCAT TATCTAGCTC CCTTTCCCCAA GAGAGATGGT GCAGCTATGC CCTATGGCCAT TGCTGAGCT CCTATGGCCAT CCTATGGCCAT CCTATGGCCAT CCTATGGCCAT CCTATGGCCAT CCTATGGCCAT CCTATGGCCAT CCACGGCCTT	ATCTGGCCAT GGAAGTGGTC CTCTCGCCAG GACTGGCAGC GATGGCAGC CCGGAGTCA ACTAACACA ACTAGCCAT ACTAGCAT ACTAGCAGC CAACCTCTCG AAAGCAGCAC CAACCTCTCG GGGGCCACC CACCTCTCG GGGGCCACC CACCCCCTACC CACCCCCTACC CACCCCCTACC CACCCCCTACC CACCCCCTACC CCCCCTACC CCCCCTACC CCCCCTACC	GAAGGGCTGA ACCAGCTGA ATCCGGCTG AAGATTGGGG ATCATCCGGA AAGTCCCTGA CCCCAGTCG GACTCACAGA CACCACCTGG TCCCCAGCG GACTCACAGA ACTCACCAGA ACTCACCAGG GACTCACAGA ACTCACCAGG ACTCACAGA ACCCCCAGGG GATTACCGGA ACTCACAGA ACCCCCAGGG TGTACCGGGC GTGTACCGGGC CTGCCCGGAT ATCGCAGGCA TCCTCCTACA	ACCAGCTGGG ACCAGCTGGG ACTACANACG ACGAGTATGC ACGAGTATGC ACGAGTATGC ACGAGTATGC ACTCCCGGACA ATTCCCTGGG ACAAGAGGAA ACACGAACA ACCACAAGG AGCACCACAAGG CGAACACCACACC CCTACCCCGT TGTCAGTTC AGTCGCTC AGTCGCCCA TCGTGGCACC ACTCACCCCA TCGTGGCACC ACTCACCCCA TCGTGGCACC ACTCACCCCA TCGTGGCACC ACTCACCCCA TCGTGGCACG ACCCACCCCA TCGTGGCACG ACTCACCCCA CGTACCCCCA TCGTGGCACG ACCCACCCCA TCGTGGCACG ACCCACCCCA CATCAAGGCCT CATCAAGGCC	120 180 240 360 420 480 540 660 720 780 840 900 960 1020 1140 1200 1260
50 55 60 65	GAATTCGGCG AGGGGCCTTT GGCCACCAG GGTCACAAG GGCTCCAAG CCAGAACCAT GCACACTAC AATGATGAC GGACCCTAC AATGATGAC GGACCCCTAC CGGACCCCTAC GGTGCCCATT CGAGCACGCT CCACCCCC CCAGCCCCC CAGGCCCCC CAGCCCCC CAGCCCCC CAGCCCCC CAGCCCCC CAGCCCC CAGCCCCC CAGCCCCC CAGCCCCC CAGCCCCC CAGCCCCC CAGCCCCC CAGCCCCCC CAGCCCCCCC CAGCCCCCCC CAGCCCCCC CAGCCCCCC CAGCCCCCCC CAGCCCCCC CAGCCCCCC CAGCCCCCC CAGCCCCCCC CAGCCCCCC CAGCCCCCC CAGCCCCCC CAGCCCCCCC CAGCCCCCC CAGCCCCCC CAGCCCCCC CAGCCCCCC CAGCCCCCCC CAGCCCCCCCC	ATGCCTCACA GTGAATGGCA GTGAATGGCA GTGATAGGCA ATCCTTGGCA ACCTGCTCA ACCTCCTA ACCAGCTCAG TCCATCAATG AGTGATCAG AAGCACCTTC GAGCAGCAC TCCAACACGC TCCAACACGC TCCAACACGC TCCAACACGC TCCATCACT CCCTTCATCAT CCCTTCATCT CCCTTCAATG TCCACCACTG AACTCCAGCT AACTCCAGCT CCCACCACTG TCCAACACGC TCCACCACTG TCCACCACTG TCCACCACTG TCCACCACTG TCCACCACTG TCCACCACTG TCCACCACTG TCCACCACTG TCCGCACCACTG TCCCACCACTG TCCCACCACCACTG TCCCACCACCACCACCACCACCACCACCACCACCACCACC	21  ACTICATCAG GACCTCTGCC CCTGCGACAT GGTACTAGA CCACCCCCAA CCTGGGAGAT GTGTCAGCTC TGGACAGCTG CTGTAACTCC GGCTCCTGGG ATAGCTGCCG ATACCTGCCAG TGCCCTTGCCAT CACTGGGAGC CCTTTCCCCAC GAGAGATGGT GCAGTTTCCCCAC TGAGTCTGCT CCTTTCCCCAC TGCTGAGTTC CCTTTCCCCAC TGCTGAGTTC CCACGCCTT SEQUEDCE	ATCTGGCCAT GGAAGTGGTC CTCTCGCCAG GACTGGCAGC GATGGCAGC CCGGAGTCA ACTAACACA ACTAGCCAT ACTAGCAT ACTAGCAGC CAACCTCTCG AAAGCAGCAC CAACCTCTCG GGGGCCACC CACCTCTCG GGGGCCACC CACCCCCTACC CACCCCCTACC CACCCCCTACC CACCCCCTACC CACCCCCTACC CCCCCTACC CCCCCTACC CCCCCTACC	GAAGGGCTGA ACCAGCTGA ATCCGGCTG AAGATTGGGG ATCATCCGGA AAGTCCCTGA CCCCAGTCG GACTCACAGA CACCACCTGG TCCCCAGCG GACTCACAGA ACTCACCAGA ACTCACCAGG GACTCACAGA ACTCACCAGG ACTCACAGA ACCCCCAGGG GATTACCGGA ACTCACAGA ACCCCCAGGG TGTACCGGGC GTGTACCGGGC CTGCCCGGAT ATCGCAGGCA TCCTCCTACA	ACCAGCTGGG ACCAGCTGGG ACTACANACG ACGAGTATGC ACGAGTATGC ACGAGTATGC ACGAGTATGC ACTCCCGGACA ATTCCCTGGG ACAAGAGGAA ACACGAACA ACCACAAGG AGCACCACAAGG CGAACACCACACC CCTACCCCGT TGTCAGTTC AGTCGCTC AGTCGCCCA TCGTGGCACC ACTCACCCCA TCGTGGCACC ACTCACCCCA TCGTGGCACC ACTCACCCCA TCGTGGCACC ACTCACCCCA TCGTGGCACG ACCCACCCCA TCGTGGCACG ACTCACCCCA CGTACCCCCA TCGTGGCACG ACCCACCCCA TCGTGGCACG ACCCACCCCA CATCAAGGCCT CATCAAGGCC	120 180 240 360 420 480 540 660 720 780 840 900 960 1020 1140 1200 1260
50 55 60 65	GAATTCGGCG AGGGGCCTTT GGCCCACCAG GGTCACAAG GGGCTCCAAG GCACACTTT GCACATGAC CTCACCTAC AATGATGAC GGACCCCT AATGACACCCT GGGGCCCCATT CGAGCACCCT GGTGGCAGAC CCTGACCCCT CATCCCCAC CAGGCCCTC CATCCCCAC CAGGCCCTC CATCCCACC AAGTGAATAC GCGCTTCCCC GAGTGACCCCT Seq ID NO: Protein Ac 1	ATGCCTCACA ATGCCTCACA GTGAATGGCA GTGAATGGCA ACCTTTGGCA ACCTCCTTA ACCTCCTCA ACCTCCTCA ACCTCCACTCAC TCCATCACTCAC	21  ACTCCATCAG GACCTCTGCC CCTGCGACAT GGTACTACGA CCTGCGAGAT CGTGCAGAT CTGGCAGAT GTTCAGCTC TGGACAGCTG GCTCCTGGG ATACCCCAGA TGCCTTGCC ACTACCCAGA TGCCTTGCT CACTGGCAT TATCTAGCTC CCTTTCCCCA TATCTAGCTC CCTTTCCCCAT TATCTAGCTC CCTTATGCCAT TATCTAGCTC CCTATGGCCAT TGCTGAGTTC CCACGGCCTT CCACGGCCTT SEQUENCE NP_003457 21	ATCTGGCCAT GGAAGTGGTC GGAGTGGGCAG GATTGGCAG GATTGGCAG CCTGGCCAC CATCATAATAGA ACTAGCATC CAACACTCTCAG AACAGCACC AACACTCTCG AAGCAGGA CGCCTATTGC CCACCTCTCG CCACCTCTCG CCACCTCTCG CCCCATATTAT TGACCATCT CTCAGCAGA CTCCTCTGCC CACCCCTAC CCCATATTAT TGACCATCTG	GGAGGGCTGA GGCAGGCGCA ATCCGGCTGA ATCCGGCTG AAGATTGGGG CTCCTGGCTG ATCATCCGGA AAGTCCCTGA ACCCCCAGTCG GACTCACCAGA CACCACCTCG CTGGACGAGCG GACTCACCAGA ACCCCCGAGCG GATTCACCAGA ACCCCCGAGCG GATTCACCAGA ACCCCCGAGCG GTGTACCGGGC TACCCCGGACG TACCCCCGACC TACAGTTCCACA TACAGTTCCACA TACAGTTCCACA TACAGTTCCACA TACAGTTCCACA TACAGTTCCACA TACAGTTCCACACA TACAGTTCCACACA TACAGTTCCACACA TACAGTTCCACACA TACAGTTCCACACACACACACACACACACACACACACACA	ACCAGCTGGG ACCAGCTGGG ACTACAAACG AGGCGTCTG CCAAAGTGCA AGGCCGTCGA ATTCCCGGACA ATTCCCTGGG ACACAGAGGAAA GCAGCAGCAG AGCAGCAGCAG AGCAGCAGCAG AGCAGCAGCAG ACACCAAAGG AGCAGCAG ACACCAACAGT TGTCCAGGT TGTCCAGGT AGTTCACGGG ACCCACCCA AGTTCACGGG ACCCACCCA TGTGGCAGG GCGAGGCCTG CATCAAGGCC TT	120 180 240 300 360 420 6600 6600 720 780 840 900 1020 1020 1140 1200 1260 1320
50 55 60 65	GAATTCGGCG AGGGGCCTTT GGCCCACCAG GGTCCAGA GGGTCCAAG GCAACCATT CAAGCATC CACGCTAC AATGATGAC GGACCCTA CGAGCCCAT GGAGCCCAT GGAGCCCAT GGTGGCAGACCCT GGTGGCAGACCCT GGTGGCCAT AGCTCCCAC CAGGCCCCC CAGCCCCTA CAGGCTCCCC GAGTGCACC GAGTGCACC Seq ID NO: Protein Ac 1   MPHNSIRSGE ILGRYYETGS	ATGCCTCACA GTGAATGGCA GTGAATGGCA GTGAATGGCA GTGTAAGGC ATCCTTGGCA ACCTCCTTA ACTGTGCCA AACCTCCTTA AGTGATCAGG TCCATCAATG TCCATCAATG AGGCACTTC GAGCGGCAGC CTCAACAGGC CTCTACTCAT CCTTCATTT CCCTTCATTG CTTCTCAATG AGCGAATG TCGCAATG TCGCAACGT TCGCAATG TCGCAATG TCGCAACGT TCGCAATG TCGCAATG TCGCAATG TCGCAACGT TCGCAATG TCGCAACGT	21  ACTCCATCAG GACCTCTGCC CCTGCGACAT GGTACTACGA CCTGGGAGAT GTGTCAGCTC GGCTCCTGGG ATACTCC GGCTCCTGGG ATACTCC GCACCCCAA CCTGGGAGAT CCTGACTC GCACCGCAT ACTCCCAGA TGCCCTTGCC CCTTTCCCCAT TATCTAGCTC CCTTTCCCCAT GGAGATGGT GCACTATGGCCAT TATCTAGCCAT GCACGACTATGC CCTATGGCCAT TGCTGACTAT GCACGCCTT SEQUENCE NP_003457 21  VNGRPLPEVV C PRVATPKVVE	ATCTGGCCAT GGAAGTGGTC GGAAGTGGCCAC GACTGGCAGC CCTGAGCCAC CATTAATAGA CCTCGCCAG ACTAGCATCA CATCGCTCAG GGCCTTATGCC CAACACCACC CAACATCTTTG TGCTGCCTCC CACCCCTAC CTCCTCTCCC CACCCCTAC CCACCTCTTGCC CACCCCTAC CCACCTCTTGCC CACCCCTAC CCACATATTAT TGACCATCTGCC CACCCCTAC CCATATTAT  A RQRIVDLAHC KIGDYKRONE	GGAGGGCTGA GGCAGGGCA ATCCGGCTG AAGATTGGGG CTCCTGGCTG ATCATCCGGA AAGTCCCTGA ACCCCAGCG GGACTCACAGGA ACCCCCAGCG CTGGCAGGG GATCTACCAGGA ACCCCGAGGG GATCTACCAGGA ACCCCGAGGG GATCTACCAGGA CTGCCCGGAT ATCGCAGGCA TACGCTGGAGGA TACGTTGCAGGCA TACGTTGCAGCAGA TACGTTGCAGGCA TACGTTGCAGGCA TACGTTGCAGGCA TACGTTGCAGGCA TACGTTGCAGGCA TACGTTGCAGGCA TACGTTGCAGGCA TACGTTGCAGGCA TACGTTGCAGGCAGA TACGTTGCAGGCA TACGTTGCAGGCA TACGTTGCAGGCA TACGTTGCAGGCAGA TACGTTGCAGGCAGA TACGTTGCAGGCAGA TACGTTGCAGGCAGA TACGTTGCAGGCAGAGA TACGTTGCAGGCAGAGA TACGTTGCAGGCAGAGAA TACGTTGCAGAGAA TACGTTGCAGAGAA TACGTTGCAGAGAA TACGTTGCAGAGAAA TACGTTGCAGAGAAAA TACGTTGCAGAAAAAAAAAA	ACCAGCTGGG ACTACAAAGG ACTACAAAGG ACTACAAAGG ACTACAAAGG ACTACAAAGG ACTACCAGGACA ACTCCCGGACA ACTCCCGGACA ACTCCCGGACA AGCAGCACCAG AGCAGCACCA AGCAGCACCAC ACTCCCCGT ACTTCACCCGT ACTTCACCCGT ACTTCACCGG ACCACACCCCA TCGTGGCACC ACTTCACCCGG TCTCACCCCT TTTCCAGTTC AGTCGGCTC ACTTCACGGG ACCCACCCCA TCGTGGCAGG CCATCAAGGCC TT  51	120 180 240 300 360 420 540 660 720 780 960 1020 1140 1200 1320
50 55 60 65 70	GAATTCGGCG AGGGGCCTTT GGCCACCAG GGTCACAAG GGGCTCCAAG CCAGAACCATTC CACGCTGATC CTCCACCTAC AATGGATGAC CGGACCCCTA CGGCCCATT CGAGCAGGCCCTA CGGGCCCCAT CGGGGCCCCA CCAGGCCCTC CATCCCCACC CAGGCCCTC CATCCCCACC CAGGCCTTC CAGGCT	ATGCCTCACA ATGCCTCACA GTGAATGGCA GTGAATGGCA GTGATAGGCA ATCCTTGGCA ACCTCCTCA ACCTCCCTA ACCTCCAG TCCATCAGG CGAGCTCAG TCCATCAGG CCTCACTCAC CCTTCACTCAC CCTTCACTCAC TCCACCAGGT CCTTCACTGGC TCCACCACTG CCTTCACTCAC CCTTCCACTG CCTTCACTGGC TCCACCACTG ACCGCACCACTG CCCTCCACTAGGC TCCACCACTG CCCACCACTG CCCACCACTC CCCACCACTG CCCACCACTC CCCACCAC	21  ACTCCATCAG GACCTCTGCC CCTGCGACAT GGTACTACGA CCTCCCCAA CCTGCGAGAT GTGTCAGCTG CTGTAACTCC GGCTCCTGGG ACTACCCAGA ATAGCTGCCTTGCCAT TATTCTAGCTC CCTTTCCCCA GAGAGATGGT CCATTGGCATT TATCTAGCTG CCTTTGCCAT TATCTAGCTT CCTTTGCCAT TATCTAGCTT CCTTTGCCAT TATCTAGCT CCTTTGCCAT TATCTAGCTT CCTTTGCCAT TATCTAGCT CCTTTGCCAT TATCTA	ATCTGGCCAT GGAAGTGGTC GGAGACCGG GCTGGCGAG CCGAGACCGG CATTAATAGA CGTGGCCACC CACCTCTCG AAAGCACTCC AAACACACCAC TGCTCCTCGC CACCTCTCG CACCTCTCG CACCTCTCG CACCTCTCG CACCCCTACC CACCCCCTACC CACCCCTACC CACCCCCTACC CACCCCCTACC CACCCCTACC CACCCCTACC CACCCCTACC CACCCCCTACC CACCCCCCTACC CACCCCCCTACC CACCCCCCTACC CACCCCCCCC	GGAGGGCTGA GGAGGGCTGA ATCCGGCTGA ATCCGGCTGA ATCCGGCTGA ATCCGGCTGA ATCCCGGA AAGTCCCTGA ACCCCAGTCGG GACTCACAGA CACCACCTCGG GACTCACAGA ACCCCCAGGCG GATCACCAGA ACCCCCGAGCG GTGTACCGGA CTCGCCAGCC CTGGCAGGCG GTTACCGGAG TACTGCAGGCA TACTGCAGCAGCA TACTGCAGCAGCA TACTGCAGCAGCA TACTGCAGCAGCA TACTGCAGCAGCA TACTGCAGCAGCA TACTGCAGCAGCA TACTGCAGCAGCA TACTGCAGCAGCAGCA TACTGCAGCAGCAGCA TACTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	ACCAGCTGGG ACCAGCTGGG ACTACAAACG AGGCGTCTG CCAAAGTGCA AGGCGTCTG CCAAAGTGCA ATTCCCTGGG ACAAGAGGAA AGCAGCACAAAGG AGACGACACAAAGG GGAAGGCAC CCTACCCCGT TGTCCAGTTC AGTTCACGGG ACCACCCCA TGGTGGCAGG CCATCACCCCT TGTCAGTTC AGTTCAGGC CTTCACTCCCT TGTCAGTTC AGTTCAGGC TT	120 180 240 300 360 420 540 660 720 780 900 960 1020 1260 1320
50 55 60 65 70	GAATTCGGCG AGGGGCCTTT GGCCCACCAG GGTCACAAG GGGCTCCAAG GCACACTT CACACTAGC AATGATGAC CTCACCTAC AATGATGAC CTCACCTAC CAGCCCTAT CGAGCACCAT CGAGCCCCAT CGAGCCCCAC GGTGGCAGAT TAGCTCCACC CAGGCCTTCCC CATCCCCACC AATGATAAC GCGCTTCCCC GAGTGCACC Seq ID NO: Protein AC 1	ATGCCTCACA GTGAATGGCA GTGAATGGCA GTGAATGGCA GTGAATGGCA GCCAAGGTGG ACCATGTTTG ACTGTGCCA AACCTCCTA ACCTCACTCA GTGATCAGG CTCAACACGC CTCTACCCGC CCTCACTCAC CCTTCCTCTT CCCTTCAATG CTCTCAGGCAATG CTCTCAGCAGGCAATG CTCTCACACAATG CTCTCACACAATG CTCTCAGCAGGCAATG CTCTCACACAATG CTCTCACACAATG CTCTCAACAATG CTCTCAAC	21  ACTCCATCAG GACCTCTGCC CCTGCGACAT GGTACTACGA CCTGGGAGAT GTGCAGCAT CTGGACAGCT CTGGACAGCT CTGACTACC GGCTCCTGGG ACTACCCCGA ACTACCCAGA TGCCCTTGCC ACTACCCAGA TGCCTTTCCCCA TATCTAGCTC CCTTTCCCCA TGCTGACT CCTATGGCCAT TATCTAGCTC CCTATGGCCAT TATCTAGCTC CCACGCCTT  Bequence NP_003457 21  VVNGRPLPEVV PKVATPKVVII NLPMDSCVAT SDQDSCRLSI LYPLPLINST PSSLSSSAFI	ATCTGGCCAT GGAAGTGGTC GGAAGTGGTCAG GATTGACAGC GATTGACAGC CCTGAGCACC CATCATAATAGA ACTAGCATCAG ACTAGCACC CAACATCTCAG CAACACCACC CAACATCACC CAACATCACC CAACATCACC CAACATCACC CAACATCACC CAACATCACC CAACATCACC CAACATCACC CACCCCTACC CACCCCTACC CACCCCTACC CACCCCTACC CACCCCTACC CACCCCTACC CACCCCTACC CACCCCCTACC CACCCCTACC CACCCCCTACC CACCCCTACC CACCCCCTACC CACCCCTACC CACCCTACC CACCCCTACC CACCCTACC CACCCCTACC CACCCCTACC CACCCCTACC CACCCCTACC CA	GGAGGGCTGA GGCAGGCGCA ATCCGGCTGA ATCCGGCTGA ATCCGGCTGA ATCCGGCTGA ATCCCTGGA AAGTCCCTGA ACCCCAGTCGG GGACTCACCAGGCA CTCGCCCAGGCC CTGGACGACGA ACCCCCAGGCC CTGGACGACGA CTCACCAGGA ACCCCCAGGCC CTGCCCGAGGC CTGCCCGGGC CTGCCCGAGGC CTGCCCAGGC CTGCCCAGCC CTGCCCAGGC CTGCCCAGC CTGCCCAGGC CTGCCCAGC CTGCCCAGGC CTGCCCAGGC CTGCCCAGGC CTGCCCAGGC CTGCCCAGGC CTGCCCAGGC CTGCCCAGGC CTGCCCAGGC C	ACCAGCTGGG ACCAGCTGGG ACTACAAACG AGGGGATTGGAACTTG GAGTGATAGG ACTACAAACG AGGGCGTCTG CCAAAGTGCA ATTCCCTGGG ACAAGAGGAA ACACCAAAGG AGCAGCACCACCCGT TGTCCAGTTC AAGTCGGCTC AAGTCAGCCGT AAGTCAGCCGT AAGTCAGCCGT CATTCACCGGG ACCACCCCA TGTTGGCAGG CCACCCCA TT  51   LEVSHGCVSK LLAEGVCDND PQSDSLGSTY HHLEPLECPP TTQTYVAAD VYGGFTGQAL	120 180 240 300 360 420 600 720 780 840 960 1020 1140 1200 1140 1200 1320
50 55 60 65 70	GAATTCGGCG AGGGGCCTTT GGCCCACCAG GGTCACAAG GGGCTCCAAG GCACACATT CAACATGAC CTCACCTAC AATGATGAC CGGACCCCA AGGCCCCAT CGAGCACCAT CGAGCCCCAC AGTGCCCAC GGTGCACCAC CCAGCCCTC CATCCCACC CAGGCCTCC CATCCCACC CAGGCCCCAC AAGTGAATAC GCGCTTCCCC GAGTGCACC Seq ID NO: Protein AC 1	ATGCCTCACA GTGAATGGCA GTGAATGGCA GTGAATGGCA GTGAATGGCA GCCAAGGTGG ACCATGTTTG ACTGTGCCA AACCTCCTA ACCTCACTCA GTGATCAGG CTCAACACGC CTCTACCCGC CCTCACTCAC CCTTCCTCTT CCCTTCAATG CTCTCAGGCAATG CTCTCAGCAGGCAATG CTCTCACACAATG CTCTCACACAATG CTCTCAGCAGGCAATG CTCTCACACAATG CTCTCACACAATG CTCTCAACAATG CTCTCAAC	21  ACTCCATCAG GACCTCTGCC CCTGCGACAT GGTACTACGA CCTCCCCAA CCTGCGAGACT GTGCACGCT GGGACAGCT GGGACAGCT GGGACAGCT GGCACGCCCCCCAA CCTGGAGATC CCGCATCCCCGG GCACGGATGC ACTACCCAGA TGCCCTTGCCAT TATCTAGCTC CCTTTCCCCA GAGAGATGGT CCATGGGCCA TGCTGAGTTC CCTTAGCCCT TGCTGAGTTC CCATGGCCA TGCTGAGTTC CCATGGCCA TGCTGAGTTC CCATGGCCA TGCTGAGTTC CCACGCCTT SEQUENCE NP_003457 21  VNGRPLPEVV VRVATPKVVE NLPMDSCVAT DSSLQSSAFI TSSLSSAFI TSSLSSAFI TSCQGSYASSI	ATCTGGCCAT GGAAGTGGTC GGAGGTGGCCAG GACTGGCAGC CCTGGCCAGC CCTGGCCACC CCCGGAGTCA CCTCAGCCAG ACTAGCATC CAACACTCTCG AAACAGCACC CAACCTCTCG AAAGCAGGA CCTCTCTG CCACCCTTATTAT TGCTGCCTCC CACCCCTACC CACCCTACC CACCCCTACC CACCCTACC CACCCCTACC CACCCCTACC CACCCCTACC CACCCTACC CACCCCTACC CACCCTACC CACCCCTACC CACCCCTACC CACCCCTACC CACCCCTACC CACCCCTACC CA	GGAGGGCTGA GGCAGGCGCA ATCCGGCTGA ATCCGGCTGA ATCCGGCTGA ATCCGGCTGA ATCCCTGGA AAGTCCCTGA ACCCCAGTCGG GGACTCACCAGGCA CTCGCCCAGGCC CTGGACGACGA ACCCCCAGGCC CTGGACGACGA CTCACCAGGA ACCCCCAGGCC CTGCCCGAGGC CTGCCCGGGC CTGCCCGAGGC CTGCCCAGGC CTGCCCAGCC CTGCCCAGGC CTGCCCAGC CTGCCCAGGC CTGCCCAGC CTGCCCAGGC CTGCCCAGGC CTGCCCAGGC CTGCCCAGGC CTGCCCAGGC CTGCCCAGGC CTGCCCAGGC CTGCCCAGGC C	ACCAGCTGGG ACTACAAAGG ACTACAAAGG ACTACAAAGG ACTACAAAGG ACTACAAAGG ACTACCAGGACA ACTCCCGGACA ACTCCCGGACA ACTCCCGGACA AGCAGCACAGA AGCAGCACAGA AGCAGCACAGA AGCAGCACAGA AGCAGCACAGA AGCAGCACAGA AGCAGCACAAAGG ACACACAC	120 180 240 300 360 420 540 660 720 780 900 960 1020 1140 1200 1320
50 55 60 65 70	GAATTCGGCG AGGGGCCTTT GGCCCACCAG GGTCAGAG CCAGAACCCT TGACAATGAC CCAGCTGATC CACCTAC AATGGATGAC CGGACCCCGA GTGCCCATT GGTGGCAGAT TAGCTCACC CAGCTGAT CCAGCTATC CGAGCCCCA CCAGCCCAC CAGCCCCAC CAGCCCAC CAGCCCCAC CAGCTCCCCAC CAGCTCCCCAC AGTGACACC Seq ID NO: Protein AC I MPHNSIRSGE ILGRYYETGS TVPSVSSINI SINGLLGIAG ERCHYPEAY PHSPFAIKQI LSGREMVGFT NSSLLSSPY	ATGCCTCACA GTGAATGGCA GTGAATGGCA GTGAATGGCA GTGAATGGCA GCCAAGGTGG ACCATGTTTG ACTGTGCCCA AACCTCCTTA ACTGTACCAG TCCATCAATG GTGATCAGG CTCTACCAGG CCTCACTCAC CCTTCCTCTT CCCTTCAATG CTCTACAGGC CTCTCAGGCAATG AGGGACAGG TCTGAGCAGG CTCTCAGGCAATG CCCTCCACTG CCTTCCAGGT CCCACCACTG CCGAGCAGGG TCTGAGCAGG TCTGGCAATG AGGGACAGG TCTGGCAATG AGGGACAGG TCTGGCAATG AGGGACAGG TCTGGCAATG AGGGACAGG TCTGGCAATG TCTGAGCAGG TCTGGCAATG TCTGAGCAGG TCTGCAGCAGG TCTGAGCAGG TCTGAATG TCTGAGCAGG TCTGAGCAGG TCTGAGCAGG TCTGAATG TCTGAGCAGG TCTGACAGG TCTGAGCAGG TCTGAGC TCTGAGCAGG TCTGAGC TCTGAGCAGG TCTGAGCAGG TCTGAGCAGG TCTGAGCAGG	ACTCCATCAG GACCTCTGCC CCTGCGACAT GGTACTACGA CCTGCGAGAGT GGTCAGGCT CTGGACAT CTGGAGAT CTGGACAGCT GGCTCCTGGG ATACTCCG GCACCGCAGA TGCCCTTGCC CCTTTCCCCA GAGAGATGCT CCTTTCCCCAC GAGAGATGGT CCTTTCCCCAC GAGAGATGGT CCCATTGCCT CCCTTTCCCCAT TATCTAGCTC CCTTTCCCCAT GAGAGATGGT CCCACGGCCTI Sequence NP_003457 21 VNGRPLPEVV PKVATPKVVE NLPMDSCVAT SDQDSCRLST CTYPLPLLINST SGQGSYASSI PTTATAFDHI	ATCTGGCCAT GGAAGTGGTC GGAGGTGGCCAG GACTGGCAGC CCTGGCCAGC CCTGGCCACC CCCGGAGTCA CCTCAGCCAG ACTAGCATC CAACACTCTCG AAACAGCACC CAACCTCTCG AAAGCAGGA CCTCTCTG CCACCCTTATTAT TGCTGCCTCC CACCCCTACC CACCCTACC CACCCCTACC CACCCTACC CACCCCTACC CACCCCTACC CACCCCTACC CACCCTACC CACCCCTACC CACCCTACC CACCCCTACC CACCCCTACC CACCCCTACC CACCCCTACC CACCCCTACC CA	GGAGGGCTGA GGCAGGCGCA ATCCGGCTGA ATCCGGCTGA ATCCGGCTGA ATCCGGCTGA ATCCCTGGA AAGTCCCTGA ACCCCAGTCGG GGACTCACCAGGCA CTCGCCCAGGCC CTGGACGACGA ACCCCCAGGCC CTGGACGACGA CTCACCAGGA ACCCCCAGGCC CTGCCCGAGGC CTGCCCGGGC CTGCCCGAGGC CTGCCCAGGC CTGCCCAGCC CTGCCCAGGC CTGCCCAGC CTGCCCAGGC CTGCCCAGC CTGCCCAGGC CTGCCCAGGC CTGCCCAGGC CTGCCCAGGC CTGCCCAGGC CTGCCCAGGC CTGCCCAGGC CTGCCCAGGC C	ACCAGCTGGG ACCAGCTGGG ACTACAAACG AGGGGATTGGAACTTG GAGTGATAGG ACTACAAACG AGGGCGTCTG CCAAAGTGCA ATTCCCTGGG ACAAGAGGAA ACACCAAAGG AGCAGCACCACCCGT TGTCCAGTTC AAGTCGGCTC AAGTCAGCCGT AAGTCAGCCGT AAGTCAGCCGT CATTCACCGGG ACCACCCCA TGTTGGCAGG CCACCCCA TT  51   LEVSHGCVSK LLAEGVCDND PQSDSLGSTY HHLEPLECPP TTQTYVAAD VYGGFTGQAL	120 180 240 300 360 420 600 720 780 840 960 1020 1140 1200 1140 1200 1320

	1	11	21	31	41	51	
	TTCAGAAGGA	GCAGAGACAC	CGGGCCCAGG	GCACCCTCGC	GGGCGGGGGG	ACCCAAGCAG	60
_	TGAGGGCCTG	CAGCOGGCOG	GCCAGGGCAG	CGGCAGGCGC	GGCCCGGACC	TACGGGAGGA	120
5	AGCCCCGAGC	CCTCGGCGGG	CTGCGAGCGA	CTCCCCCGGCG	ATGCCTCACA	ACTCCATCAG	180
	ATCTGGCCAT	GGAGGGCTGA	ACCAGCTGGG	AGGGGCCTTT	GTGAATGGCA	GACCTCTGCC	240
	GGAAGTGGTC	CGCCAGCGCA	TCGTAGACCT	GGCCCACCAG	GGTGTAAGGC	CCTGCGACAT	300
	CTCTCGCCAG	CTCCGCGTCA	GCCATGGCTG GAGTGATAGG	CCCCTCCAAC	ATCCTTGGCA	CACCCCCAA	360 420
10	GACTGGCAGC	ALCOGCCIG	ACTACAAACG	CCAGAACCCT	ACCATGTTTG	CCTGGGAGAT	480
~ •			AGGGCGTCTG				540
	CATTAATAGA	ATCATCCGGA	CCAAAGTGCA	GCAACCATTC	AACCTCCCTA	TGGACAGCTG	600
	CGTGGCCACC	AAGTCCCTGA	GTCCCGGACA	CACGCTGATC	CCCAGCTCAG	CTGTAACTCC	660
15	CCCGGAGTCA	CCCCAGTCGG	ATTCCCTGGG ACAAGAGGAA	ANTOCATOR	TCCATCAATG	ATACCTCCCG	720 780
13	ACTARCOTTA	CACTCACAGA	GCAGCAGCAG	OGGACCCOGA	AAGCACCTTC	GCACGGATGC	840
	CTTCAGCCAG	CACCACCTCG	AGCCGCTCGA	GTGCCCATTT	GAGCGGCAGC	ACTACCCAGA	900
	GGCCTATGCC	TCCCCCAGCC	ACACCAAAGG	CGAGCAGGGC	CTCTACCCGC	TGCCCTTGCT	960
20			GGAAGGCCAC				1020
20	CAACCTCTCG	ACTCACCAGA	CCTACCCCGT	GGTGGCAGCT	CCGCCCTTTT	COTOTACCAG	1080 1140
	CAAGTCGGCT	CCCACCCCCT	GCCCTTCAAT CCTCTCAGGG	CCAGAGATGG	TGGGGCCCAC	GCTGCCCGGA	1200
			CAGCGGACAG				1260
~ ~	ATGGTGGCAG	GAAGTGAATA	CTCTGGCAAT	GCCTATGGCC	ACACCCCCTA	CTCCTCCTAC	1320
25	AGCGAGGCCT	GGGGCTTCCC	CAACTCCAGC	TTGCTGAGTT	CCCCATATTA	TTACAGTTCC	1380
1			GCCCACCACT	GCCACGGCCT	TIGACCATCI	GTAGTTGCCA	1440
	TGGGGACAGT	G					
	Sea ID NO:	52 Protein	sequence				
30		cession #: 1					
	i.	11	21	31	41	51	
				PORTURE AUG	CIMPONTERO.	Lencorcover	60
			VNGRPLPEVV PKVATPKVVE				120
35			NLPMDSCVAT				180
	SINGLLGIAQ	PGSDKRKMDD	SDQDSCRLSI	DSQSSSSGPR	KHLRTDAFSQ	HHLEPLECPP	240
			LYPLPLLNST				300
			MLPPCTGSSR		WGPRCPDTHP	TSPPADRAAM	360
40	PPLPSQAWWQ	EVNTLAMPMA	TPPTPPTARP	GASPTPAC			
10	Seg ID NO:	53 DNA seg	uence				
	Nucleic Ac:	id Accession	n #: NM_0124	127			
		id Accession					
15				31	41	51	
45	Coding sequents	лепсе: 43! 11 	924 21	31   .	1	i	60
45	Coding sequents     CTTGTGGTTC	ience: 43! 11     CTCTCTACTT	924 21     GGGGAAATCA	31   . GGTGCAGCGG	 CCATGGCTAC	 AGCAAGACCC	60 120
45	Coding sequence of the control of th	11   CTCTCTACTT GGGTGCTCTG ACAATGATGT	924 21     GGGGAAATCA TGCTCTGATC TTCCTGTGAC	31   . GGTGCAGCGG ACAGCCTTGC CACCCCTCTA	CCATGGCTAC TTCTGGGGGT ACACCGTGCC	AGCAAGACCC CACAGAGCAT CTCTGGGAGC	
	Coding sequence of the control of th	lence: 43  11  CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG	924 21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA	31   . GGTGCAGCGG ACAGCCTTGC CACCCCTCTA GACGCCCGGT	CCATGGCTAC TTCTGGGGT ACACCGTGCC CGGATGACAG	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCCGC	120 180 240
45 50	Coding sequence of the control of th	lence: 43  11  CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCOGACTG	224 21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGAA CGATATGCAC	31   . GGTGCAGCGG ACAGCCTTGC CACCCCTCTA GACGCCCGGT ACCCAGCCGT	CCATGGCTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG GGCAGGCCGC	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCCGC GCTGTTGCTA	120 180 240 300
	Coding sequence of the control of th	Dence: 43  11    CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCGGACTG AGCTCTACTG	924 21   GGGGAAATCA TGCTCTGTGAC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGGCGGTG	31 	CCATGGCTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG GGCAGGCCGC CACAGTGGCT	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACGGCC	120 180 240 300 360
	Coding sequence of the control of th	LENCE: 43  11  CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCGACTG AGCTCTACTG GGAAGAAAGT	924 21     GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGGGGGTG TTTCAGAGTC	31   GGTGCAGCGG ACAGCCTTGC CACCCCTCTA GACGCCCGGT TTGGTGCATC CGTCTCGGCC	CCATGGCTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG GGCAGGCCGC CACAGTGGCT ACTACTCCCT	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACCGGCC GTCACCAGTT	120 180 240 300
50	Coding sequence of the control of th	HENCE: 43  11  CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGCTCTACTG GGAAGAAAGT AGCTCTACTG	924 21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGGCGGTG TTTCAGAGTC CTTCCAGGGG	31 	CCATGGCTAC TTCTGGGGG ACACGTGCC CGGATGACAG GGCAGGCCGC CACAGTGGCT ACTACTCCCT TCCCCCACCC ACAGAAGAAT	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACCAGCT TGGCTACTCC TCGTCCCACT	120 180 240 300 360 420 480 540
	Coding sequence of the control of th	HENCE: 43  11    CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCGGACTGG AGCTCTACTG GGAAGAAAGT AGCTCTACTG GGAAGAAAGT ACTCTAAACGA GACCCATCAA	924 21   GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGAA CGATATGCAC CGGGCGGTG TTTCAGAGTC GTTCCAGGGC CCTCATGCTC	31 	CCATGGCTAC TTCTGGGGT ACACCGTGCC CGGATGACAG GGCAGGCCGC CACAGTGGCT ACTACTCCCT TCCCCCACCC ACAGAAGAAT CTGCTGGGAC	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG	120 180 240 300 360 420 480 540 600
50	Coding sequence of the control of th	Lence: 43  11    CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCOGACTG AGCTCTACTG AGCTCTACTGA AGCTCTAACGA ACTCTAACGA GGCGGACAAC	924 21	31   GGTGCAGCGG ACAGCCTTGC CACCCCTCTA ACCCAGCCGT TTGGTGCATC CGTCTCGGCC GTCAAATCCA ATCAAACTGA ACTGAACTGA	CCATGGCTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG GGCAGGCCGC CACAGTGGCT ACTACTCCCT TCCCCCACCC ACAGAAGAAT CTGCTGGGAC TCCCTAAGGT	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACGGCC GTCACCAGTT TGGCTACTCC TCGTCCCACT TCGTCCCACT CCTCCACTGC	120 180 240 300 360 420 480 540 600 660
50	Coding sequence of the control of th	Lence: 43  11  CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCOGACTG GGAAGAAAGT ACGTCTACTG GGAAGAAAGT GGCAGCAGAT ACTCTAACGA GACCCATCAA GGGGGACAAC GCGTGCTAAAG	924 21	31   GGTGCAGCGG ACAGCCTTGCA GACGCCCGGT TIGGTGCATC CGTCTCGGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT TAGGAGGATG	CCATGGCTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG GGCAGGCCGC CACAGTGGCT TCCCCCACCC ACAGAGAAAT CTGCTGGGAC TCCCTAAGGT CTTACCCGAG	AGCAAGACCC CACAGAGCCAC CACAGAGCCAC CAGCAGCCGC GCTGTTGCTA GCTCACGGCC GTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG ACCAGTTCCCACTGCCACTGCCACTGCCACTGCCACTGCCACTGCCACTGCCACTGCCACTGCCACAGATAGAT	120 180 240 300 360 420 480 540 600 660 720
50	Coding sequence of the control of th	Lence: 431  11  CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGCTCTACTG GGAAGAAAGT ACTCTAACGA GACCCATCAA GGCGGACAAC GCGTGCTAAC TCTCGCCCGG	924 21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGGCGGTG TTTCAGAGTC CTTCCAGGG CCTCATGCTC CGTCTCCTCT CAAGAGCCC TCAGAAAAGC TGACAAAAGCA	31   GGTGCAGCGG ACAGCCTTTGC CACCCCTCTA ACCCAGCCGT TTGGTGCATC CGTCTCGGCC ATCAAACTGA ATCAAACTGA CATTGTCCCT CAAGTGCACT TGCGAGGATG GGTAGAGACCT	CCATGGCTAC TTCTGGGGGT ACACCGTGCC GGATGACAG GGCAGC CACAGTGGCT ACTACTCCCT TCCCCCACCC ACAGAGAAGAAT CTGCTGGGAC TCCCTAAGGT CTTACCCAGG CCTGCCAGG	AGCAAGACCC CACAGAGCAT CTCTGGAGC CAGCAGCAGC CAGCAGCAGCCGC GCTGTTGCTA GCTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTGC ACAGATAGAT TGATTCTGGG	120 180 240 300 360 420 480 540 600 660
50	Coding sequence of the control of th	Lence: 43  11  CTCTCTACTT GGGGGCTCTG ACAATGATGT TGGGAGCTGG GATCOGACTG GGAAGAAAGT ACTCTACTG GGCAGCAGAT ACTCTAACGA GACCCATCAA GGCGGACAAC GCGTGCTAAG TCTGGCCGG TCTGCACTGG ACAACCGGG	924 21	31   GGTGCAGCGG ACAGCCTTGA CACCCCTCTA ACCCAGCCGT TTGGTGCATC CGTCTCGGCC GTCAAATCCA ATCAAACTGA ATCAAACTGA CATTGTCCCT TCAGGTGCACT TGCGAGGATG GGTAGAGACT GGACTCGTGT AACCTCTGCA	CCATGGCTAC CCATGGCTAC CGGATGACAG GGCAGGCCGC ACAGAGGACT ACTACTCCCT TCCCCCACCC ACAGAGAGACAT CTTCCCGAGG CCTCCCAGGG CCTGCGGGAG AGTTCACCAAGAAGAAAGAAGAACAAT ACCCCAAGGAAGAAGAACAAACAAC CCCCCAAGGAACAAC CCCCCAAGGAACAACAACAACAACAACAACAACAACAACA	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACCGCC GTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCAGTGC ACAGATAGAT TGATTCTGGG TTACCCTTGT GTGGATCCAG	120 180 240 300 360 420 480 540 600 660 720 780
50	Coding sequence of the control of th	Lence: 43  11  CTCTCTACTT GGGGGCTCTG ACAATGATGT TGGGAGCTGG GATCOGACTG GGAAGAAAGT ACTCTACTG GGCAGCAGAT ACTCTAACGA GACCCATCAA GGCGGACAAC GCGTGCTAAG TCTGGCCGG TCTGCACTGG ACAACCGGG	924 21	31   GGTGCAGCGG ACAGCCTTGA CACCCCTCTA ACCCAGCCGT TTGGTGCATC CGTCTCGGCC GTCAAATCCA ATCAAACTGA ATCAAACTGA CATTGTCCCT TCAGGTGCACT TGCGAGGATG GGTAGAGACT GGACTCGTGT AACCTCTGCA	CCATGGCTAC CCATGGCTAC CGGATGACAG GGCAGGCCGC ACAGAGGACT ACTACTCCCT TCCCCCACCC ACAGAGAGACAT CTTCCCGAGG CCTCCCAGGG CCTGCGGGAG AGTTCACCAAGAAGAAAGAAGAACAAT ACCCCAAGGAAGAAGAACAAACAAC CCCCCAAGGAACAAC CCCCCAAGGAACAACAACAACAACAACAACAACAACAACA	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACCGCC GTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCAGTGC ACAGATAGAT TGATTCTGGG TTACCCTTGT GTGGATCCAG	120 180 240 300 360 420 480 540 600 660 720 780 840
50	Coding sequence of the control of th	Lence: 43  11	924 21   GGGGAAATCA TGCTCTGATC TTCCTGTGATC GGCCGGGGAA CGATATGCAC CGGGGGGGGGG	31   GGTGCAGCGG ACAGCCTTGA GACGCCCGTTA GACGCCCGT TTGGTGCATC CGTCTCGGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT CAAGTGCACT TGCGAGGATG GGTAGAGACT GGACTCGTGT AACCTCTGCA GACCCTCATT	CCATGGCTAC TTCTGGGGGT ACACCGTGCC GGATGACAG GGCAGGCCGC CACAGTGGCT ACTACTCCCT TCCCCCACCC ACAGAGAAT CTGCTGGAC TCCCTAAGGT CTTACCCAAG CCTGCCAGGG CCTGCCAGGG CCTGCCAGGG CCTCCCAACGGC CCTCCCAACGGC CCTCCCAACGGC CCTCCCAACGGC CCTCCCAACGGC CCTCCCAACGGC CCTCCCAACGGC CCTCCCAACGGC CCTCCCACACCGC CCTCCCACAC	AGCAAGACCC CACAGAGCCC CACAGAGCACCCC CACAGAGCACCCC CACACCACT GCTACCCACT TAGCCACT AAAGTGCTTG CCTCCAGTAC ACAGATAGAT TGATTCTCGG TTACCCTTGT GTGGATCCAG ATCCCCACT ATCCCACT ATCCCACT ACAGATAGAT TGATTCTGGG ATCCCCACCT ATCCCACCT ATCCCACCT ATCCCACCT ATCCCACCT ATCCCACCT ATCCCACCT ATCCCACCT ATCTTCAGA	120 180 240 300 360 420 480 540 600 660 720 780 840 900 960 1020
50	Coding sequence of the control of th	Lence: 43  11    CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCOGACTG GGAGGAGAAGT GGCAGCAGAT ACTCTAACGA GGCGGACAAC GCGTGCTAAG GCGGGACAAC GCGTGCTAAG ACAGACOGGG ACAGCCATCAA CGCCCATCAC CGCCCTGCACCC CTCCAGCCCCC	924 21	31   GGTGCAGCGG ACAGCCTTGC CACCCCTCTA ACCCAGCCGT TTGGTGCATC CGTCTCGGCC GTCAAATCCA ATCAAACTGA ACATTGTCCCT CAAGTGCACT TGCGAGGATG GGTAGAGACT GGACTCGTGT AACCTCTGCA CCAGGACTCA CACGGACTCAT TCTCCTGGA	CCATGGCTAC TCCAGGGGG ACACCGTGCC CGGATGACAG GGCAGGCCGC CCACAGTGGCT ACTACTCCCT TCCCCCACCC ACAGAAGAAT CTGCTGGGAC TCCCTAAGGT CTTACCCAGG CCTCCCAGG CCTCCCAGG CCTCCCAGC TCCCCACC TCCCCACAC TCACGGTCT TCACCAC TCAGGGTCT TCACCAG	AGCAAGACCC CACAGAGCCT CACAGAGCGC CAGCAGCGCC GCTGTTGCTA GCTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTGC ACAGATAGAT TGATTCTGGG TTACCCTTGT GTGGATCCAC ATCCCACCT ATCCCACCT ATCCCACCT ATCCCACCT ATCCCACCT ATCCCACCCT ATCCCACCCT ATCCCCACCC	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020
50 55 60	Coding sequence of the control of th	Lence: 43  11  CTCTCTACTT GGGGGCTCTG ACAATGATGT TGGGAGCTGG GATCOGACTG GGAGCAGAT ACTCTACTG GGCAGCAGAT ACTCTAACGA GCCCATCAA GCGGGACAAC GCGTGCTAAG TCTGCGCCG ACACCGGG ACACCGGG ACACCGGG ACGCCTGACC CCCGTGTCTCC	924 21	31	CCATGGCTAC CCATGGCTAC CGGATGACAG GGCAGGCGGC ACTACTCCCT TCCCCCACCC ACAGAAGAAT CTGCTGGGAC TCCCTAAGGT CTTACCCAGG CCTGCCAGGG AGTTACCAGG CCTGCCAGGG CCTCCCAACGA AGTTCACCAA GCACACCGGC CCTTCCCAAC CCACACCGGC CCTTCCCAAA AGTTCACAAA	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACCGCC GTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCACGTC ACAGATAGAT TGATTCTGG TTACCCTTGT GTGGATCCAG ATCCCACCT GATGTTCAG ATCCCACCT GATGTTCAGG CTTCCCCCCAC CTGTCCAGGG CTTCCCAGGG	120 180 240 300 360 420 480 540 600 660 720 780 840 900 960 1020
50	Coding sequence of the control of th	Lence: 43  11  CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCOGACTG AGCTCTACTG GGAAGAAAGA ACTCTAACGA GGACCATCAA GGGGGACAAC GGGTGCTAAG TCTGCACCGG TCTGCAATGG ACAGACCGGG ACAGACCGGC CCGGCCTGAC CCCGGTCTCCT GTCTCAATCT GTCTCAATCT	221 21 21 26GGAAATCA TGCTCTGATC TTCCTGTGAC TGCTCTGAC CGGGGGAA CGATATGCAC CGGGGGGTGT CTTCAGAGTC CTCATGCTC CAGAAAAGCA TCAGAAAAGCA CTCCTGCAG TGTTACAGG TGTTACACG CTGAGTCATC TGAGAAAAGCA CTCCTTTCAA ACTCCTTTCAA ACTCCTTTCAA ACTCCTTTCAA CTGAGTCATC ACTCCTTTCAA CTGAGTCATC ACTCCTTTCAA CTGAGTCATC CTGAGTCATC CTAGTTGAAAC CTAGTTGAAC CTAGTTGAAAC CTAGTTGAAAC CTAGTTGAAAC CTAGTTGAAAC CTAGTTGAAC CTAGTTGAAAC CTAGTTGAAC CTAGTTGAAAC CTAGTTGAAC CTAGTTGAAAC CT	31   GGTGCAGCGG ACAGCCTTGC CACCCCTCTTA GACGCCGGT ACCCAGCCGT TTGGTGCATC CGTCTCGGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT CAAGTGCACT CAAGTGCACT GGACTCGTGT ACCTCTGGTA ACCTCTGGTA CCAGGACTCA TCTCCTGGAC CCTGGGACC CCTGGGACC CTTTCATCCT	CCATGGCTAC TTCTGGGGGT ACACCGTGCC GGATGACAG GGCAGC CACAGTGGCT ACTACTCCT TCCCCACCC CTTACCGAG CCTTACCGAG CCTGCGGAGA AGTTACCCAAG CCTGCGGAGA AGTTACCCAAG CCTCCCAGG CCTCCCAGG CCTCCCAGA TCAGGGTCTA CAAGGTTACAAA CAAGCTCAGA	AGCAAGACCC CACAGGAGCAC CTCTGGGAGC CAGCAGCAGCCGC GCTGTTGCTA GCTCACCAGT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTAC TGATTCTGGG TTACCCTTGT TGGATTCTGGG TTACCCTTGT GTGGATCCAGT TGGATCCAGT TGATTCTGGG TTACCCTACT GATGTTGAGAC CTTCCCCACC CTGTCCCAGGG GCCCATCCCT	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1080
50 55 60	Coding sequence of the control of th	Lence: 43  11  CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCOGACTG GGATCAGACTG GGAAGAAAGT GGCAGCAGAT ACTCTAACGA GCCCATCAA GCGGGACAAC GCGTGCTAAG TCTGCACAGG ACAGCCCTGCA CCTCCAGCCCC CCGTGTCTCT TCTGACCAA	924 21	31   GGTGCAGCGG ACAGCCTTGC CACCCCTCTTA GACGCCGGT ACCCAGCCGT TTGGTGCATC CGTCTCGGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT CAAGTGCACT CAAGTGCACT GGACTCGTGT ACCTCTGGTA ACCTCTGGTA CCAGGACTCA TCTCCTGGAC CCTGGGACC CCTGGGACC CTTTCATCCT	CCATGGCTAC TTCTGGGGGT ACACCGTGCC GGATGACAG GGCAGC CACAGTGGCT ACTACTCCT TCCCCACCC CTTACCGAG CCTTACCGAG CCTGCGGAGA AGTTACCCAAG CCTGCGGAGA AGTTACCCAAG CCTCCCAGG CCTCCCAGG CCTCCCAGA TCAGGGTCTA CAAGGTTACAAA CAAGCTCAGA	AGCAAGACCC CACAGGAGCAC CTCTGGGAGC CAGCAGCAGCCGC GCTGTTGCTA GCTCACCAGT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTAC TGATTCTGGG TTACCCTTGT TGGATTCTGGG TTACCCTTGT GTGGATCCAGT TGGATCCAGT TGATTCTGGG TTACCCTACT GATGTTGAGAC CTTCCCCACC CTGTCCCAGGG GCCCATCCCT	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1080
50 55 60	Coding sequence of the control of th	Lence: 43  11  CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCOGACTG GGATCACTG GGAAGAAAGT ACTCTAACGA GACCCATCAA ACGCTGCTAAG TCTGCACTGG ACACCGGGACAAC CCGGCCTGAC CCGCCTGAC CTCCAGCCC GTCTCATCT TCTGACCCAA  54 Protein	224 21 21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGGGGGTGT TTTCAGAGTC CTTCTCTCTC CGTCTCTCTCT TCAGAGGCC TCAGAAAGCA CTCCTGCAG TGTCACAGA CTCCTGCAG TGTCTACAG CTCCTGCAG TGTCTACAG CTCCTGCAG CTCAGTAAAC CTCCTTTCA ACTCCTTTCA ACTCCTTTCA ACTCCTTTCA CTGAGTCATC CTAGTTGAAC CCCTGGGGCA ATTTAGTCCC Sequence	31   GGTGCAGCGG ACAGCCTTGC CACCCCTCTTA GACGCCGGT ACCCAGCCGT TTGGTGCATC CGTCTCGGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT CAAGTGCACT CAAGTGCACT GGACTCGTGT ACCTCTGGTA ACCTCTGGTA CCAGGACTCA TCTCCTGGAC CCTGGGACC CCTGGGACC CTTTCATCCT	CCATGGCTAC TTCTGGGGGT ACACCGTGCC GGATGACAG GGCAGC CACAGTGGCT ACTACTCCT TCCCCACCC CTTACCGAG CCTTACCGAG CCTGCGGAGA AGTTACCCAAG CCTGCGGAGA AGTTACCCAAG CCTCCCAGG CCTCCCAGG CCTCCCAGA TCAGGGTCTA CAAGGTTACAAA CAAGCTCAGA	AGCAAGACCC CACAGGAGCAC CTCTGGGAGC CAGCAGCAGCCGC GCTGTTGCTA GCTCACCAGT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTAC TGATTCTGGG TTACCCTTGT TGGATTCTGGG TTACCCTTGT GTGGATCCAGT TGGATCCAGT TGATTCTGGG TTACCCTACT GATGTTGAGAC CTTCCCCACC CTGTCCCAGGG GCCCATCCCT	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1080
50 55 60 65	Coding sequence of the control of th	Lence: 43  11    CTCTCTACTT GGGTGCTCTG GGAGCTCG GATCGACTG GATCGACTG AGCTCTACTA AGCCATCAAA GGCAGCAGAA ACTCTAACGA GGCGGACAAA GCCTGCATAAG GCCTGCATAAG ACACCCGGAC ACAGACCGG ACAGACCGGC ACCACCATCAAACCCCCCAGCCCCC CCCTGTCTCT GTCTCAATCT TCTGACCCAA  54 Protein Cession #:	924 21   GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CTTCCAGGGG CTTCCAGGGG CTTCCAGGGG CTTCCATCTC CAAGAGGCCC TCAGAAAAGCA CTCCCTGCAG TGTCTACCCA TGTCTACACC ACTCCTTCA CTGCTCATCACC ACTCCTTCA CTGCTCATCACC ACTCCTTCA CTGCTGAGC CTGAGTCATC ACTCCTTTCA CTGCTGAGC CTGAGTCATC ACTCCTTTCA CCCTGGGGCA ATTTAGTCCC Sequence NP_036559	GGTGCAGCGG ACAGCCTTGC GACGCCGGT TGGGGCCGGT TTGGTGCATC GACTCCGGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT CAAGTGCACT GGGAGGATG GGTAGAGACT ACCCTCTGGA ACCCTCTGCA GCACCTCATT TCTCCTGGAC CCTGGGACC CCTGGGACC CCTGGGACC CCTGGGACC ACCTCATT	CCATGGCTAC TTCTGGGGGT ACACCGTGCC GGATGACAG GGCAGC CACAGTGGCT ACTACTCCT TCCCCACCC CTTACCGAG CCTTACCGAG CCTGCGGAGA AGTTACCCAAG CCTGCGGAGA AGTTACCCAAG CCTCCCAGG CCTCCCAGG CCTCCCAGA TCAGGGTCTA CAAGGTTACAAA CAAGCTCAGA	AGCAAGACCC CACAGGAGCAC CTCTGGGAGC CAGCAGCAGCCGC GCTGTTGCTA GCTCACCAGT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTAC TGATTCTGGG TTACCCTTGT TGGATTCTGGG TTACCCTTGT GTGGATCCAGT TGGATCCAGT TGATTCTGGG TTACCCTACT GATGTTGAGAC CTTCCCCACC CTGTCCCAGGG GCCCATCCCT	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1080
50 55 60	Coding sequence of the control of th	Lence: 43  11  CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCOGACTG GGATCACTG GGAAGAAAGT ACTCTAACGA GACCCATCAA ACGCTGCTAAG TCTGCACTGG ACACCGGGACAAC CCGGCCTGAC CCGCCTGAC CTCCAGCCC GTCTCATCT TCTGACCCAA  54 Protein	224 21 21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGGGGGTGT TTTCAGAGTC CTTCTCTCTC CGTCTCTCTCT TCAGAGGCC TCAGAAAGCA CTCCTGCAG TGTCACAGA CTCCTGCAG TGTCTACAG CTCCTGCAG TGTCTACAG CTCCTGCAG CTCAGTAAAC CTCCTTTCA ACTCCTTTCA ACTCCTTTCA ACTCCTTTCA CTGAGTCATC CTAGTTGAAC CCCTGGGGCA ATTTAGTCCC Sequence	31   GGTGCAGCGG ACAGCCTTGC CACCCCTCTTA GACGCCGGT ACCCAGCCGT TTGGTGCATC CGTCTCGGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT CAAGTGCACT CAAGTGCACT GGACTCGTGT ACCTCTGGTA ACCTCTGGTA CCAGGACTCA TCTCCTGGAC CCTGGGACC CCTGGGACC CTTTCATCCT	CCATGGCTAC TTCTGGGGGT ACACCGTGCC GGATGACAG GGCAGC CACAGTGGCT ACTACTCCT TCCCCACCC CTTCCCACCC CTTACCCAGG CCTGCGGAGA AGTTACCCAAG CCTGCGGAGA AGTTACCCAAG CCTCCCAGG CCTCCCAGG CCTTCCCAGA TCAGGGTCTG TCAGGAT CAGGGTCTG TCAGAAC CAAGCTCAGG TCAGGGTCTG TCAAGAAC CAAGCTCAGG TGAGAAGTGG	AGCAAGACCC CACAGAGCCC CACAGAGCACCCC CACAGAGCACCCC CACACCACT TGGCTACCCACT TAGCCACT TAGCCACT AAAGTGCTTG CCTCCAGTGC ACAGATAGAT TGATTCTCGG TTACCCTTGT GTGGATCCAG TGATCCAGC TACCCACT AATGTCCAGC CTCCAGCC CTCCACTCCA	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1080
50 55 60 65	Coding sequence of the control of th	Lence: 43  11    CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCGACTG AGCTCTACTG AGCTCTACTG AGCTCTACTG AGCTCTACTG AGCAGCAGAT ACTCTAACGA GGCGGACAAC GGCGGACAAC GCCTGCAACG CTCCAGCCCG CCGGTCTCTCT TCTGACCCAA  54 Protein cession #: 11    VLCALITALI	924 21   GGGGAAATCA TGCTCTGATC TTCCTGTGATC GCCCGGGGAA CGATATGCAC CGGGGGGGTG TTTCAGAGTC GTTCCAGGGG CCTCATGCTC CAAGAGGCCC TCAGAAAAGGA CTCCTGCAG TGTCTACCC ACTCCTTCA TGACCAAGCA CTCCTTTCA TGACCATG CTAGTTCATC ACTCCTTTCA TGACCCATG CTAGTTGAAC CCCTGGGGCA ATTTAGTCCC Sequence NP_036559 21   LGVTEHVLAN	31	CCATGGGTAC TTCTGGGGGT ACACCGTGCC GGATGACAG GGCAGC CACAGTGGCT ACTACTCCT TCCCCACCC CTTCCCACCC CTTACCCAGG CCTGCGGAGA AGTTACCCAGG CCTGCCAGGG CCTCCCAGG CCTCCCAGA TCACGGTCTG TCACCAAA CAGCTCCAGG TCACGGGTCTG ATTCCAAAA CAAGCTCAGG TGAGAAGTGG  41 I TVPSGSNQDL	AGCAAGACCC CACAGAGACCC CACAGAGCACCC CACAGAGCACCCC GCTGTTGCTA GCTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTGC ACAGATAGAT TGATTCTCGG TTACCCTTGT GTGGATCCAG ATGGTCCAGC GATGTTCAGA CTTCCCCACC TGATCCAGC GATGTTCAGA CTTCCCCCAC CTGTCCAGGG GCCCATCCCT AAAAAAAAAA	120 180 240 300 360 420 540 600 660 720 780 840 900 960 1020 1140 1200
50 55 60 65	Coding sequence of the control of th	Lence: 43  11    CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCGACTG GGAAGAAAGT GGCAGCAGAA ACTCTAACGA GGCGACACTC GCCTGCAAG TCTGCAATGG ACAGACCGG ACAGCCCATCCA CTCCAGCCCC CGGTTCTCT TCTGACCCAA  54 Protein cession #:  11    VLCALITALI SDCDMHTOPW	924 21	31	CCATGGGTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG GGCAGGCCGC CCACAGTGGCT ACTACTCCCT TCCCCCACCC ACAGGGGAGA CTTACCCAGG CCTGCCAGGG CCTCCCAGGG CCTGCGGAGA AGTTCACCAA TCAGGGTCTG ATTTCCAAAA TCAGGGTCTG TGAGAAGTGG TGAGAAGTGG TGAGAAGTGG TGAGAAGTGG TGAGAAGTGG TGAGAAGTGG TTVPSGSNODL QWLLTAAHCR	AGCAAGACCC CACAGAGACCC CACAGAGCACCT CTCTGGGAGC CAGCAGCACCGC GTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTGC ACAGATAGAT TGATTCTGGG ATCCCCACT ATCCCACT TGATCCAGT TGATCCAGT TGATTCTGG TTACCCTTGT GTGGATCCAG ATCCCCACCT TAAAAAAAAAA	120 180 240 300 360 420 480 540 600 660 720 780 840 900 1020 1080 1140
50 55 60 65 70	Coding sequilibrium control co	Lence: 43  11    CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCOGACTG GGATCACAGA GGCAGAAAGA ACTCTAACGA GACCCATCAA GGCGGACAAC GCGTGCTAAG TCTGCACAGG ACACCAGGG ACGCCCTACA CTCCAGCCC CCGTGTCTCT GTCTCAATCT 11    VLCALITALL SDCDMHTOPM QQMFQGVKSI	924 21	31	CCATGGCTAC CGATGACTAC CGGATGACAG GGCAGGCCGC CGCACAGTGGCT ACTACTCCCT TCCCCACCC ACCCACCC ACCCACCC	AGCAAGACCC CACAGAGCCT CACAGAGCCT CACAGAGCCC CACAGAGCCGC CACAGTTGCTA GCTCACCACT TAGCTACTCC TCGTCCCACT TGATTCCAGTC CACAGATAGAT TGATTCTGG TTACCCTACT GTGGATCCAG TTACCCTACT ATCCCACCT ATTCCCACCT CATGTTGATTCAGG TTACCCACCT ATTCCCCACC TACTCCAGGG CCCATCCCT AAAAAAAAAA	120 180 240 300 360 480 540 660 720 780 900 960 1020 1140 1200
50 55 60 65	Coding sequence of the control of th	Lence: 43  11  CTCTCTACTT GGGGGCTCTG ACAATGATG TGGGAGCTGG GATCOGACTG GGAAGAAGA ACTCTACTG GGAAGAAGA ACTCTAACGA GACCCATCAA GCGGGACAACA CGCGTGCTAAG TCTGCAGCCG AGGCCAACTC CTCCAGCCC CCGTGTCTCT TCTGACCCAA  54 Protein cession #:  11  VLCALITALL SDCDMHTQPW QQMFQGVKSI GTTKSPQWHE	924 21	31	CCATGGCTAC TTCTGGGGGT ACACCGTGCC GGATGACAG GGCAGC CACAGTGGCT ACTACTCCCT TCCCCACCC CTTCCCAGCG CCTCCAGGG CCTCCCAGGG CCTCCCAGGG CCTCCCAGG CCTCCCAGG CCTCCCAGG TCACCGGGAAA AGTTCACAAA CAAGCTCAGG TGAGAAGTGG  41   TVPSGSNQDL QWLITAAHCR RRIRPTKDVR YPRQIDDTMF	AGCAAGACCC CACAGAGCAC CACAGAGCAC CACAGAGCAC CACAGAGCAC CACAGCAC CACAGCAC CACACAC CACAC	120 180 240 300 360 420 660 660 720 780 840 900 1020 1080 1140 1200
50 55 60 65 70	Coding sequence of the control of th	Lence: 43  11  CTCTCTACTT GGGGGCTCTG ACAATGATG TGGGAGCTGG GATCOGACTG GGAAGAAGA ACTCTACTG GGAAGAAGA ACTCTAACGA GACCCATCAA GCGGGACAACA CGCGTGCTAAG TCTGCAGCCG AGGCCAACTC CTCCAGCCC CCGTGTCTCT TCTGACCCAA  54 Protein cession #:  11  VLCALITALL SDCDMHTQPW QQMFQGVKSI GTTKSPQWHE	924 21	31	CCATGGCTAC TTCTGGGGGT ACACCGTGCC GGATGACAG GGCAGC CACAGTGGCT ACTACTCCCT TCCCCACCC CTTCCCAGCG CCTCCAGGG CCTCCCAGGG CCTCCCAGGG CCTCCCAGG CCTCCCAGG CCTCCCAGG TCACCGGGAAA AGTTCACAAA CAAGCTCAGG TGAGAAGTGG  41   TVPSGSNQDL QWLITAAHCR RRIRPTKDVR YPRQIDDTMF	AGCAAGACCC CACAGAGCAC CACAGAGCAC CACAGAGCAC CACAGAGCAC CACAGCAC CACAGCAC CACACAC CACAC	120 180 240 300 360 480 540 660 720 780 900 960 1020 1140 1200
50 55 60 65 70	Coding sequence of the control of th	Lence: 43  11  CTCTCTACTT GGGGGCTCTG ACAATGATG TGGGAGCTGG GATCOGACTG GGAAGAAGA ACTCTACTG GGAAGAAGA ACTCTAACGA GACCCATCAA GCGGGACAACA CGCGTGCTAAG TCTGCAGCCG AGGCCAACTC CTCCAGCCC CCGTGTCTCT TCTGACCCAA  54 Protein cession #:  11  VLCALITALL SDCDMHTQPW QQMFQGVKSI GTTKSPQWHE	924 21	31	CCATGGCTAC TTCTGGGGGT ACACCGTGCC GGATGACAG GGCAGC CACAGTGGCT ACTACTCCCT TCCCCACCC CTTCCCAGCG CCTCCAGGG CCTCCCAGGG CCTCCCAGGG CCTCCCAGG CCTCCCAGG CCTCCCAGG TCACCGGGAAA AGTTCACAAA CAAGCTCAGG TGAGAAGTGG  41   TVPSGSNQDL QWLITAAHCR RRIRPTKDVR YPRQIDDTMF	AGCAAGACCC CACAGAGCAC CACAGAGCAC CACAGAGCAC CACAGAGCAC CACAGCAC CACAGCAC CACACAC CACAC	120 180 240 300 360 480 540 660 720 780 900 960 1020 1140 1200
50 55 60 65 70 75	Coding sequence of the control of th	Lence: 43  11    CTCTCTACTT GGGTGCTCTG GGAGCTGG GATCGACTG GGAGCAGAT ACTCTACCTA GGGAGCAGAT ACTCTACCGA GGCGGACAGAT TCTGACCGA GCCTGCATGA CTCCAGCCCG CCGTGCTCA  54 Protein Cession #: 11    VLCALITALL SCICHITCHACCA GQMFQGVKE: GTTKSPQVHE CNGSLQGLVS  15 DNA sec	924 21   GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CTTCAGAGTC GTTCCAGGGG CTTCCAGGGG CTTCAGAAAGGA CTCCTTCT CAAGAGGCCC TCAGAAAAGG TGTCTACCAG TGTCTACCAG TGTCTACCAG CTCCTTCAACAAAGCA CTCCTTCAAC ACTCCTTTCA CTCATTGAAC CCCTGGGGCA ATTTAGTCCC Sequence NP_036559 21   LGVTEHVLAN QAALLIRPNO PHPGYSHPGE PKVLQCINIS WGDYPCARPN Quence n#: NM_002	GGTGCAGCGG ACAGCCTTGC CACCCCTCTA GACGCCGGT ACCCAGCCGT TTGGTGCATC CGTCTAGGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT TGCGAGGATG GGTAGAGACT GGACTCGTGT AACCTCTGCA CCAGGACTCA TCTCTGGAC CCAGGACTCA TCTCTGGAC CCAGGACTCA TCTCTGGAC CCTGGGAACA CTTTCATCCT AGAAATAAAC  31   NDVSCDHPSN LYCGAVLVHP SNDLMLIKLN LYCGAVLVHP SNDLMLIKLN VLSQKRCEDA	CCATGGCTAC TTCTGGGGGT ACACCGTGCC GGATGACAG GGCAGC CACAGTGGCT ACTACTCCCT TCCCCACCC CTTCCCAGCG CCTCCAGGG CCTCCCAGGG CCTCCCAGGG CCTCCCAGG CCTCCCAGG CCTCCCAGG TCACCGGGAAA AGTTCACAAA CAAGCTCAGG TGAGAAGTGG  41   TVPSGSNQDL QWLITAAHCR RRIRPTKDVR YPRQIDDTMF	AGCAAGACCC CACAGAGCAC CACAGAGCAC CACAGAGCAC CACAGAGCAC CACAGCAC CACAGCAC CACACAC CACAC	120 180 240 300 360 480 540 660 720 780 900 960 1020 1140 1200
50 55 60 65 70	Coding sequence of the control of th	Lence: 43  11    CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCGACTG GGAGGAGAAGA GCCATCAACGA GGCGACAGACTC TCTGCACCGG ACAGCCATCAA GGGGACAACTC CCAGCCCTGAC CTCCAGCCCC CGGTTCTCT TCTGACCCAA  54 Protein Cession #: 11    VLCALITALL SDCDMHTOPW COMFQGVKSI GTTKSPQVHE CNGSLQGLVS  55 DNA sec cid Accessic Luence: 681	924 21	GGTGCAGCGG ACAGCCTTGC CACCCCTCTA GACGCCCGGT ACCCAGCCGT TTGGTGCATC CGTCTCAGGCC GTCAAATCCA ATCAAACTGA ACATGTCACT GGAGGAGT GGACTCGTGGACT ACCTCGGGACT ACCTCGGGACT ACCTCTGCA CCAGGACTCA ACCTCTGCA CCTGGGAACT ACCTCTGGAACT ACCTCTGGAACT ACTTCATCCT AGAAATAAAC  31   NDVSCDHPSN LYCGAVLVHP SNDLMLIKLN VLSQKRCEDA RPGVYTNLCK	CCATGGCTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG GGCAGGCCGC CACAGTGGCT ACTACTCCT TCCCCCACCC ACCACCACCAC ACAGAGAAT CTGCTGGGAC CCTCCCAGG CCTCCCAGG CCTCCCAGG CCTCCCAGG CCTCCCAGG TCACCGAG TCACCGAG TCACCGAG TCAGGGTCTG ATTTCCAAAA TCAGGGTCTG TGAGAAGTG  41    TVPSGSNODL QWLLTAAHCR RRIRPTKDVR YPRQIDDTMF FTKWIQETIQ	AGCAAGACCC CACAGAGACCC CACAGAGCAC CACAGAGCAC CAGCAGCAGC GCTGTTGCTA GCTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTGC ACAGATAGAT TGATTCTGGG ATCCCCACT ATCCCCACT ATCCCACT ATCCCACT ATCCCACT ATCCCACT ATCCCACCT ATCCCACCT ATCCCACCT ATCCCACCT AAAAAAAA	120 180 240 300 360 480 540 660 720 780 900 960 1020 1140 1200
50 55 60 65 70 75	Coding sequence of the control of th	Lence: 43  11    CTCTCTACTT GGGTGCTCTG GGAGCTGG GATCGACTG GGAGCAGAT ACTCTACCTA GGGAGCAGAT ACTCTACCGA GGCGGACAGAT TCTGACCGA GCCTGCATGA CTCCAGCCCG CCGTGCTCA  54 Protein Cession #: 11    VLCALITALL SCICHITCHACCA GQMFQGVKE: GTTKSPQVHE CNGSLQGLVS  15 DNA sec	924 21   GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CTTCAGAGTC GTTCCAGGGG CTTCCAGGGG CTTCAGAAAGGA CTCCTTCT CAAGAGGCCC TCAGAAAAGG TGTCTACCAG TGTCTACCAG TGTCTACCAG CTCCTTCAACAAAGCA CTCCTTCAAC ACTCCTTTCA CTCATTGAAC CCCTGGGGCA ATTTAGTCCC Sequence NP_036559 21   LGVTEHVLAN QAALLIRPNO PHPGYSHPGE PKVLQCINIS WGDYPCARPN Quence n#: NM_002	GGTGCAGCGG ACAGCCTTGC CACCCCTCTA GACGCCGGT ACCCAGCCGT TTGGTGCATC CGTCTAGGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT TGCGAGGATG GGTAGAGACT GGACTCGTGT AACCTCTGCA CCAGGACTCA TCTCTGGAC CCAGGACTCA TCTCTGGAC CCAGGACTCA TCTCTGGAC CCTGGGAACA CTTTCATCCT AGAAATAAAC  31   NDVSCDHPSN LYCGAVLVHP SNDLMLIKLN LYCGAVLVHP SNDLMLIKLN VLSQKRCEDA	CCATGGCTAC TTCTGGGGGT ACACCGTGCC GGATGACAG GGCAGC CACAGTGGCT ACTACTCCCT TCCCCACCC CTTCCCAGCG CCTCCAGGG CCTCCCAGGG CCTCCCAGGG CCTCCCAGG CCTCCCAGG CCTCCCAGG TCACCGGGAAA AGTTCACAAA CAAGCTCAGG TGAGAAGTGG  41   TVPSGSNQDL QWLITAAHCR RRIRPTKDVR YPRQIDDTMF	AGCAAGACCC CACAGAGCAC CACAGAGCAC CACAGAGCAC CACAGAGCAC CACAGCAC CACAGCAC CACACAC CACAC	120 180 240 300 360 480 540 660 720 780 900 960 1020 1140 1200
50 55 60 65 70 75	Coding sequence of the	Lence: 43  11    CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCGACTG AGCTCTACTT AGCTCTACTT AGCTCTACTA AGCCATCAACGA GCAGCAGAT ACTCTAACGA GCAGCACTCAA GGGGGACAAC GCCTGCAACG CTCCAGCCCC CCGTGTCTCT TCTGACCCAA  54 Protein Cession #: 11    VLCALITALL SCOMMTGVWS: 12   GTTKSPQVHS CNGSLQGLVS  11   CNGSLQGLVS  11	924 21   GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGAA CGATATGCAC CGGGGGGGTG TTTCAGAGTC GTTCCAGGGG CTTCATCTC CAAGAGCCCC TCAGAAAAGG TGTCTACTC ACTCCTTCAC TGACAAAAGCA CTCCTGCAG TGTCTACCG TGACAAAGCA CTCCTTTCA TGACCCATG CTAGTTACACG ACTCCTTTCA CCAGGGGCA ATTTAGTCCC Sequence NP_036559 21   LGVTEHVLAN QAALLERPNO PHPGYSEHGE PKVLQCINIS WGDYPCARPN Quence n#: NM_002 .2990 21	GGTGCAGCGG ACAGCCTTGC GACGCCCGT ACCCAGCCGT TTGGTGCATC CACCCTCCA ATCAAACTGA ATCAAACTGA CATGGAGGATG GGTAGAGACT GGACTCGTGT AACCTCTGGA ACCAGCGTT AACCTCTGCA GACCTCATT TCTCCTGGAC CCTGGGACC AGACATCA GACCTCATT TCTCCTGGAC CTTTCATCCT AGAAATAAAC  31   NDVSCDHPSN LYCGAVLVHP SNDLMLIKLN VLSQKRCEDA RPGVYTNLCK 214	CCATGGCTAC TTCTGGGGGT ACACCGTGCC GGATGACAG GGCAGC CACAGTGGCT ACTACTCCT TCCCCACCC CTTCCCCACCC CTTACCCAGG CCTGCGGGAG AGTTACCCAAG AGTTACCCAAG CCTCCCAGG CCTCCCAGG CCTCCCAGG CCTCCCAGG TCACGGTCTG ATTCCAAAA CAAGCTCAGG TGAGAAGTGG  41   TVPSGSNQDL QWLLTAAECR RRIRPTKDVR RRIRPTKDVR PRQLDDIMF FTKWIQETIQ	AGCAAGACCC CACAGAGCAC CACAGAGCAC CACAGAGCAC CAGCAGCAGC GCTGTTGCTA GCTCACCAGT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTGC ACAGATAGAT TGATTCTGGG TTACCCTTGT GATGTTCAGAC CTTCCCCACC TACACAGAT AAAAAAAAAA	120 180 240 300 360 480 540 660 720 780 900 960 1020 1140 1200
50 55 60 65 70 75	Coding sequilibrium control co	Lence: 43  11  CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCOGACTG AGCTCTACTG AGACTGACTG AGACCATCAA ACTCTAACGA GCGGACAAAC GCGTGCTAAG TCTGGACCGG ACAGACCGGG ACAGCCATCAA CGCCCTACAC CCGTGTCTCT GTCTCAATCT TCTGACCCAA  54 Protein Cession #: 11  VLCALITALL SDCDMHTOPW CMGSLQGLVS  12  CMGSLQGLVS  11  CGTCTCCCCCCC CGTCTCTCCCCCCCCCCCCCC	924 21	GGTGCAGCGG ACAGCCTTGC CACCCCTCTA GACGCCGGT ACCCAGCGT ACCCAGCGT TTGGTGCATC CGTCTAGAACTGA ACTAAACTGA CATTGTCCCT TGCGAGGATG GGTAGAGACT ACCCTCAGT ACCCTCAGT TCTCTGGAC CCTGGGAACTCA ACCCTCATT TCTCCTGGAC CCTGGGAACA CTTTCATCCT AGAAATAAAC  31   NDVSCDHPSN LYCGAVLVHP SNDLMLIKLN VLSQKRCEDA RPGVYTNLCK  214  31   CCCGGAGCTTC AGACCGCGCTC AGACCGCGCTC AGACCGCGCTC AGACCGCGCCTC AGACCGCGCCTC AGACCGCGCTC AGACCGCGCCTC AGACCGCGCCC AGACCGCGCCC AGACCGCGCCC AGACCGCGCCC AGACCGCGCCC AGACCGCGCCC AGACCGCGCCC AGACCCCCCC AGACCGCGCCC ACCCCCCCC	CCATGGCTAC CCATGGCTAC CCATGGCTAC CGGATGACAG GGCAGGCGGC CCACAGTGGCT ACTACTCCT TCCCCCACCC ACAGAGAAT CTGCTGGGAC TCCCTAAGGT CCTCACCAGG CCTGCCAGG CCTGCCAGG CCTCCCAGG TCACCCAA TCAGGTCTC TTACCCAGA TCAGGGTCTG ATTTCCAAAA CAAGCTCAG TCAGGGTCTG ATTTCAAAAC CAAGCTCAGG CTTCCAGA TCAGGGTCTG TVPSGSNQDL VPSGSNQDL CWLLTAAHCR RRIRPTKDVR YPRQIDDTMF FTKWIQETIQ  41  1  CTCCCTTGCC GCAAAGCTGC GCAAAGCTGC GCAAAGCTGC GCAAAGCTGC GCAAAGCTGC CCCCTTGCC GCAAAGCTGC CGCAAGCTGC CGCAAGCTGCC CGCA	AGCAAGACCC CACAGAGACCC CACAGAGCAC CACAGAGCAC CAGCAGCAGC GCTGTTGCTA GCTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTGC ACAGATAGAT TGATTCTGGG ATCCCCACT ATCCCCACT ATCCCACT ATCCCACT ATCCCACT ATCCCACT ATCCCACCT ATCCCACCT ATCCCACCT ATCCCACCT AAAAAAAA	120 180 240 300 360 420 600 720 780 840 960 1020 1020 1140 1200

	TOCCOTOGAC	CTCGCCGGCG	TACCCTCCCA	CAGATCCAGC	ATCACCCAGT	GAATGTACAT	240
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	CTAAGCTGAT	TTATGCAGCA	GAAGCCCCAC	CGGCTGGAGA	GAAACAAAAG	CTCTTTTCTT	360
5	TGTCCCGGAG	CAGGCTGCGG	AGCCCTTGCA	GAGCCCTCTC	TCCAGTCGCC	GCCGGGCCCT	420
)	CCCCTACCC	AGGAGGTGCT	TCTCGCGGAG GCCGAGCGGT	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	ACCCCTTCCT	480 540
	CCCAGCCGCG	GGGTCCGCCT	GCTAGGCCTG	CGGAAAACGT	CCTAGCGACA	CTCGCCCGCG	600
	GGCCCCGAGG	TCGCCCGGGA	GGCCGAGCCC	GCGTCCGGAA	GGCAGCCAGG	OGGCGGGGGC	660
	GGGGGGGCT	GTTTTGCATT	ATGTGCGGCT	CGGCCCTGGC	TTTTTTTACC	GCTGCATTTG	720
10			CGAGGTCCCG				780
			CAAGGTGAAG				840 900
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	ATTTTATGCT	GAAAGTTCAT	CCTCTGAAGA	AATATCCTGT	GGATCTTTAT	TATCTTGTTG	1140
	ATGTCTCAGC	ATCAATGCAC	AATAATATAG	AAAAATTAAA	TTCCGTTGGA	AACGATTTAT	1200
			TCCCGTGACT				1260
20			AGCATCCACC CCCCATGGAT				1320 1380
20	ACAATTTAGA	TGAGAAAGCA	GTTCATAGAC	ACAICCAIGI	TGGAAACATA	GATACACCAG	1440
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			TTTAACATTA				1920
30	CAGGCATGGA	AGGATGCAGA	AACGTGACGA	GCAATGATGA	AGTTCTTTTC	AATGTAACAG	1980
-	TTACAATGAA	AAAATGTGAT	GTCACAGGAG	GAAAAAACTA	TGCAATAATC	AAACCTATTG	2040
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	CATATCACCA	TEGALATETE	TGTGCTGGGC	ATGGAGAGTG	TGAAGCAGGC	AGATGCCAAT	2400
	GCTTCAGTGG	CTGGGAAGGT	GATCGATGCC	AGTGCCCTTC	AGCAGCAGCC	CAGCACTGTG	2460
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	GCAAGGAAAA	CTGGAATTGT	ATGCAATGCC	TTCACCCTCA	CAATTTGTCT	CAGGCTATAC	2640 2700
	TIGATCAGIG	CAAAACCICA	TGTGCTCTCA AGCTACTTGA	CAATATTTTT	CATCATTTC	ATAGTTACAT	2760
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			GCTCATGAAA				3000
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55			CACTTCAACA				3480
			TCACTCTTTC GTGTGTAGTT				3540 3600
	AAAGATTATT	CCATACTAAA	TCCAGCATTC	TIMIGCATOL	COUNTRICT	Jana Calandar Cala	3660
	TTTTTACAGG	ATAAGTTTAT	GTATGTCACA	GATGACTGGA	TTAATTAAGT	GCTAAGTTAC	3720
60	TACTGCCATA	AAAAACTAAT	AATACAATGT	CACTTTATCA	GAATACTAGT	TTTAAAAGCT	3780
	GAATGTTAA						
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		56 Protein					
65	Protein Ac	cession #: 1	NP_002205 21	31	41	51	
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		AAFVCLQNDR	RGPASFLWAA		QGEDNRCASS	NAASCARCLA	60
	LGPECGWCVQ	EDFISGSRS	ERCDIVSNLI	SKGCSVDSIE	YPSVHVIIPT	ENEINTQVTP	
70						NDLSRKMAFF	
70						TENITEPEKA	
						ALDSKLAGIV YKDLLPLLPG	
						SRKPGMEGCR	
						CEDNRGPKGK	
75	CVDETFLDSK	CFQCDENKCE	FDEDQFSSES	CKSHKDQPVC	SGRGVCVCGF	CSCHKIKLGK	540
	VYGKYCEKDD	PSCPYHHGNI	CAGHGECEAG	RCQCFSGWEG	DRCQCPSAAF	QHCVNSKGQV	600
	CSGRGTCVCG	RCECTDPRSI	GRFCEHCPTC	YTACKENWNC	MOCLHPHNLS	QAILDQCKTS	660
						WNSNKIKSSS	720
80	DIKVSASKKI	KULLQSVCTE	AVTYRREKPE	. EINMIIDKUN	AREIFRONE		
20	Sea ID NO	57 DNA sec	nuence				
			n #: NM_001	719			
		quence: 123	1418				
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					29	93	

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                                                                                              120
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                                                                                              660
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TCTTCAAGGC CACGGAGGTC CACTTCCGCA GCATCCGGTC CACGGGGAGC AAACAGCGCA
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                                                                                             1200
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AGACGCTGGT CCACTTCATC AACCCGGAAA CGGTGCCCAA GCCCTGCTGT GCGCCCACGC
                                                                                             1260
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25
                                                                                             1500
                                                                                             1560
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                                                                                             1800
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                                                  31
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LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHHREFRFDL SKIPEGEAVT AAEFRIYKDY
                                                                                              120
40
         IRERFDNETF RISVYQVLQE HLGRESDLFL LDSRTLWASE EGWLVFDITA TSNHWVVNPR
                                                                                               240
         HNLGLQLSVE TLDGQSINPK LAGLIGRHGP QNKQPFMVAF FKATEVHFRS IRSTGSKQRS
                                                                                              300
         QNRSKTPKNQ EALRMANVAE NSSSDQRQAC KKHELYVSFR DLGWQDWIIA PEGYAAYYCE
                                                                                              360
         GECAFPLNSY MNATNHAIVQ TLVHFINPET VPKPCCAPTQ LNAISVLYFD DSSNVILKKY
                                                                                              420
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                      11
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         CCTCAGCTCC TTTTCCTGAG CCCGCCGCGA TGGGAGCTGC GCGGGGATCC CCGGCCAGAC
55
                                                                                              240
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                                                                                               360
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                                                                                               600
         ACATTGATGG GCACCTCGG CCCACCTACC AATGGTTCCG AGATGGGACC CCCCTTTCTG ATGGTCAGAG CAACCACACA GTCAGCAGCA AGGAGCGGAA CCTGACGTC CGGCCAGCTG
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         GTCCTGAGCA TAGTGGGCTG TATTCCTGCT GCGCCCACAG TGCTTTTGGC CAGGCTTGCA
                                                                                               780
65
         GCAGCCAGAA CTTCACCTTG AGCATTGCTG ATGAAAGCTT TGCCAGGGTG GTGCTGGCAC
CCCAGGACGT GGTAGTAGCG AGGTATGAGG AGGCCATGTT CCATTGCCAG TTCTCAGCCC
                                                                                               840
                                                                                               900
         AGCCACCCCC GAGCCTGCAG TGGCTCTTTG AGGATGAGAC TCCCATCACT AACCGCAGTC
                                                                                               960
         GCCCCCCACA CCTCCGCAGA GCCACAGTGT TTGCCAACGG GTCTCTGCTG CTGACCCAGG
                                                                                             1020
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70
                                                                                              1140
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         GCCACGCGGC CAACCTGGCT GGTCAGCGGA GACAGGATGT CAACATCACT GTGGCCACTG
                                                                                              1380
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TGGATTGCCT GACCCAGGCC ACACCAAAAC CTACAGTTGT CTGGTACAGA AACCAGATGC
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                                                                                              1440
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                                                                                              1560
                                                                                              1620
          TGGAGGTGTA TGATGGGACA TGGTACCGTT GTATGAGCAG CACCCCAGCC GGCAGCATCG
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	TLLVNELKSK FKEIPVTVYT TEVHEGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac: Coding sequ 1	ESDIMITINGV TKIITKVVEP KKYTKIIDGV IEGGDGHLFE 67 DNA sequid Accessionence: 1-92' 11	IHVVDKLLYP KIKVIEGSLQ PVEITEKETR DEEIKRLLQG uence n #: EOS sec 7 21     GGGCCCCGCC	ADTPVGNDQL PIIKTEGPTL EERIITGPEI DTPVRKLQAN Quence 31	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL  41   GGCGTCTGCG	IQIKFVRGST FRLIKEGETI ETEETLKKLL REGRSQ 51   GCTGGGGCGA	720 780
50	TLLVNELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac- Coding sequ 1   ATGCCTGGGG CTAGGGCTGG	ESDIMITINGV TKIITKVVEP KKYTKIIDGV IEGGDGHLFE 67 DNA sequid Accession ience: 1-92' 11   GGTGCTCCCG TACTCCTGGG	IHVVDKLLYP KIKVIEGSLQ PVEITEKETR DEEIKRLLQG uence n #: EOS sec 7 21 ) GGGCCCCGCC CTGGGTCTCC	ADTPVGNDQL PIIKTEGPTL EERIITGPEI DTPVRKLQAN Quence 31   GCCGCGGACG TCGTCTTCTC	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL  41   GGCGTCTGCG CCACCICCTC	IQIKFVRGST FRLIKEGETI ETEETLKKLL REGRSQ 51   GCTGGCGCGA GCATCCTCC	720 780 60 120
	TLLVNELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac: Coding sequ 1   ATGCCTGGGG CTAGCGCTGG TTCTCCTCCT	ESDIMITINGV TKIITKVVEP KKYTKIIDGV IEGGDGHLFE 67 DNA seq id Accessio: eence: 1-92' 11   GGTGCTCCCG TACTCCTGGG CGGGCCCGTT	IHVVDKLLYP RIKVIEGSLQ PVEITEKETR DEEIKRLLQG uence n #: EOS ser 7 21   GGGCCCCGCC CTGGGTCTCC CCTGGCTTCC	ADTPVGNDQL PIIKTEGPTL EERIITGPEI DTPVRKLQAN Quence 31 GCCGGGGACG TCGTCTTCTC GCCGTGTCCG	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL  41   GGCGTCTGCG CCACCTCCTC CCCAGCCCCCC	IQIKFVRGST FRLIKEGETI ETEETLKKLL REGRSQ 51   GCTGGCGCGA GCCTGCCGGAC	720 780 60 120 180
50	TLLVNELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac: Coding sequ 1   ATGCCTGGGG CTAGCGCTGG TTCTCCTCCT	ESDIMITINGV TKIITKVVEP KKYTKIIDGV IEGGDGHLFE 67 DNA seq id Accessio: eence: 1-92' 11   GGTGCTCCCG TACTCCTGGG CGGGCCCGTT	IHVVDKLLYP RIKVIEGSLQ PVEITEKETR DEEIKRLLQG uence n #: EOS ser 7 21   GGGCCCCGCC CTGGGTCTCC CCTGGCTTCC	ADTPVGNDQL PIIKTEGPTL EERIITGPEI DTPVRKLQAN Quence 31 GCCGGGGACG TCGTCTTCTC GCCGTGTCCG	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL  41   GGCGTCTGCG CCACCTCCTC CCCAGCCCCCC	IQIKFVRGST FRLIKEGETI ETEETLKKLL REGRSQ 51   GCTGGCGCGA GCCTGCCGGAC	720 780 60 120
50	TLLVNELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac: Coding sequi   ATGCCTGGGG CTAGGGCTGG TTCTCCTCCT CAGTGCCCCG	ESDIMITINGV TKIITKVVEP KKYTKIIDGV LEGGDGHLFE 67 DNA seq dd Accession Lence: 1-92' 11  GGTGCTCCCG TACTCCTGGG CGGCGCCGTT CGCTGGGGA	IHVVDKLLYP KIKVIEGSLQ PVEITEKETR DEEIKRLLQG Umence n #: EOS sec 7 21 ) GGGCCCCGCC CTGGTTCTC CCTGGTTTCC GTGCTCCGAG	ADTPVGNDQL PILKTEGPTL EERLITGPEI DTPVRKLQAN Quence 31 GCCGCGGACG TCGTCTTCTC GCCGTGTCCG GCAGCGCGCA	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL  41   GGCGTCTGCG CCACCTCCTC CCCAGCCCCC CAGTCAAGTG	IQIKFVRGST FRLIKEGETI FTEETLKKLL REGRSQ 51   GCTGGCGCGA GCATCCTCC GCTGCCGGAC CGTTAACCGC	720 780 60 120 180
50	TLLVNELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac: Coding sequil ATGCCTGGGG CTAGCGCTGG TTCTCCTCTC CAGTGCCCCC AATCTGACCG	ESDIMITINGV TKIIITKVVEP KKYTKIIDGV IEGGDGHLFE 67 DNA seq id Accession Lence: 1-92' 11   GGTGCTCCCG TACTCCTGGG CGGCGCCGTT CGCTGTGCGA AGGTGCCCAC	IHVVDKLLYP KIKVIEGSLQ PVEITEKETR DEEIKRLLQG uence n #: EOS sec 7 21   GGGCCCGGC CTGGTTCCC CTGGTTCCC GTGCTCCGAG GGACCTGCCC	ADTPVGNDQL PIKTEGPTL EERIITGPEI DTPVRKLQAN Quence 31   GCCGGGGACG TCGTCTTCTC GCCGTGTCCCG GCAGCGCGCA GCCTACGTGC	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL  41   GGCGTCTGCG CCACCCCTC CCCAGCCCCCC CAGTCAAGTG GCAACCTCTT	IQIKFVRGST FRLIKEGETI ETEETLKKLL REGRSQ  51   GCTGGCGCGA GGCATCCTCC GCTGCCGGAC CGTTAACCGC CCTTACCGGC	720 780 60 120 180 240 300
50	TLLVNELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Accoding sequence ATGCCTGGGG CTAGGGCTGG TTCTCCTCT CAGTGCCCCG AATCTGACCG AACCAGCTGG	ESDIMITINGV TKIIITKVVEP KKYTKIIDGV IEGGDGHLFE 67 DNA sequid Accession Lence: 1-92' 11   GGTGCTCCCG TACTCCTGGG CGGCGCGTT CGCTGTGCGA AGGTGCCCAC CCAGCAACCA	IHVVDKLLYP KIKVIEGSLQ PVEITEKETR DEEIKRLLQG  uence n #: EOS sec 7 21   GGGCCCCGCC CCTGGCTTCC GTGCTCCGAG GGACCTGCCC CTTCCTTTAC	ADTPVGNDQL PIIKTEGPTL EERIITGPEI DTPVRKLQAN Quence 31   GCCGCGGACG TCGTCTTCTC GCCGTGTCCG GCAGCGCCG GCAGCGCGCA GCCTACGTGC CTGCCGCGGG	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL  41   GGCGTCTGCG CCACCTCCTC CCCAGCCCCC CAGTCAACT ATGTGCTGGG	IQIKFVRGST FRLIKEGETI ETEETLKKLL REGRSQ  51   GCTGGCGGA GGCATCCTCC GCTGCCGAC CCTTACCCGC CCTACCGCC CCAACTGCCC	720 780 60 120 180 240 300 360
50 55	TLLVNELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac: Coding sequ     ATGCCTGGGG CTAGGGCTGG TTCTCCTCCT CAGTGCCCCG AATCTGACCG AACCAGCTGG AACCAGCTGG AGCCTCAGGC	ESDIMITINGV TKIITKVVEP KKYTKIIDGV IEGGDGHLFE 67 DNA seq dd Accession Lence: 1-92' 11   GGTGCTCCCG TACTCCTGGG AGGTGCCCAC CCCAGCAACCA ACCTGGACTA ACCTGGACTA	IHVVDKLLYP KIKVIEGSLQ PVEITEKETR DEEIKRLLQG Ueence n #: EOS see 7 21 ) GGGCCCCGCC CTGGGTTCC CTGGTTCCCTTCAG GGACCTGCCC CTTCCTTTAC AAGTAATAAT	ADTPVGNDQL PILKTEGPTI ERRIITGPEI DTPVRKLQAN  quence  31   GCCGCGGACG TCGTTCTTC GCCGTGTCCG GCCTACGTGC CTGCCGCGGG TCGCTGGTGA	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL  41   GGCGTCTGCG CCACCTCCTC CCCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGG GCCTGACCTA	IQIKFVRGST FRLIKEGETI ETEETIKKLL REGRSQ  51   GCTGGCGCGA GCATCCTCC GCTGCCGGAC CCTTACCGGC CCTACCGGC CCTGCCCC CGTGTCCTTC-	720 780 60 120 180 240 300 360 420
50	TLLVNELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac: Coding sequi ATGCCTGGGG CTAGCGCTGG TTCTCCTCCT CAGTGCCCCG AATCTGACCG AGCCTCAGG AGCCTCAGG AGCCTCAGG CGCAACCTGA	ESDIMITINGV TKIIITKVVEP KKYTKIIDGV IEGGDGHLFE 67 DNA seq id Accessio: dence: 1-92' 11   GGTGCTCCCG TACTCCTGGG CGGCGCCGTT GCCTGGCGA AGGTGCCCAC CCAGCAACCA ACCTGGACTT CACATCTAGA	IHVVDKLLYP KIKVIEGSLQ PVEITEKETR DEEIKRLLQG Uence n #: EOS sec 7 21     GGGCCCCGCC CTGGGTTCC CTGGGTTCC GTGCTCCGAG GGACCTGCCC CTTCCTTTAC AAGTAATAAT AAGCCTCCAC	ADTPVGNDQL PIIKTEGPTL EERIITGPEI DTPVRKLQAN quence 31   GCCGGGGACG TCGTCTTCTC GCAGGGGCACG GCAGGGCGCA GCCTACGTGC CTGCCGCGGG TCGCGCGGG TCGCTGGTGA	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL  41   GGCGTCTGCG CCACTCCTC CCCAGCCCCC CAGTCAAGTG GCAACTCTT ATTIGCTGGC GCCTGACCTA ATGCCTCAA	IQIKFVRGST FRLIKEGETI FEETIKKLL REGRSQ  51   GCTGGCGCGA GCATCCTCC GCTGCCGGAC CGTTAACCGC CCTACCGC CCAACTGCCC CGTGTCCTTCC	720 780 60 120 180 240 300 360 420 480
50 55	TLLVNELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac: Coding sequit ATGCCTGGGG CTAGCGCTGG TTCTCCTCT CAGTGCCCCG AACTGACCGG AGCCTCAGGC CGCAACCTGG AATGGCACCC	ESDIMITINGV TKIIITKVVEP KKYTKIIDGV IEGGDGHLFE 67 DNA seq idd Accession Lence: 1-92' 11   GGTGCTCCCG TACTCCTGGG CGGCGCGTT CGCTGTGCGA AGGTGCCCAC CCAGCAACCA ACCTGGACTT CACATCTAGA TGGCTGAGTT	IHVVDKLLYP KIKVIEGSLQ PVEITEKETR DEEIKRLLQG  uence n #: EOS ser 7 21   GGGCCCCGCC CTGGTTCCC CTGGTTCCC GTGCTCCGAG GGACCTGCCC CTTCCTTTAC AAGTAATAAT AAGCCTCCAA GGCACGCCTAC	ADTPVGNDQL PIIKTEGPTL EERIITGPEI DTPVRKLQAN  31   GCCGGGGACG TCGTCTTCTC GCCGTGTCCG GCAGCGCGCA GCCTACGTGC CTGCCGCGGG TCGCTGGTGA CTGGAGGACA CCCCACATTA	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL  41	IQIKFVRGST FRLIKEGETI FEETLKKLL REGRSQ  51   GCTGGCGGAC GGCATCCTCC GCTGCCGGAC CCTTACCGGC CCAACTGCCC CGTGCCTTCAC GGTCCTTCAC GGACAACAAT	720 780 60 120 180 240 300 360 420 480 540
50 55	TLLVNELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac: Coding sequit ATGCCTGGGG CTAGCGCTGG TTCTCCTCT CAGTGCCCCG AACTGACCGG AGCCTCAGGC CGCAACCTGG AATGGCACCC	ESDIMITINGV TKIIITKVVEP KKYTKIIDGV IEGGDGHLFE 67 DNA seq idd Accession Lence: 1-92' 11   GGTGCTCCCG TACTCCTGGG CGGCGCGTT CGCTGTGCGA AGGTGCCCAC CCAGCAACCA ACCTGGACTT CACATCTAGA TGGCTGAGTT	IHVVDKLLYP KIKVIEGSLQ PVEITEKETR DEEIKRLLQG  uence n #: EOS ser 7 21   GGGCCCCGCC CTGGTTCCC CTGGTTCCC GTGCTCCGAG GGACCTGCCC CTTCCTTTAC AAGTAATAAT AAGCCTCCAA GGCACGCCTAC	ADTPVGNDQL PIIKTEGPTL EERIITGPEI DTPVRKLQAN  31   GCCGGGGACG TCGTCTTCTC GCCGTGTCCG GCAGCGCGCA GCCTACGTGC CTGCCGCGGG TCGCTGGTGA CTGGAGGACA CCCCACATTA	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL  41	IQIKFVRGST FRLIKEGETI FEETLKKLL REGRSQ  51   GCTGGCGGAC GGCATCCTCC GCTGCCGGAC CCTTACCGGC CCAACTGCCC CGTGCCTTCAC GGTCCTTCAC GGACAACAAT	720 780 60 120 180 240 300 360 420 480
50 55	TLLVNELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac: Coding sequence TCCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	ESDIMITINGV TKIIITKVVEP KKYTKIIDGV IEGGDGHLFE 67 DNA seq idd Accession Lence: 1-92' 11   GGTGCTCCCG TACTCCTGGG CGGCGCGTT CGCTGTGCGA ACGTGCCCAC ACCTGGACTA ACCTGGACTT CACATCTAGA TGGCTGAGTT GCGAGTT GCGAGTT GCGAGTT GCGAGTT GCGAGTT GCGACTT GCGACTT GCGACTGCCA	IHVVDKLLYP KIKVIEGSLQ PVEITEKETR DEEIKRLLQG  uence n #: EOS sec 7 21   GGGCCCCGCC CCTGGCTCCC CCTGGCTCCC GTGCTCCGAG GGACCTGCCC CTTCCTTTAC AAGTAATAAT AAGCCTCCAA GCAAGGTCTA CATGGCAGAC CATGGCAGAC	ADTPVGNDQL PIIKTEGPTL EERIITGPEI DTPVRKLQAN  31   GCCGGGGACG TCGTCTTCTC GCCGTGTCCG GCAGCGCGCA GCCTACGTGC CTGCCGCGGG TCGCTGGTGA CTGGAGGACA ATGGTGACCT ATGGTGACCCC ATGGTGACCCC	LEILNKLIKY TKVKLIEGEPE KYTRISTGGG KKVQGSRRRL  41   GGCGTCTGCG CCACCTCCTC CCCAGCCCCC CAGTCAAGTC ATGTCTGGG GCCACCTCTT ATGTGCTGGC GCCTGACCTA ATGCCCTCAA GGGTTTTCCT GGCTCAAGGA	IQIKFVRGST FRLIKEGETI ETEETLKKLL REGRSQ  51    GCTGGCGGA GGCATCCTCC GCTGCCGGAC CCTTACCGGC CCTACCGC CCTACCGC CCACTGCCC GGTCCTTC- GGTCCTTC- GGTCCTTC- GGACAACAAT AACAGAGGTA	720 780 60 120 180 240 300 360 420 480 540
50 55	TLLVNELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Nucleic Ac: Coding sequ 1   ATGCCTGGGG TTCTCCTCCT CAGTGCCCGG AATCTGACCG AACCAGCTGG AGCCTCAGGC CGCAACCTGA AATGGCACCC CCCTGGGTCT GTGCAGGCC CTGGGGTCT GTGCAGGCCA	ESDIMITINGV TKIITKVVEP KKYTKIIDGV LEGGDGHLFE 67 DNA seq dd Accessio. Lence: 1-92' 11   GGTGCTCCCG TACTCCTGGG AGGTGCCAC CCAGCACCA AGGTGCCAC CCAGCACCA ACCTGGACT CACATCTAGA TGGCTGAGTT CACATCTAGA TGGCTGAGTT CACATCTAGA AGACCGGCT AAGACCGCCAC AAGACCGCCAC AAGACCGCCAC AAGACCGCCT AAGACCGCCT AAGACCGCCT AAGACCGCCT	IHVVDKLLYP KIKVIEGSLQ FVEITEKETR DEEIKRLLQG  ##: EOS sei 7 21   GGGCCCCGCC CTGGGTTCC CTGGTTCCGAG GGACCTGCCC CTTCCTTAAC AAGTATAAT AAGCCTCAC GCAAGGTCTA CATGGCAGAC CACCTGTGCA	ADTPVGNDQL PILKTEGPTI EERIITGPEI DTPVRKLQAN  quence  31   GCCGCGGGACG TCGTTCTC GCAGCGCGCA GCCTACGTGC CTGCCGCGGCA CCCACATTA ATGGTGACCT TATCCGGAAA	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL  41   GGCGTCTGCG CCACCTCCTC CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGCTGGT GCCTGACCTA ATGCCTCTA ATGCCTCTA ATGCCTCTA ATGCCTCAA GGGTTTTCCT GGCTCAAGGA AAATGAGGAA	IQIKFVRGST FRLIKEGETI FRETIKKLL REGRSQ  51   GCTGGCGCGA GCATCCTCC GCTGCCGGAC CCTTACCGGC CCTACCGGC CCTACCGGC CCTGCCTCCGGTCCTTCCGGTCCTTCAC GGACAACAAT ACCAGAGGTA TCGGGTCCTC	720 780 60 120 180 240 300 420 480 540 600 660
<ul><li>50</li><li>55</li><li>60</li></ul>	TLLVNELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac: Coding sequil ATGCCTGGGG CTAGCGCTGG TTCTCCTCT CAGTGCCCG AATCTGACCGG AACCAGCTGG AACCAGCTGG AATGGCACCC CCCTGGGTCT GTGCAGGGCA TTGGAGGGCA TTGGAGGGCA	ESDIMITINGV TKIIITKVVEP KKYTKIIDGV LEGGDGHLFE 67 DNA seq id Accessio. lence: 1-92' 11   GGTGCTCCCG TACTCCTGGG CGGCGCCTGTA ACGTGTCCAA ACCTGGACTT CACATCTAGA TGGCTGACTT GCGACTGCAC TACATCTAGA TGGCTGACTT ACAATCTAGA TGGCTGACTT ACAATCTAGA TGGCTGACTT ACAATCTAGA TGGCTGACTT ACAATCTAGA TGGCTGACTT ACAATGCCAA ACAGTGCCCA ACAGTGCCCA ACAGTGCTCA ACAGTGCTCA	IHVVDKLLYP KIKVIEGSLQ PVEITEKETR DEEIKRLLQG  in #: EOS sei 7 21   GGGCCCCGCC CTGGGTCTCC CTGGCTCCC GTGCTCCGAG GGACCTGCCC CTTCCTTTAC AAGTAATAAT AAGCCTCAAC GCAAGGTCTA CATGGCAGGC CACCTGTCAC CACCTGTCAC CACCTGTCAC CCTGGACTGT	ADTPVGNDQL PIIKTEGPTL EERIITGPEI DTPVRKLQAN  Quence  31   GCCGGGGACG GCCTTTCTC GCCGTGTCG GCAGGGCGCA GCCTAGTGC CTGCCGCGGG TCGCTGGGG TCGCTGGGAGACA CCCCACATTA ATGGTGACCT TATCCGGAAA GACCCGATTC	LEILNKLIKY TKVKLEGEPE KYTRISTGGG KKVQGSRRRL  41    GGCGTCTGCG CCACCCCTC CCCAGCCCCC CAGCCAGC GCAGCCCTC ATGTGCTGGG GCAACCTCTT ATGTGCTGGG GCTGACCTA ATGCCCTCAA GGGTTTTCCT GGCTCAAGGA AAATGAGGAA ATTCCCCCATC	IQIKFVRGSTI FRLIKEGETI FRLIKEGETI ETEETLKKLL REGRSQ  51   GCTGGCGCGA GGCATCCTCC GCTGCCGGAC CCTTACCGGC CCTTACCGGC CCTACCGGC CCAACTGCCC CGTGTCCTTCAC GGACAACAAT AACAGAGGTA ATCGGGTCCTTC CCTGCAAACC CCTGCAAACC	720 780 60 120 180 240 360 420 540 600 660 720
50 55	TLLVNELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac: Coding sequit ATGCCTGGGG CTAGGGCTGG TTCTCCTCT CAGTGCCCG AACTGACGCAACTGA AATGGCACGC CCCTGGGTCT GTGCAGGGCA TTGGAACTCA TCTATATGTCT	ESDIMITINGV TKIIITKVVEP KKYTKIIIGV IEGGDGHLFE 67 DNA seq id Accession Lence: 1-92' 11   GGTGCTCCCG TACTCCTGGG CGGCGCGTT CGCTGTGCGA ACGTGCCCA ACGTGACTT CACATCTAGA ACTGGACT CACATCTAGA ACGTGCCA ACGTGACTT CCAGCAACCA ACGTGCCA ACGTGCCA ACGTGCCA ACGTGCCA ACGTGCCT ACGTGCTCA ACGTGCCT ACGTGCTCA ACGTGCCT ACGTGCTCT ACGTGCTCT ACGTGCTCT ACGTGTATT CCTGGGTAT	IHVVDKLLYP KIKVIEGSLQ PVEITEKETR DEEIKRLLQG  impression in #: EOS second  condition in	ADTPVGNDQL PIIKTEGPTL EERIITGPEI DTPVRKLQAN  31 GCCGGGGACG TCGTCTTCTC GCCGTGTCCG GCAGCGCGA GCTTACGTGC CTGCTGGTGA CTGCAGGACA CTCACATTA ATGGTGACCT TATCCGGAACA CCCACATTA ATGGTGACCT CTGATGACCT CTGATAGGCG CTGATAGGCG CTGATAGGCG CTGATAGGCG CTGATAGGCG CTGATAGGCG CTGATAGGCG	LEILNKLIKY TKVKLIEGEPE KYTRISTGGG KKVQGSRRRL  41    GGCGTCTGCG CCACCTCCTC CCCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGC GCCTGACCTA ATGCCCTCAA GGGTTTTCCT GGCTCAAGGA AAATGAGGAA ATTCCCCCATC CTATTTTCCT	IQIKFVRGST FRLIKEGETI ETEETLKKLL REGRSQ  51    GCTGGCGGA GGCATCCTCC GCTGCCGGAC CCTTACCGGC CCAACTGCCC GGTCCTTCAC GGTCCTTCAC GGACAACAAT AACAGAGGTA TCGGGTCCTC CCTGCAACC CCTGGTTCTTG	720 780 120 180 240 360 420 480 540 660 660 720 780
<ul><li>50</li><li>55</li><li>60</li></ul>	TLLVNELKSK FKEIPVTVYT TEVIHEPII QEEVIKVTKF Seq ID NO: Nucleic Ac: Coding sequ     ATGCCTGGGG CTAGGGCTGG AATCTGACCC AATCTGACCCG AACCAGCTGG AGCCTCAGGC CGCAACCTGA AATGGCACCC CCCTGGGTCT GTGCAGGCA TGGGAACTCA TCTTATGTCT TATTTGAACC	ESDIMITINGV TKIITKVVEP KKYTKIIDGV IEGGDGHLFE 67 DNA seq dd Accessio. lence: 1-92' 11   GGTGCTCCCG TACTCCTGGG AGGTGCCCAC CCAGCAACCA ACCTGGACTT CACATCTAGA TGGCTGACTT CACATCTAGA TGGCTGACTC ACAGTGCTC ACAGTGCTC ACAGTGCTC ACAGTGCTC ACAGTGCTC ACAGTGCTC ACAGTGCTC ACAGTGCTCA CCAGGGGTT GCACAGGGGT GCACAGGGT GCACAGGGGT GCACAGGGGT GCACAGGGGT GCACAGGGGT GCACAGGGT GCACAGGT GCACAGGGT GCACAGGT GCACAGGGT GCACAGGGT GCACAGGGT GCACAGGGT GCACAGGGT GCACAGGGT GCACAGGGT GCACAGGGT GCACAGGGT GCACAGGT GCACAGGGT GCACAGGGT GCACAGGGT GCACAGGGT GCACAGGT GCACAG	INVUKLLYP KIKVIEGSLQ FVEITEKETR DEEIKRLLQG  I #: EOS sei 7 21   GGGCCCCGCC CTGGGTTCCC CTGGTTCCCGTTCC GTGCTTCCCTTTAC AAGTAATAAT AAGCCTCAC GCAAGGTCTA CACCTGTGCA CACCTGTGCA CTGGATGT CACCTGTAC AAAAAAGTGG	ADTPVGNDQL PILKTEGPTI ERRIITGPEI DTPVRKLQAN  Quence  31 GCCGCGGGACG TCGTTCTTC GCAGTGCC GCCTACGTGC CTGCAGCGCATTA ATGGTGACCT TATCCGGAAA GACCCATTA TATCCGGAAA GACCCATTA GACCCATTA TATCCGGAAA GACCCATTA TATCCGGAAA GACCCATTA GACCCATTA	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL  41    GGCGTCTGCG CCACCTCCTC CCAGCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGG GCCTGACCTA ATGCCCTCAA GGGTTTTCCT GGGTCAAGGA AAATGAGGAA TTCCCCCATC TCAGAGGATGC	IQIKFVRGST FRLIKEGETI FREIKKLL REGRSQ  51   GCTGGCGCGA GCATCCTCC GCTGCCGGAC CCTTACCGGC CCAACTGCCC CGTGCCTTCAC GGACAACAT TCGGGTCCTTC GGACACCAT TCGGGTCTTC CCTGCAAACC CCTGGAAACC CCTGGAAACC CCTGGTTTTG CTGCAGGGAT	720 780 120 180 240 300 360 420 480 540 660 720 840
<ul><li>50</li><li>55</li><li>60</li></ul>	TLLVNELKSK FKEIPVTVYT TEVIHEPII QEEVIKVTKF Seq ID NO: Nucleic Ac: Coding sequ     ATGCCTGGGG CTAGGGCTGG AATCTGACCC AATCTGACCCG AACCAGCTGG AGCCTCAGGC CGCAACCTGA AATGGCACCC CCCTGGGTCT GTGCAGGCA TGGGAACTCA TCTTATGTCT TATTTGAACC	ESDIMITINGV TKIITKVVEP KKYTKIIDGV IEGGDGHLFE 67 DNA seq dd Accessio. lence: 1-92' 11   GGTGCTCCCG TACTCCTGGG AGGTGCCCAC CCAGCAACCA ACCTGGACTT CACATCTAGA TGGCTGACTT CACATCTAGA TGGCTGACTC ACAGTGCTCA AGAGCCGCT ACAGTGCTCA ACAGTGCTCA ACAGTGCTCA ACAGTGCTCA ACAGTGCTCA ACAGTGCTCA ACAGTGCTCA CCACAGGGTT CCACAGGGGTT CCACAGGGGTT GCACAGGGGTT GCACAGGGGTT GCACAGGGGTT GCACAGGGGTT	INVUKLLYP KIKVIEGSLQ FVEITEKETR DEEIKRLLQG  I #: EOS sei 7 21   GGGCCCCGCC CTGGGTTCCC CTGGTTCCCGTTCC GTGCTTCCCTTTAC AAGTAATAAT AAGCCTCAC GCAAGGTCTA CACCTGTGCA CACCTGTGCA CTGGATGT CACCTGTAC AAAAAAGTGG	ADTPVGNDQL PILKTEGPTI ERRIITGPEI DTPVRKLQAN  Quence  31 GCCGCGGGACG TCGTTCTTC GCAGTGCC GCCTACGTGC CTGCAGCGCATTA ATGGTGACCT TATCCGGAAA GACCCATTA TATCCGGAAA GACCCATTA GACCCATTA TATCCGGAAA GACCCATTA TATCCGGAAA GACCCATTA GACCCATTA	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL  41    GGCGTCTGCG CCACCTCCTC CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGG GCCTGACCTA ATGCCCTCAA GGGTTTTCCT GGGTCAAGGA AAATGAGGAA TTCCCCCATC TCAGAGGATGCC TCAGAGGAGGA	IQIKFVRGST FRLIKEGETI FREIKKLL REGRSQ  51   GCTGGCGCGA GCATCCTCC GCTGCCGGAC CCTTACCGGC CCAACTGCCC CGTGCCTTCAC GGACAACAT TCGGGTCCTTC GGACACCAT TCGGGTCTTC CCTGCAAACC CCTGGAAACC CCTGGAAACC CCTGGTTTTG CTGCAGGGAT	720 780 120 180 240 360 420 480 540 660 660 720 780
<ul><li>50</li><li>55</li><li>60</li></ul>	TLLVNELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac: Coding sequi ATGCCTGGGG TTCTCCTCCT CAGTGCCCGG AATCTGACCG AACCAGCTGG AGCCTCAGG AGCCTCAGGCCCGCAACCTGA ATGGCACCC CCCTGGGTCT GTGCAGGCC TGTGCAGGCC TGTGAACTCA TCTTATGTCT TATTTGAACCT TATTTGAACCT CACATGGAAGCC CCCCACATGGAAGCC	ESDIMITINGV TKIITKVVEP KKYTKIIDGV LEGGDGHLFE 67 DNA seq dd Accession Lence: 1-92' 11   GGTGCTCCCG TACTCCTGGG CGGCGCCTT CGCTGGGACTA ACCTGGACTA ACCTGGACTA CACATCTAGA TGCTGAGTT CCCAGGTGCTA TGCGAGTGCCA ACGTGCTGCA ACGTGCTGCA TGCGAGTGCTA CCAGCTGCTA ACGTGCTGAGTT CCCAGGGTAT CCCAGGGGTAT CCCAGGGGTAT GCTATCATTA	IHVVDKLLYP KIKVIEGSLQ FVEITEKETR DEEIKRLLQG  IH: EOS Sei CTGGTCTCC CTGGTTCC GTGCTTCC GTGTTCCGAG GGACCTGCCC CTTCCTTTAC GCAAGGTCTA CACCTGCAC CACCTGTGCA CCTGGACTGT TGTTTTAGCC AAAAAAGTGG AAAAAGTGG CAAGATATGAA	ADTPVGNDQL PIIKTEGPTL EERIITGPEI DTPVRKLQAN  31 GCCGGGGACG TCGTCTTCTC GCCGTGTCCG GCAGCGCGA GCTTACGTGC CTGCTGGTGA CTGCAGGACA CTCACATTA ATGGTGACCT TATCCGGAACA CCCACATTA ATGGTGACCT CTGATGACCT CTGATAGGCG CTGATAGGCG CTGATAGGCG CTGATAGGCG CTGATAGGCG CTGATAGGCG CTGATAGGCG	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL  41    GGCGTCTGCG CCACCTCCTC CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGG GCCTGACCTA ATGCCCTCAA GGGTTTTCCT GGGTCAAGGA AAATGAGGAA TTCCCCCATC TCAGAGGATGCC TCAGAGGAGGA	IQIKFVRGST FRLIKEGETI FREIKKLL REGRSQ  51   GCTGGCGCGA GCATCCTCC GCTGCCGGAC CCTTACCGGC CCAACTGCCC CGTGCCTTCAC GGACAACAT TCGGGTCCTTC GGACACCAT TCGGGTCTTC CCTGCAAACC CCTGGAAACC CCTGGAAACC CCTGGTTTTG CTGCAGGGAT	720 780 120 180 240 300 360 420 480 540 660 720 840
<ul><li>50</li><li>55</li><li>60</li></ul>	TLLVNELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac: Coding sequi ATGCCTGGGG TTCTCCTCCT CAGTGCCCGG AATCTGACCG AACCAGCTGG AGCCTCAGG AGCCTCAGGCCCGCAACCTGA ATGGCACCC CCCTGGGTCT GTGCAGGCC TGTGCAGGCC TGTGAACTCA TCTTATGTCT TATTTGAACCT TATTTGAACCT CACATGGAAGCC CCCCACATGGAAGCC	ESDIMITINGV TKIITKVVEP KKYTKIIDGV IEGGDGHLFE 67 DNA seq dd Accessio. lence: 1-92' 11   GGTGCTCCCG TACTCCTGGG AGGTGCCCAC CCAGCAACCA ACCTGGACTT CACATCTAGA TGGCTGACTT CACATCTAGA TGGCTGACTC ACAGTGCTCA AGAGCCGCT ACAGTGCTCA ACAGTGCTCA ACAGTGCTCA ACAGTGCTCA ACAGTGCTCA ACAGTGCTCA ACAGTGCTCA CCACAGGGTT CCACAGGGGTT CCACAGGGGTT GCACAGGGGTT GCACAGGGGTT GCACAGGGGTT GCACAGGGGTT	IHVVDKLLYP KIKVIEGSLQ FVEITEKETR DEEIKRLLQG  IH: EOS Sei CTGGTCTCC CTGGTTCC GTGCTTCC GTGTTCCGAG GGACCTGCCC CTTCCTTTAC GCAAGGTCTA CACCTGCAC CACCTGTGCA CCTGGACTGT TGTTTTAGCC AAAAAAGTGG AAAAAGTGG CAAGATATGAA	ADTPVGNDQL PILKTEGPTI ERRIITGPEI DTPVRKLQAN  Quence  31 GCCGCGGGACG TCGTTCTTC GCAGTGCC GCCTACGTGC CTGCAGCGCATTA ATGGTGACCT TATCCGGAAA GACCCATTA TATCCGGAAA GACCCATTA GACCCATTA TATCCGGAAA GACCCATTA TATCCGGAAA GACCCATTA GACCCATTA	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL  41    GGCGTCTGCG CCACCTCCTC CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGG GCCTGACCTA ATGCCCTCAA GGGTTTTCCT GGGTCAAGGA AAATGAGGAA TTCCCCCATC TCAGAGGATGCC TCAGAGGAGGA	IQIKFVRGST FRLIKEGETI FREIKKLL REGRSQ  51   GCTGGCGCGA GCATCCTCC GCTGCCGGAC CCTTACCGGC CCAACTGCCC CGTGCCTTCAC GGACAACAT TCGGGTCCTTC GGACACCAT TCGGGTCTTC CCTGCAAACC CCTGGAAACC CCTGGAAACC CCTGGTTTTG CTGCAGGGAT	720 780 120 180 240 300 360 420 480 540 660 720 840
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	TLLVNELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac: Coding sequit ATGCCTGGGG CTAGCGCTGG TTCTCCTCTC CAGTGCCCCG AACTGACCCC CACCTGGACCTGG ACCTCAGGC CCCTGGGTCT GTGCAGGGCA TTGGAACTCA TCTTATGTCT TATTTGAACC CACATGGAACT AGTTCTAACT	ESDIMITINGV TKIITKVVEP KKYTKIIDGV LEGGDGHLFE 67 DNA seq id Accession Lence: 1-92' 11    GGTGCTCCCG TACTCCTGGG CGGCGCGTT CGCTGTGCGA AGGTGCCCAC CCAGCAACCA ACCTGGACTT GCAATCTAGAA TGCTGAGTT GCGACTGCCA AGACCGGCT ACCTCGGGTAT GCGACTGCCA AGACCGGCT CCAGCGATCT CCAGCTACT CGCAGTATT CGCAGTGTCT CGCAGTAT CCAGGGGTAT CCAGGGGTAT CCAGGGGTAT CGCAGGGGTAT CGCAGGGGTAT CGGATGTCCT	IHVVDKLLYP KIKVIEGSLQ PVEITEKETR DEEIKRLLQG  #: EOS sei 7 21   GGGCCCCGCC CTGGCTTCC CTGGCTCCC GTGCTCCGAG GGACCTGCCC CTTCCTTTAC AAGTAATAAT AAGCCTGCAC CACCTGTGCA CACCTGTGCA CATGGCAGAC CACCTGTGCA TGTTTTAGCC AAAAAAGTGG CAGATATGAA CGGATGA	ADTPVGNDQL PILKTEGPTI ERRIITGPEI DTPVRKLQAN  Quence  31 GCCGCGGGACG TCGTTCTTC GCAGTGCC GCCTACGTGC CTGCAGCGCATTA ATGGTGACCT TATCCGGAAA GACCCATTA TATCCGGAAA GACCCATTA GACCCATTA TATCCGGAAA GACCCATTA TATCCGGAAA GACCCATTA GACCCATTA	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL  41    GGCGTCTGCG CCACCTCCTC CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGG GCCTGACCTA ATGCCCTCAA GGGTTTTCCT GGGTCAAGGA AAATGAGGAA TTCCCCCATC TCAGAGGATGCC TCAGAGGAGGA	IQIKFVRGST FRLIKEGETI FREIKKLL REGRSQ  51   GCTGGCGCGA GCATCCTCC GCTGCCGGAC CCTTACCGGC CCAACTGCCC CGTGCCTTCAC GGACAACAT TCGGGTCCTTC GGACACCAT TCGGGTCTTC CCTGCAAACC CCTGGAAACC CCTGGAAACC CCTGGTTTTG CTGCAGGGAT	720 780 120 180 240 300 360 420 480 540 660 720 840
<ul><li>50</li><li>55</li><li>60</li></ul>	TLLVNELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac: Coding sequit ATGCCTGGGG TTCTCCTCCT CAGTGCCCGG AATCTGACGG AACCAGCTGG AACCAGCTGG AACCAGCTGA AATGGCACCC CCCTGGGTCT CTGCCAGGCCC CCCTGGGTCT TGTGCAGGGCA TTGGAACTCA TCTTATGTCT TATTTTGAACC CACATGGAAG AGTTCTAACT Seq ID NO:	ESDIMITINGV TKIITKVVEP KKYTKIIDGV IEGGDGHLFE 67 DNA seq dd Accessio: lence: 1-92' 11   GGTGCTCCCG TACTCCTGGG AGGTGCCCAC CCAGCACCAA AGGTGCCCAC CCAGCACCAA ACCTGGGACTT CACATCTAGA TGGCTGAGTT CACATCTAGA TGGCTGAGTT CACATCTAGA TGGCTGAGTT CACATCTAGA TGGCTGAGTT CACATGCTCA CAGTGCTCA CGGTATCCTCA CGGTTGTCCT 68 Protein	IHVVDKLLYP KIKVIEGSLQ FVEITEKETR DEEIKRLLQG  IH: EOS Sei 7 21   GGGCCCCGCC CTGGGTTCC CTGGTTCCCGTTCC GTGCTTCCCGAG GGACCTGCCC CTTCCTTTAC AAGTATATAT AAGCCTCAC GCAAGGTCTA CACCTGTGCA CCTGGACTGT TGTTTTAGCC AAAAAAGTGG CAGATATGAA CGAGTGA GCAGTGA	ADTPVGNDQL PILKTEGPTI EERLITGPEI DTPVRKLQAN  quence  31   GCCGCGGGACG TCGTTCTCT GCCGCGGG CCTGCTGGTGA CCCCACATTA ATGGTGACCT TATCCGGAAA GACCCGATCT TATCCGGAAA GACCCGATTA GACCCGATTA GACCCGATTA GACCCGATTA CTGTATAGGCG ATGCATAACA ATCAATGCGG	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL  41    GGCGTCTGCG CCACCTCCTC CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGG GCCTGACCTA ATGCCCTCAA GGGTTTTCCT GGGTCAAGGA AAATGAGGAA TTCCCCCATC TCAGAGGATGCC TCAGAGGAGGA	IQIKFVRGST FRLIKEGETI FREIKKLL REGRSQ  51   GCTGGCGCGA GCATCCTCC GCTGCCGGAC CCTTACCGGC CCAACTGCCC CGTGCCTTCAC GGACAACAT TCGGGTCCTTC GGACACCAT TCGGGTCTTC CCTGCAAACC CCTGGAAACC CCTGGAAACC CCTGGTTTTG CTGCAGGGAT	720 780 120 180 240 300 360 420 480 540 660 720 840
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<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	TLLVNELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac: Coding sequit ATGCCTGGGG TTCTCCTCCT CAGTGCCCGG AATCTGACGG AACCAGCTGG AACCAGCTGG AACCAGCTGA AATGGCACCC CCCTGGGTCT CTGCCAGGCCC CCCTGGGTCT TGTGCAGGGCA TTGGAACTCA TCTTATGTCT TATTTTGAACC CACATGGAAG AGTTCTAACT Seq ID NO:	ESDIMITINGV TKIITKVVEP KKYTKIIDGV IEGGDGHLFE 67 DNA seq dd Accessio: lence: 1-92' 11   GGTGCTCCCG TACTCCTGGG AGGTGCCCAC CCAGCACCAA AGGTGCCCAC CCAGCACCAA ACCTGGGACTT CACATCTAGA TGGCTGAGTT CACATCTAGA TGGCTGAGTT CACATCTAGA TGGCTGAGTT CACATCTAGA TGGCTGAGTT CACATGCTCA CAGTGCTCA CGGTATCCTCA CGGTTGTCCT 68 Protein	IHVVDKLLYP KIKVIEGSLQ FVEITEKETR DEEIKRLLQG  IH: EOS Sei 7 21   GGGCCCCGCC CTGGGTTCC CTGGTTCCCGTTCC GTGCTTCCCGAG GGACCTGCCC CTTCCTTTAC AAGTATATAT AAGCCTCAC GCAAGGTCTA CACCTGTGCA CCTGGACTGT TGTTTTAGCC AAAAAAGTGG CAGATATGAA CGAGTGA GCAGTGA	ADTPVGNDQL PILKTEGPTI EERLITGPEI DTPVRKLQAN  quence  31   GCCGCGGGACG TCGTTCTCT GCCGCGGG CCTGCTGGTGA CCCCACATTA ATGGTGACCT TATCCGGAAA GACCCGATCT TATCCGGAAA GACCCGATTA GACCCGATTA GACCCGATTA GACCCGATTA CTGTATAGGCG ATGCATAACA ATCAATGCGG	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL  41    GGCGTCTGCG CCACCTCCTC CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGG GCCTGACCTA ATGCCCTCAA GGGTTTTCCT GGGTCAAGGA AAATGAGGAA TTCCCCCATC TCAGAGGATGCC TCAGAGGAGGA	IQIKFVRGST FRLIKEGETI FREIKKLL REGRSQ  51   GCTGGCGCGA GCATCCTCC GCTGCCGGAC CCTTACCGGC CCAACTGCCC CGTGCCTTCAC GGACAACAT TCGGGTCCTTC GGACACCAT TCGGGTCTTC CCTGCAAACC CCTGGAAACC CCTGGAAACC CCTGGTTTTG CTGCAGGGAT	720 780 120 180 240 300 360 420 480 540 660 720 840
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<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	TLLVNELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac: Coding sequil ATGCCTGGGG TTCTCCTCCT CAGTGCCCGG AATCTGACOG AACCAGCTGG AACCAGCTGG AACCTGAGCCCCC CCCTGGGTCT GTGCAGGCACCTGA TTGGAACTCA TCTTATGTCT TATTTGAACC CACATGGAAC AGTTCTAACT Seq ID NO: Protein Ac 1	ESDIMITINGV TKIITKVVEP KKYTKIIDGV LEGGDGHLFE 67 DNA seq dd Accessio. Lence: 1-92' 11   GGTGCTCCCG TACTCCTGGG AGGTGCCCAC CCACCAACCAA AGGTGCCCAC CCACCAACCAA AGCTGGACTT CACATCTAGA TGGCTGAGTT CACATCTAGA TGGCTGAGTT CACATCTAGA TGGCTGAGTT CACATCTAGA TGGCTGAGTT CACATCTAGA TGGCTGAGTT CACATCTAGA TCCTGGGTAT CCGGGTAT CCGGGTAT CCGGTATCATTA CCGATGTCCT 68 Protein cession #: 11	IHVVDKLLYP KIKVIEGSLQ FVEITEKETR DEEIKRLLQG  IH: EOS Set T 21  GGGCCCCGCC CTGGGTTCC GTGCTTCCC GTGCTTCCC GTGCTTCCC GTGCTCCAG GGACCTGCC CTCCTTAC CAGGTATATAAT AAGCCTCAC GCAAGGTCTA CACCTGTGCA CCTGGACTGT TGTTTTAGC CACCTGTGCA CAGGTGA CAGGTGA GAGATATGAA CAGGTGA Sequence EOS Sequence 21	ADTPVGNDQL PILKTEGPTI EERIITGPEI DTPVRKLQAN  quence  31   GCCSCGGACG TCGTTCTC GCCGTGTCCG GCAGCGCGCA GCCTACGTGA CTCGCGCGG TCGCTGGTGA CCCCACATTA ATGGTGACCT TATCCGGAAA GACCCGATTC CTGATAGGCG ATGATAGGCG ATGCATACGG ATGCATACGG	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL  41  GGCGTCTGCG CCACCTCCTC CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTCTGGG GCCTGACCTA ATGCCCTCAA GGGTTTACGT GGCTCTACGT AATGCCCTCAA TCCCCCATC TCACAGATGT TCACAGATGT ACCCCATC TCACAGATT	IQIKFVRGST FRLIKEGETI FREIKKLL REGRSQ  51   GCTGGCGCGA GCATCCTCC GCTGCCGGAC CCTTACCGGC CCTACCGGC CCTACCGGC CCTACCGGC CCTGCACACTACCC CCTGCTCCTCC CGGTCCTTCC CGGTCCTTCC CCTGGTCTTC CCTGCAAACC CCTGGTTTTG CTGCAGGGAT AACAAACCTC	720 780 120 180 240 300 360 420 480 540 660 720 840
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	TLLVNELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac: Coding sequi  ATGCCTGGGG CTAGCGCTGG TTCTCCTCTCT TCAGTGCCCCG AATCTGACCG AACCAGCTGG AGCCTCAGG AGCCTCAGG AGCCTCAGG TGGAACCTGA ATGGCACCC CCCTGGGTCT TGTGAAGGC TGTGAAGCTCA TCTTATGTCT TATTTGAACT CACATGGAAG AGTTCTAACT Seq ID NO: Protein Ac  I MPGGCSRGPA	ESDIMITINGV TKIITKVVEP KKYTKIIDGV LEGGDGHLFE 67 DNA sequid Accession lence: 1-92' 11   GGTGCTCCCG TACTCCTGGG CGGCGCCGTT CACTCTGGGACTT CACATCTAGA TGGCTGACTT CACATCTAGA TGCTGGGATT CCAGGGGTT CCAGGGGGTT CCAGGGGGTT CCAGGGGGTT CCAGGGGTT CCAGGGGTT CGATGTCCT 68 Protein CCCSSION #: 11   ACDGRILLAR	INVUDELLYP KIKVIEGSLQ PVEITEKETR DEEIKRLLQG  I #: EOS Sei  GGGCCCCGCC CTGGTTCC CTGGTTCC CTGGTTCC CTTCCTTTAC AAGTAATAAT AAGCCTCAC GCACTGTCA CACCTGTGCA CACCTGTCA CACCTCA CACCTGTCA CACCTCA CACCTGTCA CACCTCA CACCTCA CACCTGTCA CACCTCA CA	ADTPVGNDQL PILKTEGPTL EERIITGPEI DTPVRKLQAN  Quence  31   GCCGCGGGACG TCGTCTTCTC GCAGGGCGCGCA GCCTACGTGC CTGCCGCGGG TCGCTGCGCGGG TCGCTGCGCGCG ACGCGCACTTA ATGGTGACA CCCCACATTA ATGGTGACC CTGATAGGCG ATCCATAACA ATCAATGCGG ATCATAACA ATCAATGCGG	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL     GGCGTCTGCG CCACTCCTC CCCAGCCCCC CAGTCAAGTG GCAACTCTT ATGTGCTGGC GCCTGACCTA ATGCCTCAA GGGTTTTCCT GGCTCAAGGA TTCCCCCATC CTATTTTCCT TCAGAGATG ACCCCAGATT       FSSSAPFLAS	IQIKFVRGST FRLIKEGETI FRLIKEGETI ETEETLKKLL REGRSQ  51   GCTGGCGCGA GGCATCCTCC GCTGCCGGAC CCTTACCGGC CCTACCGGC CCTACCGGC CCTACCGCC CCTGCTCTCAC GGACAACAAT AACAGAGGTA TCGGGTCCTC CCTGCAAACC CCTGGTTTTG CTGCAGGGAT AACAAACCTC	720 780 120 120 120 240 300 360 420 540 600 720 780 840 900
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	TLLVNELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac: Coding sequil ATGCCTGGGG CTAGCGCTGG TTCTCCTCT CAGTGCCCG AACCAGCTGG AACCAGCTGG AACCAGCTGG AACCAGCTGG AACCAGCTGG AATGGCACCC CCCTGGGTCT GTGCAGGGCA TTGGAAGCTC ATTATGACC CACATGGAA TCTTATGTCT TATTTGAACC CACATGGAAC AGTTCTAACT Seq ID NO: Protein Ac 1   MPGGCSRGPA QCPALCECSE	ESDIMITINGV TKIIITKVVEP KKYTKIIDGV KKYTKIIDGV 67 DNA seq id Accessio. lence: 1-92' 11    GGTGCTCCCG TACTCCTGGG CGGCGCCTGTA ACGTGTCCAA ACCTGGACTT CACATCTAGA TGCTGACTT ACAATCTAGA TGCTGACTT ACAATCTAGA TCCTGGGTAT CACATCTAGA TCCTGGGTAT CACATCTAGA TCCTGGGTAT CACATCTAGA TCCTGGGTAT CACATCTAGA TCCTGGGTAT CCAAGTGCCA ACGGGTAT CCAAGTGCCA CCAGCAACCA CCGGTTAT CCAATCTAGA TCCTGGGTAT CCAGTGTCCT CGGATTCCT 68 Protein ccssion #: 1   ACGGTGCLLAAF AARTVKCVMM	IHVVDKLLYP KIKVIEGSLQ PVEITEKETR DEEIKRLLQG  in #: EOS sei 7 21   GGGCCCCGCC CTGGGTCTCC CTGGCTCCCA GGACCTGCCC CTTCCTTTAC AAGTAATAAT AAGCCTCCAC GCAACGTCTA CATGGCAGCA CACCTGTGCA TGTTTTAGCC AAAAAAGTGA CCTGGACTGT TGTTTTAGCC AAAAAAGTGA CGAGTGA  GGAGTGA  Sequence EOS sequence 21   LALVLLGWVS NITEVPTDLE	ADTPVGNDQL PIIKTEGPTL EERIITGPEI DTPVRKLQAN  31   GCCGGGGACG GCCTTCTCC GCCGTGTCCG GCAGGGCGCA GCCTACGTGC CTGCGCGGGG TCGCTGGTGA CCCCACATTA ATGGTGACCT TATCCGGAAA ACCCCGATTC CTGATAGGCG ATGCATAACA ATCAATGCGG  10 1 1 2 2 31   31   31   32 33 34 VRNLFLTG	LEILNKLIKY TKVKLIEGEPE KYTRISTGGG KKVQGSRRRL  41    GGCGTCTGCG CCACCCCCC CCAGCCCCCC CCAGCCCCCC GCAGCCCCT ATGTGCTGGC GCAACCTCTT ATGTGCTGGC GCCTGACCTA ATGCCCTCAA GGGTTTTCCT GGCTCAAGGA AAATGAGGAA ATTCCCCCATC CTATTTTCCT TCAGAGATGC ACCCCAGATT  41    FSSSAPFLAS NQLASNHFLY	IQIKFVRGST FRLIKEGETI FRLIKEGETI FREIREKLL REGRSQ  51   GCTGGCGCGA GGCATCCTCC GCTGCCGGAC CCTTACCGGC CCTTACCGGC CCTTACCGGC CCTTCCCGGACTCCC CCTGTCCTTCAC GGACAACAAT AACAAAGGGTA TCGGGTCCTTC CCTGCAAACC CCTGGTTTTG CTGCAGGGAT AACAAACCTC	720 780 120 180 240 360 420 480 540 660 720 780 840 900
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	TLLVNELKSK FKEIPVTVYT TEVIHEGPII QEEVTKVTKF Seq ID NO: Nucleic Ac: Coding sequit  ATGCCTGGGG TTCTCCTCT CAGTGCCCGG AACTGGACCGG AACTGACCGG AACCAGCTGG AACCAGCTGG CGCAACCTGA AATGGCACCC CCCTGGGTCT GTGCAGGGCA TCGTATGTCT TATTTGAACC CACATGGAAC AGTTCTAACT Seq ID NO: Protein Ac  1   MPGGCSRGPA MPGGCSRGPA QCPALCECSE SLRHLDLSNN	ESDIMITINGV TKIITKVVEP KKYTKIIDGV LEGGDGHLFE 67 DNA seq dd Accessio. Lence: 1-92' 11   GGTGCTCCCG TACTCCTGGG AGGTGCCCAC CCAGCAACCA ACCTGGACTT CACATCTAGA TGGCTGAGTT CACATCTAGA TGGCTGAGTT CACATCTAGA TGGCTGAGTT CACATCTAGA TGGCTGAGTT CACATCTAGA TGGCTGATT CACATCTAGA TGGCTGATT CACATCTAGA TCCTGGGTAT GCAAGGGCT GGATTCATT CCAGGGGT TCCTGGGTAT TCCAGGGGT TCCTGGGTAT TCCAGGGGT TCCAGGGT TCCAGGT TCCAGGGT TCCAGGT TCCAGGGT TCCAGGT TCCAGGGT T	IHVVDKLLYP KIKVIEGSLQ FVEITEKETR DEEIKRLLQG  I #: EOS sei    GGGCCCCGCC CTGGGTTCTCC CTGGTTCTCCTTTAC AAGTAATAAT AAGCCTCAC GCAAGGTCTAC CACCTGTGCA CACCTGGACTGT IGTTTTAGGC AAAAAAGTGG CAGATATGAA CGAGTGA  Sequence EOS sequence 21   LALVLLGWVS NLTEVPTDLE NLTEVPTDLE RNLTHLESLE	ADTPVGNDQL PILKTEGPTL ERRILTGPEI DTPVRKLQAN  Quence  31   GCCGCGGGACG TCGTTCTTC GCCGCGGC CTGCTGGTGA CTGGAGGACA CCCCACATTA ATGGTACCT TATCCGGAAA GACCCGATTC CTGATAGGC ATGCATAGCA ATCATGCGG ATGCATAGCA ATCATGCGG SSSPTSSASS AYVRNLFLTGG LEDNALKVLB	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL  41  GGCGTCTGCG CCACTCCTC CCAGCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGC GCCTGACCTA ATGCCCTAA GGGTTTTCCT GGCTCAAGGA AAATGAGGAA TTCCCCCATC CTATTTTCT TCAGGAGAA ACCCCAGATT  41  FSSSAPFLAS NQLASNHFLY NGTLAELQGL	IQIKFVRGST FRLIKEGETI FREIKKLL REGRSQ  51   GCTGGCGCGA GCATCCTCC GCTGCCGGC CCTACCGGC CCTACCGGC CCACTGCCC CCTGCAACC CCTGCAACC CCTGCAAACC CCTGCAAACC CCTGCAAACC CCTGCAAACC CCTGCAAACC CCTGCAAACC CCTGCAAACC CCTGCAAACC CTGCACAACC CTGCACACC CTGCAAACC CTGCACACC CTGCAAACC CTGCACACC CTGCAAACC CTGCACACC CTCCACACC CTCACACC CTCCACACC CTC	720 780 120 180 240 360 420 480 540 600 660 720 780 840 900
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	TLLVNELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac: Coding sequi  ATGCCTGGGG TTCTCCTCT CAGTGCCCGG AATCTGACCG AACCAGCTGG AGCCTCGGG AGCCTCGGACTCT GTGCAGGCC CCCTGGGTCT TATTGACCT TATTTGACC CACATGGAAG AGTTCTAACT Seq ID NO: Protein Ac  1 MPGGCSRGPA QCPALCECSE SLRHLDLSNN PWVDCCHMAD	ESDIMITINGV TKIITKVVEP KKYTKIIDGV LEGGDGHLFE 67 DNA seq dd Accession Lence: 1-92' 11   GGTGCTCCCG TACTCCTGGG AGGTGCCAC CCAGCACCAA ACCTGGCAT ACCTGGCAT TCACATCTAGA TGCTGAGTT CCAGATCTAGA TGCTGGTAT CCAGATCTAGA TCCTGGGTA ACAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA CCAGTGCTGCA CCAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA CCAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA CCAGTGCTGCA ACAGTGCTGCA CCAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA CCAGTGCTGCA ACAGTGCTGCA ACAGTGCTCA ACAGTGCTGCA ACAGTGCTA A	IHVVDKLLYP KIKVIEGSLQ FVEITEKETR DEEIKRLLQG  IH: EOS Set TOTAL GGGCCCCGCC CTGGGTTCC GTGCTTCCCTTAC GGACCTGCCC CTTCCTTTAC GCAAGGTCTA CACCTGTGCA CCACCTGTGCA CCACCTGTGCA CCACCTGTGCA CACCTGTGCA CACCTGTGCA CAGTATAGAA CAGGAAGTGA LEALVLLGWVS LLALVLLGWVS LLAUVLLGWVS LLAUVLLGWVS LLAUVLLGWVS LLAUVLLGWVS LLAUVLLGWVS LLAUVLLGWVS LLAUVLLGWVS	ADTPVGNDQL PILKTEGPTL EERIITGPEI DTPVRKLQAN  Quence  31   GCCGCGGGACG TCGTTTCTC GCAGCGCGCA GCCTACGTGC GCAGCGCGCA CCCCACATTA ATGGTGACCT TATCCGGAAA GACCCGATTC CTGATAGCCG ATGATACA ATCAATGCGG ATGCATAACA ATCAATGCGG ATCATTAACA ATCAATGCGG LEDNALKVLH SSSSPTSSASS AYVRNLFLTG LEDNALKVLH TYPEKMENRVL	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL     GGCGTCTGCG CCACTCCTC CCAGCCCCC CCAGCCCCT ATGTGCTGGG GCAACCTCTT ATGCTGGG ACCTCTA ATGCCCTCAA GGGTTTTCCT ATGCCCCAT ATGCCCCAT ATGCCCCAT ATGCCCATC CTATTTTCCT ACCCCATC TCAGAGATG ACCCCAGATT	IQIKFVRGST FRLIKEGETI FRLIKEGETI FRETIKKLL REGRSQ  51   GCTGGCGCGA GGCATCCTCC GCTGCCGGAC CCTACCGGC CCTACCGGC CCTACCGGC CCTACCGGC CCTGCCTCC GGTCCTTC CGGTCCTTC CGGTCCTTC CCTGCAAACC CCTGGTCTTC CTGCAAACC CCTGGTCTTC CTGCAAACC CCTGGTTCTC CTGCAAACC CCTGGTTCTC CTGCAAACC CCTGCAAACC CCTGCAAACC CCTGCAAACC CTGCAAACC CTGCAAACC CTGCAAACC CTGCAAACC CTGCAAACC TGCACAGGGT AACAAACCTC  51   AVSAQPPLPD LPRDVIAQLP PHIRVFLDNN DPILPPSLQT	720 780 120 120 120 240 300 360 420 480 540 660 720 780 840 900
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	TLLVNELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac: Coding sequi  ATGCCTGGGG TTCTCCTCT CAGTGCCCGG AATCTGACCG AACCAGCTGG AGCCTCGGG AGCCTCGGACTCT GTGCAGGCC CCCTGGGTCT TATTGACCT TATTTGACC CACATGGAAG AGTTCTAACT Seq ID NO: Protein Ac  1 MPGGCSRGPA QCPALCECSE SLRHLDLSNN PWVDCCHMAD	ESDIMITINGV TKIITKVVEP KKYTKIIDGV LEGGDGHLFE 67 DNA seq dd Accession Lence: 1-92' 11   GGTGCTCCCG TACTCCTGGG AGGTGCCAC CCAGCACCAA ACCTGGCAT ACCTGGCAT TCACATCTAGA TGCTGAGTT CCAGATCTAGA TGCTGGTAT CCAGATCTAGA TCCTGGGTA ACAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA CCAGTGCTGCA CCAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA CCAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA CCAGTGCTGCA ACAGTGCTGCA CCAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA CCAGTGCTGCA ACAGTGCTGCA ACAGTGCTCA ACAGTGCTGCA ACAGTGCTA A	IHVVDKLLYP KIKVIEGSLQ FVEITEKETR DEEIKRLLQG  IH: EOS Set TOTAL GGGCCCCGCC CTGGGTTCC GTGCTTCCCTTAC GGACCTGCCC CTTCCTTTAC GCAAGGTCTA CACCTGTGCA CCACCTGTGCA CCACCTGTGCA CCACCTGTGCA CACCTGTGCA CACCTGTGCA CAGTATAGAA CAGGAAGTGA LEALVLLGWVS LLALVLLGWVS LLAUVLLGWVS LLAUVLLGWVS LLAUVLLGWVS LLAUVLLGWVS LLAUVLLGWVS LLAUVLLGWVS LLAUVLLGWVS	ADTPVGNDQL PILKTEGPTL EERIITGPEI DTPVRKLQAN  Quence  31   GCCGCGGGACG TCGTTTCTC GCAGCGCGCA GCCTACGTGC GCAGCGCGCA CCCCACATTA ATGGTGACCT TATCCGGAAA GACCCGATTC CTGATAGCCG ATGATACA ATCAATGCGG ATGCATAACA ATCAATGCGG ATCATTAACA ATCAATGCGG LEDNALKVLH SSSSPTSSASS AYVRNLFLTG LEDNALKVLH TYPEKMENRVL	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL     GGCGTCTGCG CCACTCCTC CCAGCCCCC CCAGCCCCT ATGTGCTGGG GCAACCTCTT ATGCTGGG ACCTCTA ATGCCCTCAA GGGTTTTCCT ATGCCCCAT ATGCCCCAT ATGCCCCAT ATGCCCATC CTATTTTCCT ACCCCATC TCAGAGATG ACCCCAGATT	IQIKFVRGST FRLIKEGETI FRLIKEGETI FRETIKKLL REGRSQ  51   GCTGGCGCGA GGCATCCTCC GCTGCCGGAC CCTACCGGC CCTACCGGC CCTACCGGC CCTACCGGC CCTGCCTCC GGTCCTTC CGGTCCTTC CGGTCCTTC CCTGCAAACC CCTGGTCTTC CTGCAAACC CCTGGTCTTC CTGCAAACC CCTGGTTCTC CTGCAAACC CCTGGTTCTC CTGCAAACC CCTGCAAACC CCTGCAAACC CCTGCAAACC CTGCAAACC CTGCAAACC CTGCAAACC CTGCAAACC CTGCAAACC TGCACAGGGT AACAAACCTC  51   AVSAQPPLPD LPRDVIAQLP PHIRVFLDNN DPILPPSLQT	720 780 120 180 240 360 420 480 540 600 660 720 780 840 900
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	TLLVNELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac: Coding sequit ATGCCTGGGG CTAGGGCTGG TTCTCCTCCT CAGTGCCCCG AATCTGACCG AATCTGACCG AACCAGCTGG AGCCTCAGGC CCCCTGGGTCT TGTGCAGCC CCCTGGGTCT TATTTGACCT TATTTGACCT TATTTGAACT Seq ID NO: Protein Ac 1   MPGGCSRGPA QCPALCECSE SLRHLDLSM SYVFLGIVLA	ESDIMITINGV TKIITKVVEP KKYTKIIDGV LEGGDGHLFE 67 DNA seq dd Accession Lence: 1-92' 11   GGTGCTCCCG TACTCCTGGG AGGTGCCAC CCAGCACCAA ACCTGGCAT ACCTGGCAT TCACATCTAGA TGCTGAGTT CCAGATCTAGA TGCTGGTAT CCAGATCTAGA TCCTGGGTA ACAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA CCAGTGCTGCA CCAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA CCAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA CCAGTGCTGCA ACAGTGCTGCA CCAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA CCAGTGCTGCA ACAGTGCTGCA ACAGTGCTCA ACAGTGCTGCA ACAGTGCTA A	IHVVDKLLYP KIKVIEGSLQ FVEITEKETR DEEIKRLLQG  IH: EOS Set TOTAL GGGCCCCGCC CTGGGTTCC GTGCTTCCCTTAC GGACCTGCCC CTTCCTTTAC GCAAGGTCTA CACCTGTGCA CCACCTGTGCA CCACCTGTGCA CCACCTGTGCA CACCTGTGCA CACCTGTGCA CAGTATAGAA CAGGAAGTGA LEALVLLGWVS LLALVLLGWVS LLAUVLLGWVS LLAUVLLGWVS LLAUVLLGWVS LLAUVLLGWVS LLAUVLLGWVS LLAUVLLGWVS LLAUVLLGWVS	ADTPVGNDQL PILKTEGPTL ERRILTGPEI DTPVRKLQAN  Quence  31   GCCGCGGGACG TCGTTCTTC GCCGCGGC CTGCTGGTGA CTGGAGGACA CCCCACATTA ATGGTACCT TATCCGGAAA GACCCGATTC CTGATAGGC ATGCATAGCA ATCATGCGG ATGCATAGCA ATCATGCGG SSSPTSSASS AYVRNLFLTGG LEDNALKVLB	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL     GGCGTCTGCG CCACTCCTC CCAGCCCCC CCAGCCCCT ATGTGCTGGG GCAACCTCTT ATGCTGGG ACCTCTA ATGCCCTCAA GGGTTTTCCT ATGCCCCAT ATGCCCCAT ATGCCCCAT ATGCCCATC CTATTTTCCT ACCCCATC TCAGAGATG ACCCCAGATT	IQIKFVRGST FRLIKEGETI FRLIKEGETI FRETIKKLL REGRSQ  51   GCTGGCGCGA GGCATCCTCC GCTGCCGGAC CCTACCGGC CCTACCGGC CCTACCGGC CCTACCGGC CCTGCCTCC GGTCCTTC CGGTCCTTC CGGTCCTTC CCTGCAAACC CCTGGTCTTC CTGCAAACC CCTGGTCTTC CTGCAAACC CCTGGTTCTC CTGCAAACC CCTGGTTCTC CTGCAAACC CCTGCAAACC CCTGCAAACC CCTGCAAACC CTGCAAACC CTGCAAACC CTGCAAACC CTGCAAACC CTGCAAACC TGCACAGGGT AACAAACCTC  51   AVSAQPPLPD LPRDVIAQLP PHIRVFLDNN DPILPPSLQT	720 780 120 120 120 240 300 360 420 480 540 660 720 780 840 900
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	TLLVNELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac: Coding sequi  ATGCCTGGGG TTCTCCTCT CAGTGCCCGG AATCTGACCG AACCAGCTGG AGCCTCGGG AGCCTCGGACTCT GTGCAGGCC CCCTGGGTCT TATTGACCT TATTTGACC CACATGGAAG AGTTCTAACT Seq ID NO: Protein Ac  1 MPGGCSRGPA QCPALCECSE SLRHLDLSNN PWVDCCHMAD	ESDIMITINGV TKIITKVVEP KKYTKIIDGV LEGGDGHLFE 67 DNA seq dd Accession Lence: 1-92' 11   GGTGCTCCCG TACTCCTGGG AGGTGCCAC CCAGCACCAA ACCTGGCAT ACCTGGCAT TCACATCTAGA TGCTGAGTT CCAGATCTAGA TGCTGGTAT CCAGATCTAGA TCCTGGGTA ACAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA CCAGTGCTGCA CCAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA CCAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA CCAGTGCTGCA ACAGTGCTGCA CCAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA CCAGTGCTGCA ACAGTGCTGCA ACAGTGCTCA ACAGTGCTGCA ACAGTGCTA A	IHVVDKLLYP KIKVIEGSLQ FVEITEKETR DEEIKRLLQG  IH: EOS Set TOTAL GGGCCCCGCC CTGGGTTCC GTGCTTCCCTTAC GGACCTGCCC CTTCCTTTAC GCAAGGTCTA CACCTGTGCA CCACCTGTGCA CCACCTGTGCA CCACCTGTGCA CACCTGTGCA CACCTGTGCA CAGTATAGAA CAGGAAGTGA LEALVLLGWVS LLALVLLGWVS LLAUVLLGWVS LLAUVLLGWVS LLAUVLLGWVS LLAUVLLGWVS LLAUVLLGWVS LLAUVLLGWVS LLAUVLLGWVS	ADTPVGNDQL PILKTEGPTL EERIITGPEI DTPVRKLQAN  Quence  31   GCCGCGGGACG TCGTTTCTC GCAGCGCGCA GCCTACGTGC GCAGCGCGCA CCCCACATTA ATGGTGACCT TATCCGGAAA GACCCGATTC CTGATAGCCG ATGATACA ATCAATGCGG ATGCATAACA ATCAATGCGG ATCATTAACA ATCAATGCGG LEDNALKVLH SSSSPTSSASS AYVRNLFLTG LEDNALKVLH TYPEKMENRVL	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL     GGCGTCTGCG CCACTCCTC CCAGCCCCC CCAGCCCCT ATGTGCTGGG GCAACCTCTT ATGCTGGG ACCTCTA ATGCCCTCAA GGGTTTTCCT ATGCCCCAT ATGCCCCAT ATGCCCCAT ATGCCCATC CTATTTTCCT ACCCCATC TCAGAGATG ACCCCAGATT	IQIKFVRGST FRLIKEGETI FRLIKEGETI FRETIKKLL REGRSQ  51   GCTGGCGCGA GGCATCCTCC GCTGCCGGAC CCTACCGGC CCTACCGGC CCTACCGGC CCTACCGGC CCTGCCTCC GGTCCTTC CGGTCCTTC CGGTCCTTC CCTGCAAACC CCTGGTCTTC CTGCAAACC CCTGGTCTTC CTGCAAACC CCTGGTTCTC CTGCAAACC CCTGGTTCTC CTGCAAACC CCTGCAAACC CCTGCAAACC CCTGCAAACC CTGCAAACC CTGCAAACC CTGCAAACC CTGCAAACC CTGCAAACC TGCACAGGGT AACAAACCTC  51   AVSAQPPLPD LPRDVIAQLP PHIRVFLDNN DPILPPSLQT	720 780 120 120 120 240 300 360 420 480 540 660 720 780 840 900
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<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	TLLVNELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac: Coding sequi  ATGCCTGGGG TTCTCCTCT CAGTGCCCGG AATCTGACCG AACCAGCTGG AGCCTCGGG AGCCTCAGGCCCC CCCTGGGTCT TATTTGACC CACATGGAACTCA TCTTATGTCT TATTTGAACC CACATGGAAG AGTTCTAACT Seq ID NO: Protein Ac  1 MPGGCSRGPA QCPALCECSE SLRHLDLSNN PWVDCCHMAD SYVFLGIVLA SSNSDVLE Seq ID NO:	ESDIMITINGV TKIITKVVEP KKYTKIIDGV LEGGDGHLFE 67 DNA seq dd Accession lence: 1-92' 11   GGTGCTCCCG TACTCCTGGG AGGTGCCAC CCAGCACCAA ACGTGCCAC ACGTGCAGATT CACATCTAGA TGCTGAGTT CCGAGTGCTA AGAGCGGCT ACAGTGCTAGA TCCTGGGTA TCCTGGGTA TCCTGGGTA CCAGTGCTGCA AGAGTGCCTG CCAGTGCTGCA AGAGTGCTGCA AGAGTGCTGCA AGAGTGCTGCA AGAGTGCTGCA AGAGTGCTGCA CCAGTGCTGA CCAGTGCTGA CCAGTGCTGCA AGAGTGCTGCA AGAGTGCTGCA CCAGTGCTGCA CCAGTGCTCA CCAGTGCTGCA CCAGTGCTA CCAGTGCTGCA CCAGTGCTA CCAG	IHVVDKLLYP KIKVIEGSLQ FVEITEKETR DEEIKRLLQG  IH: EOS Set TOTAL GGGCCCCGCC CTGGGTTCC GTGCTTCCCTTAC GGACCTGCCC CTTCCTTTAC GCAAGATCTA AAGCCTCAC GCAAGTCTA CACCTGTGCA CCACCTGTGCA CCACCTGTGCA CACCTGTGCA CACCTGTGCA CAGTATAGAA CAGGAAAGTGA LALVLLGWVS LAUVLLGWVS	ADTPVGNDQL PILKTEGPTL EERIITGPEI DTPVRKLQAN  GUENCE  31   GCCGCGGGACG TCGTTTCTC GCAGCGCGCA GCCTACGTGC GCAGCGCGCA TCGTGTGATACA ATGGTGACCT TATCCGGAAA ATGGTGACCT ATCAATGCG ATCAATGCG ATCAATGCGG ATCAATACA ATCAATGCGG ATCAATACA ATCAATGCGG ATCAATACA ATCAATGCGG ATCAATACA ATCAATGCGG  1   CCCACATTA ATCAATGCGG ATGCATTACA ATCAATGCGG ATCAATGCAGA ATCAATGCGG ATGCATTACA ATCAATGCGG ATCAATGCGG ATGCATTACA ATCAATGCGG ATGCATTACA ATCAATGCGG ATGCATTACA ATCAATGCGG ATGCATTACA ATCAATGCGG ATGCATTACA ATCAATGCGG ATGCATTACA ATCAATGCGG ATCAATGCGATACA ATCAATGCGG ATCAATGCGATACA ATCAATGCGGATACA ATCAATGCGGATACA ATCAATGCGGATACA ATCAATGCGGATACA ATCAATGCGGATACA ATCAATGCGGATACA ATCAATGCGATACA ATCAATGCGATACA ATCAATGCGATACA ATCAATGCAATG	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL     GGCGTCTGCG CCACTCCTC CCAGCCCCC CCAGCCCCT ATGTGCTGGG GCAACCTCTT ATGCTGGG ACCTCTA ATGCCCTCAA GGGTTTTCCT ATGCCCCAT ATGCCCCAT ATGCCCCAT ATGCCCATC CTATTTTCCT ACCCCATC TCAGAGATG ACCCCAGATT	IQIKFVRGST FRLIKEGETI FRLIKEGETI FRETIKKLL REGRSQ  51   GCTGGCGCGA GGCATCCTCC GCTGCCGGAC CCTACCGGC CCTACCGGC CCTACCGGC CCTACCGGC CCTGCCTCC GGTCCTTC CGGTCCTTC CGGTCCTTC CCTGCAAACC CCTGGTCTTC CTGCAAACC CCTGGTCTTC CTGCAAACC CCTGGTTCTC CTGCAAACC CCTGGTTCTC CTGCAAACC CCTGCAAACC CCTGCAAACC CCTGCAAACC CTGCAAACC CTGCAAACC CTGCAAACC CTGCAAACC CTGCAAACC TGCACAGGGT AACAAACCTC  51   AVSAQPPLPD LPRDVIAQLP PHIRVFLDNN DPILPPSLQT	720 780 120 120 120 240 300 360 420 480 540 660 720 780 840 900
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<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	TLLVNELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac: Coding sequit ATGCCTGGGG CTAGCGCTGG TTCTCCTCTT TCAGTGCCCGCAACCTGGA AATCTGACCG AACCAGCTGG AGCCTCAGGC CCCCTGGGTCT GTGCAGGGCACTGA ATGGCACCC CCCTGGGTCT TATTTGAACC Seq ID NO: Protein Ac I MPGGCSRGPA QCPALCECSE SLRHLDLSNN PWVCDCHMAD SYVFLGIVLA SSNSDVLE Seq ID NO: Nucleic Ac	ESDIMITINGV TKIITKVVEP KKYTKIIDGV LEGGDGHLFE 67 DNA sequid Accession lence: 1-92' 11   GGTGCTCCCG TACTCCTGGG TACTCCTGGG TACTCCTGGG AGGTGCCCAC CCAGCACCAA AGGTGCCCAC CCAGCACCAA ACGTGACTT CACATCTAGA TGCTGGGTAT CCAGTGGTAT CCAGTGTAT CCAGTGTA	INVUKLLYP KIKVIEGSLQ PVEITEKETR PVEITEKETR DEEIKRLLQG  ##: EOS sei  GGGCCCCGCC CTGGGTTCC CTGGCTTCC CTGGCTTCC CTGGCTTCC AAGTAATAAT AAGCCTCCAC GCAAGGTCTA CATGGCAGAC CACCTGGATGT CACTGGATGT TGTTTTAGCC AAAAAAGTGC CAGATATGAA CAGGTGA	ADTPVGNDQL PILKTEGPTL EERIITGPEI DTPVRKLQAN  GUENCE  31   GCCGCGGGACG TCGTTTCTC GCAGCGCGCA GCCTACGTGC GCAGCGCGCA TCGTGTGATACA ATGGTGACCT TATCCGGAAA ATGGTGACCT ATCAATGCG ATCAATGCG ATCAATGCGG ATCAATACA ATCAATGCGG ATCAATACA ATCAATGCGG ATCAATACA ATCAATGCGG ATCAATACA ATCAATGCGG  1   CCCACATTA ATCAATGCGG ATGCATTACA ATCAATGCGG ATCAATGCAGA ATCAATGCGG ATGCATTACA ATCAATGCGG ATCAATGCGG ATGCATTACA ATCAATGCGG ATGCATTACA ATCAATGCGG ATGCATTACA ATCAATGCGG ATGCATTACA ATCAATGCGG ATGCATTACA ATCAATGCGG ATGCATTACA ATCAATGCGG ATCAATGCGATACA ATCAATGCGG ATCAATGCGATACA ATCAATGCGGATACA ATCAATGCGGATACA ATCAATGCGGATACA ATCAATGCGGATACA ATCAATGCGGATACA ATCAATGCGGATACA ATCAATGCGATACA ATCAATGCGATACA ATCAATGCGATACA ATCAATGCAATG	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL     GGCGTCTGCG CCACTCCTC CCAGCCCCC CCAGCCCCT ATGTGCTGGG GCAACCTCTT ATGCTGGG ACCTCTA ATGCCCTCAA GGGTTTTCCT ATGCCCCAT ATGCCCCAT ATGCCCCAT ATGCCCATC CTATTTTCCT ACCCCATC TCAGAGATG ACCCCAGATT	IQIKFVRGST FRLIKEGETI FRLIKEGETI FRETIKKLL REGRSQ  51   GCTGGCGCGA GGCATCCTCC GCTGCCGGAC CCTACCGGC CCTACCGGC CCTACCGGC CCTACCGGC CCTGCCTCC GGTCCTTC CGGTCCTTC CGGTCCTTC CCTGCAAACC CCTGGTCTTC CTGCAAACC CCTGGTCTTC CTGCAAACC CCTGGTTCTC CTGCAAACC CCTGGTTCTC CTGCAAACC CCTGCAAACC CCTGCAAACC CCTGCAAACC CTGCAAACC CTGCAAACC CTGCAAACC CTGCAAACC CTGCAAACC TGCACAGGGT AACAAACCTC  51   AVSAQPPLPD LPRDVIAQLP PHIRVFLDNN DPILPPSLQT	720 780 120 120 120 240 300 360 420 480 540 660 720 780 840 900
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	TLLVNELKSK FKEIPVTVYT TEVIREPII QEEVTKVTKF Seq ID NO: Nucleic Ac: Coding sequil ATGCCTGGGC TTGGCCTGG ATTCTGACCG AACTGAACG AACCAGTGC CCCTGGGTCT GTGCAGGCC GTGCAGGCC GTGCAGGCC GTGCAGGCC CCCTGGGTCT GTGCAGGCC TTGGAACTCA ATTGTATTTATATCT TATTTGAACT Seq ID NO: Protein Ac 1   MPGGCSRGPA QCPALCECSE SLRHLDLSNN PWVCDCHMAL SSNSDVLE Seq ID NO: Nucleic Ac Coding sec	ESDIMITINGV TKIITKVVEP KKYTKIIDGV IEGGDGHLFE 67 DNA seq id Accession lence: 1-92' 11  GGTGCTCCGG TACTCCTGGG AGGTGCCAC CCAGCAACCA ACCTGGACTT CACATCTAGA TGGTGTGTAGA AGGTGCCAC ACATGTAGA TGGTAGATT CCAGGGGAT CCAGGGGAT CCAGGGGAT TCAGGGGAT TCAGGGAT TCAGGGGAT TCAGGGAT TCAGGGGAT TCAGGGGAT TCAGGGGAT TCAGGGAT TCAGGGGAT TCAGGGGAT TCAGGGGAT TCAGGGGAT TCAGGGGAT TCAGGGAT TCAGGAT TCAGGGAT TCAGGGAT TCAGGGAT TCA	INVUKLLYP KIKVIEGSLQ FVEITEKETR DEEIKRLLQG  In #: EOS sei T 21   GGGCCCCGCC CTGGGTTCCC GTGCTCCGAG GGACCTGCCC CTTCCTTTAC AAGTAATAAT AAGCCTCCAC GCAAGGTCTAC CACCTGTGCA CACCTGCA CACCTGTGCA CACCTGTGCA CACCTGTGCA CACCTGTGCA CACCTGTGCA CACCTGC	ADTPVGNDQL PILKTEGPTL ERRILTGPEI DTPVRKLQAN  Quence  31   GCCGGGGACG TCGTTCTTC GCCGTGGC GCCTACGTGC CTGCTGGTGA CTGGAGGACA CCCCACATTA ATGGTGACCT TATCCGGAAA GACCCATTC CTGATAGGCG ATGCATAACA ATCAATGCGG SSSPTSSASS AYVRNLFLTG LEDNALKVLH YPEKMRNRVL MHNIRDACRD	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL     GGCGTCTGCG CCACTCCTC CCAGCCCCC CCAGCCCCT ATGTGCTGGG GCAACCTCTT ATGCTGGG ACCTCTA ATGCCCTCAA GGGTTTTCCT ATGCCCCAT ATGCCCCAT ATGCCCCAT ATGCCCATC CTATTTTCCT ACCCCATC TCAGAGATG ACCCCAGATT	IQIKFVRGST FRLIKEGETI FRLIKEGETI FRETIKKLL REGRSQ  51   GCTGGCGCGA GGCATCCTCC GCTGCCGGAC CCTACCGGC CCTACCGGC CCTACCGGC CCTACCGGC CCTGCCTCC GGTCCTTC CGGTCCTTC CGGTCCTTC CCTGCAAACC CCTGGTCTTC CTGCAAACC CCTGGTCTTC CTGCAAACC CCTGGTTCTC CTGCAAACC CCTGGTTCTC CTGCAAACC CCTGCAAACC CCTGCAAACC CCTGCAAACC CTGCAAACC CTGCAAACC CTGCAAACC CTGCAAACC CTGCAAACC TGCACAGGGT AACAAACCTC  51   AVSAQPPLPD LPRDVIAQLP PHIRVFLDNN DPILPPSLQT	720 780 120 120 120 240 300 360 420 480 540 660 720 780 840 900
50 55 60 65 70 75 80	TLLVNELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac: Coding sequit ATGCCTGGGG TTCTCCTCCT CAGTGCCCCG AATCTGACCG AATCTGACCG AATCTGACCC CCCTGGGTCT GTGCAGGGCACTGA ATTGGAACTCA TTTATGTACC CACATGGAAC TCTTATGTC Seq ID NO: Protein Ac 1 MPGGCSRGPA QCPALCECSE SLRHLDISNN PWVCDCHMAD SYVFLGIVLA SSNSDVLE Seq ID NO: Nucleic Ac Coding sec Cding sec	ESDIMITINGV TKIITKVVEP KKYTKIIDGV KKYTKIIDGV LEGGDGHLFE 67 DNA seq dd Accessio. lence: 1-92' 11    GGTGCTCCCG TACTCCTGGG AGGTGCCAC CCAGCACCAA AGGTGCCCAC CCAGCACCAA AGGTGCTGAGT CACATCTAGA TGGCTGAGTT CACATCTAGA TGGCTGAGTT CACATCTAGA TGGCTGAGTT CACATCTAGA TGGCTGAGTT CACATCTAGA TGGCTGAGTT CACATCTAGA TGGCTGAGTT ACAGTGCTGA AGATCTCTA AAGACTGCGCT ACAGTGCTGA GGTATCATTA CGGATGTCCT 68 Protein cession #: 11    AGDGRLRLAF AARTVKCVWR SUNSLITVSS WYTWLKETEN LIGAIFLLVI 69 DNA sec cid Accessic puence: 26. 11	INVUKLLYP KIKVIEGSLQ PVEITEKETR PVEITEKETR DEEIKRLLQG  ##: EOS sei  GGGCCCCGCC CTGGGTTCC CTGGCTTCC CTGGCTTCC CTGGCTTCC AAGTAATAAT AAGCCTCCAC GCAAGGTCTA CATGGCAGAC CACCTGGATGT CACTGGATGT TGTTTTAGCC AAAAAAGTGC CAGATATGAA CAGGTGA	ADTPVGNDQL PILKTEGPTI EERIITGPEI DTPVRKLQAN  Quence  31   GCCSCGGACG TCGTTCTCT GCCGTGTCCG GCAGCGCGCA GCCTACGTGC TCGCTGGTGA ATGGAGACA CCCCACATTA ATGGTGACCT TATCCGGAAA GACCCGATTC CTGATAGGCG ATGCATACA ATCAATGCGG ATGCATAACA ATCAATGCGG  10 1 1 2 2 31   31   4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL   GCGTCTGCG CCACTCCTC CCCAGCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGC GCCTGACCTA ATGCCCTAA GGGTTTTCCT TCATGAGGA AAATGAGGAA TTCCCCATC TCAAGATG ACCCCAGATT   41    FSSSAPFLAS NQLASNHFLY NGTLAELQGL LEINSADLDC HMEGYHYRYE	IQIKFVRGST FRLIKEGETI FRLIKEGETI FRETEKKLL REGRSQ  51   GCTGGCGCGA GGCATCCTCC GCTGCCGGAC CCTTACCGGC CCTACCGGC CCTACCGGC CCTACCGCC CCTGCAACACT ACCAGAGGTA ACCAGAGGTA TCGGGTCCTC CCTGCAAACCC CCTGGTTTTC CTGCAGAACCC CCTGGTTTC TGCAGGGAT AACAAACCTC  51   AVSAQPPLPD LPRDVLAQLP PHIRVIAQLP PHIRVIANI DPILPPSLQT INADPRLTNL	720 780 120 120 120 240 300 360 420 480 540 660 720 780 840 900
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	TLLVNELKSK FKEIPVTVYT TEVIREPII QEEVTKVTKF Seq ID NO: Nucleic Ac: Coding sequil ATGCCTGGGC TTGGCCTGG ATTCTGACCG AACTGAACG AACCAGTGC CCCTGGGTCT GTGCAGGCC GTGCAGGCC GTGCAGGCC GTGCAGGCC CCCTGGGTCT GTGCAGGCC TTGGAACTCA ATTGTATTTATATCT TATTTGAACT Seq ID NO: Protein Ac 1   MPGGCSRGPA QCPALCECSE SLRHLDLSNN PWVCDCHMAL SSNSDVLE Seq ID NO: Nucleic Ac Coding sec	ESDIMITINGV TKIITKVVEP KKYTKIIDGV IEGGDGHLFE 67 DNA seq id Accession lence: 1-92' 11  GGTGCTCCGG TACTCCTGGG AGGTGCCAC CCAGCAACCA ACCTGGACTT CACATCTAGA TGGTGTGTAGA AGGTGCCAC ACATGTAGA TGGTAGATT CCAGGGGAT CCAGGGGAT CCAGGGGAT TCAGGGGAT TCAGGGAT TCAGGGGAT TCAGGGAT TCAGGGGAT TCAGGGGAT TCAGGGGAT TCAGGGAT TCAGGGGAT TCAGGGGAT TCAGGGGAT TCAGGGGAT TCAGGGGAT TCAGGGAT TCAGGAT TCAGGGAT TCAGGGAT TCAGGGAT TCA	INVUKLLYP KIKVIEGSLQ FVEITEKETR DEEIKRLLQG  In #: EOS sei T 21   GGGCCCCGCC CTGGGTTCCC GTGCTCCGAG GGACCTGCCC CTTCCTTTAC AAGTAATAAT AAGCCTCCAC GCAAGGTCTAC CACCTGTGCA CACCTGCA CACCTGTGCA CACCTGTGCA CACCTGTGCA CACCTGTGCA CACCTGTGCA CACCTGC	ADTPVGNDQL PILKTEGPTL ERRILTGPEI DTPVRKLQAN  Quence  31   GCCGGGGACG TCGTTCTTC GCCGTGGC GCCTACGTGC CTGCTGGTGA CTGGAGGACA CCCCACATTA ATGGTGACCT TATCCGGAAA GACCCATTC CTGATAGGCG ATGCATAACA ATCAATGCGG SSSPTSSASS AYVRNLFLTG LEDNALKVLH YPEKMRNRVL MHNIRDACRD	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL   GCGTCTGCG CCACTCCTC CCCAGCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGC GCCTGACCTA ATGCCCTAA GGGTTTTCCT TCATGAGGA AAATGAGGAA TTCCCCATC TCAAGATG ACCCCAGATT   41    FSSSAPFLAS NQLASNHFLY NGTLAELQGL LEINSADLDC HMEGYHYRYE	IQIKFVRGST FRLIKEGETI FRLIKEGETI FRETIKKLL REGRSQ  51   GCTGGCGCGA GCATCCTCC GCTGCCCCCCTGTTCCTCC GGTCCTTCCCCC CCTGTCCTCC CCTGCAACC CCTGCAAACC CCTGCAAACC CCTGCAAACC CCTGCAAACC CCTGCAAACC CCTGCAAACC CCTGCAAACC CTGCACTTTG AACAGAGGTA AACAAACCTC  51   AVSAQPPLPD LPRDVLAQLP PHIRVFLDNN DPILPPSLQT INADPRLTNL	720 780 120 120 120 240 300 360 420 480 540 660 720 780 840 900
50 55 60 65 70 75 80	TLLVNELKSK FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac: Coding sequit ATGCCTGGGG TTCTCCTCCT CAGTGCCCCG AATCTGACCG AATCTGACCG AATCTGACCC CCCTGGGTCT GTGCAGGGCACTGA ATTGGAACTCA TTTATGTACC CACATGGAAC TCTTATGTC Seq ID NO: Protein Ac 1 MPGGCSRGPA QCPALCECSE SLRHLDISNN PWVCDCHMAD SYVFLGIVLA SSNSDVLE Seq ID NO: Nucleic Ac Coding sec Cding sec	ESDIMITINGV TKIITKVVEP KKYTKIIDGV KKYTKIIDGV LEGGDGHLFE 67 DNA seq dd Accessio. lence: 1-92' 11    GGTGCTCCCG TACTCCTGGG AGGTGCCAC CCAGCACCAA AGGTGCCCAC CCAGCACCAA AGGTGCTGAGT CACATCTAGA TGGCTGAGTT CACATCTAGA TGGCTGAGTT CACATCTAGA TGGCTGAGTT CACATCTAGA TGGCTGAGTT CACATCTAGA TGGCTGAGTT CACATCTAGA TGGCTGAGTT ACAGTGCTGA AGATCTCTA AAGACTGCGCT ACAGTGCTGA GGTATCATTA CGGATGTCCT 68 Protein cession #: 11    AGDGRLRLAF AARTVKCVWR SUNSLITVSS WYTWLKETEN LIGAIFLLVI 69 DNA sec cid Accessic puence: 26. 11	INVUKLLYP KIKVIEGSLQ FVEITEKETR DEEIKRLLQG  In #: EOS sei T 21   GGGCCCCGCC CTGGGTTCCC GTGCTCCGAG GGACCTGCCC CTTCCTTTAC AAGTAATAAT AAGCCTCCAC GCAAGGTCTAC CACCTGTGCA CACCTGCA CACCTGTGCA CACCTGTGCA CACCTGTGCA CACCTGTGCA CACCTGTGCA CACCTGC	ADTPVGNDQL PILKTEGPTI EERIITGPEI DTPVRKLQAN  Quence  31   GCCSCGGACG TCGTTCTCT GCCGTGTCCG GCAGCGCGCA GCCTACGTGC TCGCTGGTGA ATGGAGACA CCCCACATTA ATGGTGACCT TATCCGGAAA GACCCGATTC CTGATAGGCG ATGCATACA ATCAATGCGG ATGCATAACA ATCAATGCGG  10 1 1 2 2 31   31   4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL   41    GGCGTCTGCG CCACTCCTC CCCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTCTGGG GCCTGACCTA ATGCCCTCAA GGGTTTTCCT TCACAGGAA TTCCCCCATC TCAAGGAAGT  41    FSSSAPFLAS NQLASHHFLY NGTLAELQGL LELNSADLDC HMEGYHYRYE  41	IQIKFVRGST FRLIKEGETI FRLIKEGETI FRETEKKLL REGRSQ  51   GCTGGCGCGA GGCATCCTCC GCTGCCGGAC CCTTACCGGC CCTACCGGC CCTACCGGC CCTACCGCC CCTGCAACACT ACCAGAGGTA ACCAGAGGTA TCGGGTCCTC CCTGCAAACCC CCTGGTTTTC CTGCAGAACCC CCTGGTTTC TGCAGGGAT AACAAACCTC  51   AVSAQPPLPD LPRDVLAQLP PHIRVIAQLP PHIRVIANI DPILPPSLQT INADPRLTNL	720 780 120 120 120 240 300 360 420 480 540 660 720 780 840 900

					~~~~~		60
			CCGCCATGGT				
			CCGGACAGGG				120
			AGGAAACCAA				180
_			TCACGTTCCT				240
5	CGGGATGCAG	CAGTCAGTAC	GCACCGGCCT	ACCCAGCGTG	CGGCCCCTGC	TCCACTGCGC	300
	GCCCGGCTTC	TECTTCCCCC	GCGTGGCCTG	CATCCAGACG	GAGAGCGGCG	GCCGCTGCGG	360
	CCCCCCCCCC	CCCCCTTCA	CGGGCAACGG	CTCGCACTGC	ACCGACGTCA	ACCACTCCAA	420
	CCCCTCCCC	TOTTOTO	GAGTCCGCTG	TATCAACACC	AGCCCGGGGT	TOCCOCTO	480
	COCCUACCCC	100110000	GWG1CCGC1G	TAT CANCACC	VOCCCCCCCCC	CERTIFICACION	540
10	GGCTTGCCCG	CCGGGGTACA	GCGGCCCCAC	CUNCUAGGGC	01000000100	CITICGCCAA	
10			CGGACATCAA				600
			ACACCCGGGG				660
			CCGGCTGCCA				720
	CTCGCCCAGC	GAGTGCCACG	AGCATGCAGA	CIGCGTCCTA	GAGCGCGATG	GCTCGCGGTC	780
	GTGCGTGTGT	CGCGTTGGCT	GGGCCGGCAA	CGGGATCCTC	TGTGGTCGCG	ACACTGACCT	840
15			AGCTGCGCTG				900
15	CTCACTCTC	CCCAACTCAC	GGCAGGAGGA	TOTOGOACOGO	CATCCCATCC	GAGACCCCTC	960
	CGIGACIGIG	CCCAACTCAG	* COCCOCATION	CAROCARAGE	CACAACRCCC	CCCTCCTCCC	1020
	CGATCCGGAT	GCCGACGGG	ACGGGGTCCC	CAATGAAAAG	GACAACIGCC	CGCTGGTGCG	
			CGGACGAGGA				1080
~~			AAAAGGACAC				1140
20	CGACGACATC	GACGGCGACC	GGATCCGCAA	CCAGGCCGAC	AACTGCCCTA	GGGTACCCAA	1200
			ATGGCGATGG				1260
	CANGAGCAAC	CCCCATCACC	CGGATGTGGA	CCACCACTTT	GTGGGAGATG	CTTGTGACAG	1320
			ACGGACATCA				1380
							1440
25			CAGACCACGA				
25			ACAGTCGGGA				1500
			GCGTGGGCGA				1560
			TGTGTCCGGA				1620
	GGCCTTCCAG	ACAGTCGTGC	TGGACCCGGA	GGGTGACGCG	CAGATTGACC	CCAACTGGGT	1680
	GGTGCTCAAC	CAGGGAAGGG	AGATCGTGCA	GACAATGAAC	AGCGACCCAG	GCCTGGCTGT	1740
30			GCGTGGACTT				1800
50			TCATCTTTGG				1860
							1920
			AAACGTATTG				
			CTGTGAAGTC				1980
	CGCTCTGTGG	CATACAGGAG	ACACAGAGTC	CCAGGTGCGG	CIGCIGIGGA	AGGACCCGCG	2040
35	AAACGTGGGT	TGGAAGGACA	AGAAGTCCTA	TCGTTGGTTC	CTGCAGCACC	GGCCCCAAGT	2100
	GGGCTACATC	AGGGTGCGAT	TCTATGAGGG	CCCTGAGCTG	GTGGCCGACA	GCAACGTGGT	2160
	CTTGGACACA	ACCATGOGG	GTGGCCGCCT	GGGGGTCTTC	TGCTTCTCCC	AGGAGAACAT	2220
	CITOGRACIO	A A COTTO COOT	ACCGCTGCAA	TCACACCATC	CCAGAGGACT	ATGAGACCCA	2280
	CATCIGGGCC	MACCIGCGII	ACCOCIGCAA	1GACACCATC	CCADAGGACI	ar coords ac	2340
40			GACCAGGGTG				
40			CACCCAGCCC		CGTCCTGAGG	GGGAAGTGAG	2400
	AAGGGCTCAG	AGAGGACAAA	ATAAAGTGTG	TGTGCAGGG			
	Seq ID NO:	70 Protein	sequence				
45	Protein Acc	cession #: 1	1P_000086.1	31	41	51	
45				31 1	<b>41</b>	51 I	
45	Protein Acc	cession #: 1 11 	VP_000086.1 21 	1	1	1	60
45	Protein Acc	cession #: 1 11       LTLAALGASG	VP_000086.1 21     QGQSPLGSDL	] GPQMLRELQE	 TNAALQDVRD	 WLRQQVREIT	60
45	Protein Acci 1       MVPDTACVLL   PLKNTVMECD	cession #: 1 11       LTLAALGASG   ACGMQQSVRT	NP_000086.1 21     QGQSPLGSDL GLPSVRPLLH	 GPQMLRELQE CAPGFCFPGV	 TNAALQDVRD ACIQTESGGR	 WLRQQVREIT CGPCPAGFTG	120
	Protein Acci 1     MVPDTACVLL   PLKNTVMECD   NGSHCTDVNE	cession #: 1 11     LTLAALGASG ACGMQQSVRT CNAHPCFPRV	NP_000086.1 21     QGQSPLGSDL GLPSVRPLLH RCINTSPGFR	 GPQMLRELQE CAPGFCFPGV CEACPPGYSG	 TNAALQDVRD ACIQTESGGR PTHQGVGLAP	 WLRQQVREIT CGPCPAGFTG AKANKQVCTD	120 180
45 50	Protein Acci 1     MVPDTACVLL   PLKNTVMECD   NGSHCTDVNE	cession #: 1 11     LTLAALGASG ACGMQQSVRT CNAHPCFPRV	NP_000086.1 21     QGQSPLGSDL GLPSVRPLLH	 GPQMLRELQE CAPGFCFPGV CEACPPGYSG	 TNAALQDVRD ACIQTESGGR PTHQGVGLAP	 WLRQQVREIT CGPCPAGFTG AKANKQVCTD	120
	Protein Acc 1     MVPDTACVLL   FLKNTVMECD   NGSHCTDVNE   INECETGQHN	cession #: 1 11	NP_000086.1 21     QGQSPLGSDL GLPSVRPLLH RCINTSPGFR	GPQMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG	 TNAALQDVRD ACIQTESGGR PTHQGVGLAP CQRGAQRFCP	 WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH	120 180
	Protein Acci 1     MVPDTACVLL   FLKNTVMECD   NGSHCTDVNE   INECETGQHN   ADCVLERDGS	cession #: 1 11	NP_000086.1 21     QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT	GPQMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL	TNAALQDVRD ACIQTESGGR PTHQGVGLAP CQRGAQRFCP RCPEPQCRKD	 WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ	120 180 240
	Protein Acci 1     MVPDTACVLL   PLKNTVMECD   NGSHCTDVNE   INECETGQHN   ADCVLERDGS   EDVDRDGIGD	cession #: 1  11    LTLAALGASG ACGMQQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG	NP_000086.1 21     QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPL	GPOMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD	TNAALQDVRD ACIQTESGGR PTHQGVGLAP CQRGAQRFCP RCPEPQCRKD EDKWGDACDN	 WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK	120 180 240 300 360
	Protein Acci 1     MVPDTACVLL FLKNTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA	cession #: 1    LTLAALGASG ACGMQQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI	NP_000086.1 21   QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPL RNQADNCPRV	GPOMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG	TNAALQDVRD ACIQTESGGR PTHQGVGLAP CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDNC	 WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD	120 180 240 300 360 420
50	Protein Acci 1 MVPDTACVLL PLENTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC	cession #: 1	NP_000086.1 21   QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPT HQDSRDNCPT	 GPQMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPPCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDD	URQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS	120 180 240 300 360 420 480
	Protein Acci   	cession #: 1  LTLAALGASG ACGMQQSVRT CNAHPCFFRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV	NP_000086.1 21	 GPQMLRELQE CAPGPCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTDD PNSDQKDSDD VPNSAQEDSD DKVVDKIDVC	TNAALQDVRD ACIQTESGGR PTHQGVGLAP CQRGAQRFCP RCPEPQCRKD EDKWGDACDNC DGIGDACDNC HDGQGDACDDD PENAEVILID	 WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQRNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD	120 180 240 300 360 420 480 540
50	Protein Acci   	cession #: 1	NP_000086.1 21   QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GMGILGRDT VPNEKDNCPL RNQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL	 GPQMLRELQE CAPGPCFPGY CEACPPGYSG PGFVGDQASG DLDGPPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DRVVDKIDVC AVGYTAFNGV	TNAALQDVRD ACIQTESGGR PTHQGVGLAP CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDD PENABVTLTD DFEGTFHVNT	 WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI	120 180 240 300 360 420 480 540
50	Protein Acci   	cession #: 1	NP_000086.1 21	 GPQMLRELQE CAPGPCFPGY CEACPPGYSG PGFVGDQASG DLDGPPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DRVVDKIDVC AVGYTAFNGV	TNAALQDVRD ACIQTESGGR PTHQGVGLAP CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDD PENABVTLTD DFEGTFHVNT	 WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI	120 180 240 300 360 420 480 540 600 660
50	Protein Acci      MVPDTACVLL   FLKNTVMECD   NGSHCTDVNE   INECETGQHN   ADCVLERDGS   EDVDRDGIGD   DTDQDGRGDA   VDHDFVGDAC   RDNCRLVPNP   PEGDAQIDPN   FGYQDSSFY	cession #: 1  LTLAALGASG ACSMQQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDFDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT	NP_000086.1 21   QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GMGILGRDT VPNEKDNCPL RNQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL	GPOMLRELQE CAPGPCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEPGIQLKAV	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDN PENAEVILID DFEGTFHVNT KSSTGPGEQL	ULRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT	120 180 240 300 360 420 480 540
50	Protein Acci      MVPDTACVLL   PLENTVMECD   NGSHCTDVNE   INECETGQHN   ADCVLERDGS   EDVDRDGIGD   DTDQDGRGDA   VDHDFVGDAC   RDNCRLVPNP   PEGDAQLDPN   FGYQDSSSFY   ESQVRLLWKD	cession #: 1  LTLAALGASG ACSMQQSVRT CNAHPCFPRT CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDGT DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKCMKCY	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPL ENQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YMQANPFRAV	 GPQMLRELQE CAPGPCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNFDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEPGIQLKAV QVGYIRVRFY	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDN PENAEVILID DFEGTFHVNT KSSTGPGEQL	ULRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT	120 180 240 300 360 420 480 540 600 660
50	Protein Acci      MVPDTACVLL   PLENTVMECD   NGSHCTDVNE   INECETGQHN   ADCVLERDGS   EDVDRDGIGD   DTDQDGRGDA   VDHDFVGDAC   RDNCRLVPNP   PEGDAQLDPN   FGYQDSSSFY   ESQVRLLWKD	cession #: 1  LTLAALGASG ACSMQQSVRT CNAHPCFPRT CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDGT DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKCMKCY	NP_000086.1 21	 GPQMLRELQE CAPGPCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNFDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEPGIQLKAV QVGYIRVRFY	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDN PENAEVILID DFEGTFHVNT KSSTGPGEQL	ULRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT	120 180 240 300 360 420 480 540 600 660
50	Protein Acci	cession #: 1  LTLAALGASG ACGMQQSVRT CNAHPCFPRV CVPNSVLINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMKQMEQT PRNVGWKDKK NIIWANLRYR	NP_000086.1 21   QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GMGILCGRDT VPNEKDNCPL RNQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANPFRAV SYRWPLQHRP CNDTIPEDYE	 GPQMLRELQE CAPGPCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNFDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEPGIQLKAV QVGYIRVRFY	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDN PENAEVILID DFEGTFHVNT KSSTGPGEQL	ULRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT	120 180 240 300 360 420 480 540 600 660
50	Protein Acci      MVPDTACVLL   FLKNTVMECD   NGSHCTDVNE   INECETGQHN   ADCVLERDGS   EDVDRDGIGD   DTDQDGRGDA   VDHDFVGDAC   RDNCRLVPNP   PEGDAQIDPN   FGYQDSSSFY   ESQVRLLWKD   RLGVFCFSQE   Seq ID NO:	cession #: 1  LTLAALGASG ACGMQOSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMMKQMEQT PRNVGWKDKK NIIWANLRYR  71 DNA seq	NP_000086.1 21	GPOMLRELQE GPOMLRELQE CAPGPCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNFDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEPGIQLKAV QVGYIRVRFY THQLRQA	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDN PENAEVILID DFEGTFHVNT KSSTGPGEQL	ULRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT	120 180 240 300 360 420 480 540 600 660
50	Protein Acci      MVPDTACVLL   PLENTYMECD   NGSHCTDVNE   INECETGQHN   ADCVLERDGS   EDVDRDGIGD   DTDQDGRGDA   VDHDFVGDAC   RDNCRLVPNP   PEGDAQIDPN   FGYQDSSSFY   ESQVRLLWKD   RLGVFCFSQE   Seq ID NO:   Nucleic Ac	cession #: 1  LTLAALGASG ACGMQQSVRT CNAHPCFPRI CVPNSVCINT RSCVCRVGWA ACDFDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR  71 DNA seq id Accessio	NP_000086.1 21	GPOMLRELQE GPOMLRELQE CAPGPCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNFDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEPGIQLKAV QVGYIRVRFY THQLRQA	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDN PENAEVILID DFEGTFHVNT KSSTGPGEQL	ULRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT	120 180 240 300 360 420 480 540 600 660
50	Protein Acci      MVPDTACVLL   PLKNTVMECD     NGSHCTDVNE     INECETGQHN     ADCVLERDGS     EDVDRDGIGD     DTDQDGRGDD     CDDCRLVPNP     PEGDAQIDPN     FGYQDSSSF     ESQVRLLWKD     RLGVFCFSQE     Seq ID NO:     Nucleic Ac     Coding seq	cession #: 1  LTLAALGASG ACGMQQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMHKQMEQT PRNVGWKDKK NIIWANLRYR  71 DNA seq id Accessio uence: 71	NP_000086.1 21	GPOMLRELQE CAPGPCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEPGIQLKAV QVGYIRVRFY THQLRQA	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDD PENAEVILTD DFEGTFHVNT KSSTGPGEQL EGPELVADSN	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG	120 180 240 300 360 420 480 540 600 660
50 55 60	Protein Acci      MVPDTACVLL   PLENTYMECD   NGSHCTDVNE   INECETGQHN   ADCVLERDGS   EDVDRDGIGD   DTDQDGRGDA   VDHDFVGDAC   RDNCRLVPNP   PEGDAQIDPN   FGYQDSSSFY   ESQVRLLWKD   RLGVFCFSQE   Seq ID NO:   Nucleic Ac	cession #: 1  LTLAALGASG ACGMQQSVRT CNAHPCFPRI CVPNSVCINT RSCVCRVGWA ACDFDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR  71 DNA seq id Accessio	NP_000086.1 21	GPOMLRELQE GPOMLRELQE CAPGPCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNFDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEPGIQLKAV QVGYIRVRFY THQLRQA	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDN PENAEVILID DFEGTFHVNT KSSTGPGEQL	ULRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT	120 180 240 300 360 420 480 540 600 660
50	Protein Acci      MVPDTACVLL   PLENTYMECD     NGSHCTDVNE     INECETGQHN     ADCVLERDGS     EDVDRDGIGD     DTDQDGRGDA     VDHDFVGDAC     RDNCRLVPNP     PEGDAQIDPN     FGYQDSSSFY     ESQVRLLWKD     RLGVFCFSQE     Coding seq	cession #: 1  LTLAALGASG ACGMQQSVRT CNAHPCFPRI CVPNSVCINT RSCVCRVGWA ACDFDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR  71 DNA seq id Accessio uence: 71 11    '	NP_000086.1 21   QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPL HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANFFRAV SYRWPLQHRP CNDTIPEDYE uence n #: NM_024 919 21	GPQMLRELQE GPQMLRELQE CAPGPCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AVGYTAFNGV AEPGIQLKAV QVGYIRVRFY THQLRQA	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDD PENAEVILID DFEGTFHVNT KSSTGPGEQL EGPELVADSN	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNFDQAD DDDNDGVPDS FRAFQTVVLD VTDDYAGFI RNALWHTGDT VVLDTTMRGG	120 180 240 300 360 420 480 540 600 720
50 55 60	Protein Acci	cession #: 1  LTLAALGASG ACGMQQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDFDADEDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq id Accessio uence: 71 11    GGAAGGCAGC	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPL RNQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANPFRAV SYRWPLQHRP CNDTIPEDYE uence n #: NM_024 919 21 GGCAGCTCCA	GPOMLRELQE GPOMLRELQE CABGFCFPGV CEACPFGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AFEGIQLKAV QVGYIRVRFY THQLRQA  626 31   CTCAGCCAGT	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDD PENABVILTD DFEGTFHVNT KSSTGPGEQL EGPELVADSN	WLRQQVREIT GEPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG	120 180 240 300 360 420 480 540 660 720
50 55 60	Protein Acci      MVPDTACVLL   PLENTVMECD     NGSHCTDVNE     INECETGQHN     ADCVLERDGS     EDVDRDGIGD     DTDQDGRGDA     VDHDFVGDAC     RDNCRLVPNP     PEGDAQIDPN     FGYQDSSFY     ESQVRLLWKD     RLGVFCFSQE     Seq ID NO:     Nucleic Ac     Coding seq     1	Cession #: 1  LTLAALGASG ACGMQOSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADEGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMMKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq id Accessio uence: 71 11    GGAAGGCAGC	NP_000086.1 21	GPOMLRELQE GPOMLRELQE CAPGFCFPGV CEACPFGYSG PGFVGDQASG DLDGFPDEKL VRNPQORNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEPGIQLKAV OVGYIRVRFY THQLRQA 626 31   CTCAGCCAGT CCTCAGCCAGT	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDN PENAEVILTD DFEGTFHVNT KSSTGPGEQL EGPELVADSN  41   ACCCAGATAC	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG	120 180 240 300 360 420 540 600 720
50 55 60	Protein Acci    MVPDTACVLL FLKNTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Ac Coding seq 1   GAGTCACCAA TTCCCCCAGCC TATTCTGGCT	cession #: 1  LTLAALGASG ACSMQOSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq id Accession uence: 71 11	NP_000086.1 21	GPOMLRELQE GPOMLRELQE CAPGPCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKLDVC AVGYTAFNGV AEPGIQLKAV QVGYIRVRFY THQLRQA  626 31   CTCAGCCAGT CCTCTTCTGG TGGCTTTGGT	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCKED EDKWGDACDN DGIGDACDNC HDGQGDACDD PENAEVILID KSSTGPGEQL EGPELVADSN  41   ACCCAGATAC AGCATAATTA ATTTCAGGGA	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VIDDDYAGFI RNALWHTGDT VVLDTTMRGG  51   GCTGGGAACC GCATCATCAT GACACTCCAT	120 180 240 300 360 420 480 540 660 720
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	Protein Acci    MVPDTACVLL FLKNTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Ac Coding seq 1   GAGTCACCAA TTCCCCCAGCC TATTCTGGCT	cession #: 1  LTLAALGASG ACSMQOSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq id Accession uence: 71 11	NP_000086.1 21	GPOMLRELQE GPOMLRELQE CAPGPCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKLDVC AVGYTAFNGV AEPGIQLKAV QVGYIRVRFY THQLRQA  626 31   CTCAGCCAGT CCTCTTCTGG TGGCTTTGGT	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCKED EDKWGDACDN DGIGDACDNC HDGQGDACDD PENAEVILID KSSTGPGEQL EGPELVADSN  41   ACCCAGATAC AGCATAATTA ATTTCAGGGA	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VIDDDYAGFI RNALWHTGDT VVLDTTMRGG  51   GCTGGGAACC GCATCATCAT GACACTCCAT	120 180 240 300 360 420 540 600 720
50 55 60	Protein Acci      MVPDTACVLL   PLKNTVMECD   NGSHCTDVNE   INECETGQHN   ADCVLERDGS   EDVDRDGIGD   DTDQDGRGDA   VDHDFVGDAC   RDNCRLVPNP   PEGDAQIDPN   FGYQDSSSFY   ESQVRLLWKD   RLGVFCFSQE   Seq ID NO:   Nucleic Ac   Coding seq   I   GAGTCACCAA   TTCCCCAGCC   CACAGTCACT   CACAGTCACT	cession #: 1  LTLAALGASG ACGMQQSVRT CNAHPCFPRI CVPNSVCINT RSCVCRVGWA ACDPDADEDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR  71 DNA seq id Accessio uence: 71 11   ' GGAAGGCAGC ATGGCTTCCC GGAGCAATTG ACTGTCGCCT	NP_000086.1 21	GPOMLRELQE GPOMLRELQE CAPGFCFPGV CEACPFGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEFGIQLKAV QVGYIRVRFY THQLRQA  626 31   CTCAGCCAGT CCTCTTCTGG TGGCTTTGGT CATTGGGGAG	TNAALQDVRD ACIQTESGGR PTHQGVGLAP CQRGAQRFCP ECHEMORY ECHE	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG  51   GCTGGGAACC GCATCATCAT TGAGCTGCAC	120 180 240 300 360 420 480 540 660 720
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	Protein Acci      MVPDTACVLL   FLKNTVMECD     NGSHCTDVNE     NGSHCTDVNE     NECETGQHN     ADCVLERDGS     EDVDRDGIGD     DTDQDGRGDA     VDHDFVGDAC     RDNCRLVPNP     PEGDAQIDPN     FGYQDSSFY     ESQVRLLWKD     RLGVFCFSQE     Coding seq     GAGTCACCAA     TTTCTGGCT     CACAGTCACT     TTTTGAACCT     CTTTTTGAACCT     CTTTTTGAACCT     CACAGTCACT     CACA	Cession #: 1  LTLAALGASG ACGMQQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDFDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR  71 DNA seq id Accessio uence: 71 11    GGAAGGCAGC ATGGCTTCCC GGAGCAATTG ACTGTCGCCT	NP_000086.1 21	GPOMLRELQE GPOMLRELQE CAPGPCFPGV CEACPFGYSG PGFVGDQASG DLDGFPDEKI VRNPDQRNTD PNSDQKDSDG VVNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEPGIQLKAV OVGYIRVRFY THQLRQA  626 31   CTCAGCCAGT CCTCTTCTGG TGGCTTTGGT TGATTACAA	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDD DGIGDACDDC DGIGDACDDC DFENBEVILTD DFEGTFHVNT KSSTGPGEQL EGPELVADSN  41  ACCCAGATAC AGCATAATTA ATTTCAGGGA AGTGGAATCC TCGCTGAAGG	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGG CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG  51   GCTGGGAACC GCATCATCAT GACACTCCAT TGAGCTGCAC AAGGTGTTTT	120 180 240 300 360 420 600 600 720
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	Protein Acci      MVPDTACVLL   FLKNTVMECD   NGSHCTDVNE   INECETGQHN   ADCVLERDGS   EDVDRDGIGD   DTDQDGRGDA   VDHDFVGDAC   RDNCRLVPNP   PEGDAQIDPN   FGYQDSSSFY   ESQVRLLWKD   RLGVFCFSQE   Seq ID NO:   Nucleic Accoding seq   1   GAGTCACCAA   TTCCCCAGCC   TATTCTGGCT   CACAGTCACT   TTTTGAACCT   AGGCTTGGTC	Cession #: 1  LTLAALGASG ACGMQOSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADEGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMMKQMEQT PRNVGWKDKK NIIWANLRYR  71 DNA seq id Accessio uence: 71 11  GGAAGGCAGC GGAAGGCAGC GGAGGAATTG ACTGTCGCCT GACATCAACC CATGAGTTCA	NP_000086.1 21   QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPL ENQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANPFRAV SYRWFLQHRP CNDTIPEDYE Uence n #: NM_024 919 GGCAGCTCCA TGGGGCAGAT CACTCATCAT CAGCTGGGAA ATTCTGATAT AAGAAGGCAA	GPOMLRELQE GPOMLRELQE CAPGFCFPGV CEACPFGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEPGIQLKAV QVGYIRVRFY THQLRQA  626 31   CTCAGCCAGT CCTCAGCCAGT CCTCTTCTGG TGGCTTTGGT CATTGGGGA AGATGAGCTG AAGATGAGCTG	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDD PENAEVILTD DFEGTFHVNT KSSTGPGEQL EGPELVADSN  41   ACCCAGATAC AGCATAATTA ATTTCAGGGA GATGGAATGC TCGGGTGAAGG TCGGAGCAGG	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG  51   GCTGGGAACC GCATCATCAT GACACTCCAT TGAGCTGCAC AAGGTGTTTT ATGAAATGTT	120 180 300 360 420 540 600 720
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	Protein Acci    MVPDTACVLL PLENTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Ac Coding seq 1   GAGTCACCAA TTCCCCAGCC TATTCTGGCT CACAGTCACT AGGCTTGGTC CAGAGGCCGG	cession #: 1  LTLAALGASG ACGMQSVRT CNAHPCFPRY CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR  71 DNA seq id Accessio uence: 71 11	NP_000086.1 21   QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPL HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANFFRAV SYRWPLQHRP CNDTIPEDYE  LUENCE I #: NM_024 919 21   GGCAGCTCCA TGGGCAGAT CACTCATCAT CAGCTGGGAA TTTCTGATAT AAGAAGCAA ATTGCTGATCA	GPOMLRELQE GPOMLRELQE CAPEFCFFGV CEACPFGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEFGIQLKAV QVGYIRVRFY THQLRQA  626  31   CTCAGCCAGT CCTCTTCTGG TGGCTTTGGT CATTCGCGAG GCTGATACAA AGATGAGCTG AGTGATAGTT	TNAALQDVRD ACIQTESGGR PTHQGVGLAP CQRGAQRFCP ECHEMORY ECHE	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG  51   GCTGGGAACC GCATCATCAT TGACATCCAT TGACATCCAT TGAGGTGTTTT ATGAAATGTT CTTTGCGGCT	120 180 240 360 420 540 600 600 720
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	Protein Acci      MVPDTACVLL   FLKNTVMECD     NGSHCTDVNE     INECETGQHN     ADCVLERDGS     EDVDRDGIGD     DTDQDGRGDA     VDHDFVGDAC     RDNCRLVPNP     PEGDAQIDPN     FGYQDSSFY     ESQVRLLWKD     RLGVFCFSQE     Coding seq     GAGTCACCAA     TTCCCAGCC     TATTCTGGCT     CACAGTCACT     TTTTGAACCT     AGGCTTGGTC     CAGAGGCCGG     GAAGAGCCGG     GAAGAGCCTG     CACAGTCACT     CACAGGCCCTATTCTGCT     CACAGGCCCG     CACAGGCCCCG     CACAGGCCCG     CACAGGCCCG	CESSION #: 11  LTLAALGASG ACGMQQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDFDADGDG GDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq id Accessio uence: 71 11    GGAAGGCAGC ATGGCTTCCC GGAGCAATTG GACATCAAAC CAGGAGTGAA ACAGCAGTGA CAACTCACAG CAACTCACAG	NP_000086.1 21	GPOMLRELQE GPOMLRELQE CAPGPCFPGV CEACPFGYSG PGFVGDQASG PGFVGDQASG DLDGFPDEKL VNNPDQRNTD PNSDQKDSDG VVNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEFGIQLKAV QVGYIRVRFY THQLRQA  626 31   CTCAGCCAGT CCTCTTCTGG TGGCTTTGGT TGATTCATCAAAAGGTTG AGTGATAGTT CTACAAAATGTT CTACAAAATGTT	TMAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDD DGIGDACDDC DGIGDACDDC DFEMBEVILTD DFEGTFHVNT KSSTGPGEQL EGPELVADSN  41  ACCCAGATAC AGCATAATTA ATTTCAGGGA AGTGGAATGC TCGGRGCAGG GGCAATGCCT TATATCATCA	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG  51   GCTGGGAACC GCATCATCAT GACACTCCAT TGAGCTGCAC AAGGTGTTTT ATGAAATGTT CTTTGCGGCT CTTCTTAAAGG	120 180 240 300 360 420 600 660 720 60 120 120 240 300 360 420
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	Protein Acci      MVPDTACVLL   PLENTVMECD     MSHCTDVNE     INECETGQHN     ADCVLERDGS     EDVDRDGIGD     DTDQDGRGDA     VDHDFVGDAC     RDMCRLVPNP     PEGDAQIDPN     FGYQDSSFY     ESQVRLLWKD     RLGVFCFSQE     Seq ID NO: Nucleic Ac     Coding seq     GAGTCACCAA     TTTCCCCAGCC     TTTTCAGCT     CAGGTCACTA     TTTTGAACCT     AGGCTTAGTC     CAGGGGCAAT     CAGGGGGAAT     CAGGGGAAT     CAGGAGAT     CAGGGGAAT     CAGGGGAAT     CAGGGGAAT     CAGGAGGAAT     CAGGGAAT     CAGGGAAT     CAGGAGAT     CAGGAT	Cession #: 1  LTLAALGASG ACGMQOSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADEGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMMKQMEQT PRNVGWKDKK NIIWANLRYR  71 DNA seq id Accessio uence: 71 11   ' GGAAGGCAGC GGAGGCAATTG ACTGTCGCCT GGCATCAAAC CATGAGTTCA CAACACAGGGT CAACACAGGGT CAACACAGGG GCTAACCTTG GCTTACAGG GGTAACCTTG	NP_000086.1 21	GPOMLRELQE GPOMLRELQE CAPGPCFPGV CEACPFGYSG PGFVGDQASG DLDGFPDEKV VRNPDQRNTD PNSDQKDSDG VVNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEPGIQLKAV QVGYIRVRFY THQLRQA  626 31   CTCAGCCAGT CCTCAGCCAGT CCTCTTCTGG TGGCTTTGGGAT CATTGGGAG CGTGATACAA AGATGATCT TGGAGCCTTC	TMAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDD DGIGDACDNC HDGQGDACDD PENAEVILTD DFEGTFHVNT KSSTGPGEQL EGPELVADSN  41   ACCCAGATAC AGCATAATTA ATTTCAGGAA GATGGAATCC TGGGTGAAGG TCGGAGCAGG GGCAATGCCT TATATCATCC	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGG CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG  51   GCTGGGAACC GCATCATCAT GACACTCCAT TGAGCTGCAC AAGGTGTTTT ATGAAATGTT CTTTTGCGGCT CTTCTAAAGG AAGTGAATGTT	120 180 240 300 360 420 600 650 720 60 120 180 240 360 420 420 540
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	Protein Acci    MVPDTACVLL FLKNTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Ac Coding seq 1   GAGTCACCAA TTCCCCAGCC TATTCTGGCT CACAGTCACT TTTTGAACCT TTTTGAACT TGGGTTGGTC CAGAGGCCGG GAAAAACGTGA CAGGGGAAT GGACTATAAT GGACTATAAT	cession #: 1  LTLAALGASG ACGMQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq id Accessio uence: 71 11    GGAGGCAGC ACGGCAATTG CATGGCTTCCC GGAGCAATTG CATGGCTTCCC CATGGCTTCCC CATGGCTTCCC CATGAGTTCAAAC CATGAGTTCA ACAGCAGTGT CACAGTCACATG GCCAGCTCAG GCTAACCTTG GCCAGCTCAG	NP_000086.1 21	GPOMLRELQE GPOMLRELQE CAPGPCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AVGYTAFNGV AUGUST THQLRQA  626 31   CTCAGCCAGT CCTCTTCTGG TGGCTTTGGT CATTGGGAGA AGATGAGCTG AGTGATACAA AGATGAGCTG TGGAGCCTT TGGAGCCTT CTACAAATGTT CTACAAATGTT TGGAGGCCTT GGTGTAAGGCCTT	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD DGIGDACDNC HDGQGDACDN DFGGTFHVNT KSSTGPGQL EGPELVADSN 41   ACCCAGATAC AGCATAATTA ATTTCAGGGA GATGGAATCC TGGCTGAGG GGCAATGCCT TATATCATCA AGCATGGGTGAGCCCCCCATGGT	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG  51   GCTGGGAACC GCATCATCAT GACACTCCAT TGAGCTGCAC AAGGTGTTTT ATGAAATGTT CTTTGCGGCT CTTCTAAAGG AAGTGAATGT TCCCCCAGCC	120 180 360 420 540 600 720 60 120 180 240 300 420 480 540
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	Protein Acci    MVPDTACVLL FLKNTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Ac Coding seq 1   GAGTCACCAA TTCCCCAGCC TATTCTGGCT CACAGTCACT TTTTGAACCT TTTTGAACT TGGGTTGGTC CAGAGGCCGG GAAAAACGTGA CAGGGGAAT GGACTATAAT GGACTATAAT	cession #: 1  LTLAALGASG ACGMQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq id Accessio uence: 71 11    GGAGGCAGC ACGGCAATTG CATGGCTTCCC GGAGCAATTG CATGGCTTCCC CATGGCTTCCC CATGGCTTCCC CATGAGTTCAAAC CATGAGTTCA ACAGCAGTGT CACAGTCACATG GCCAGCTCAG GCTAACCTTG GCCAGCTCAG	NP_000086.1 21	GPOMLRELQE GPOMLRELQE CAPGPCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AVGYTAFNGV AUGUST THQLRQA  626 31   CTCAGCCAGT CCTCTTCTGG TGGCTTTGGT CATTGGGAGA AGATGAGCTG AGTGATACAA AGATGAGCTG TGGAGCCTT TGGAGCCTT CTACAAATGTT CTACAAATGTT TGGAGGCCTT GGTGTAAGGCCTT	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD DGIGDACDNC HDGQGDACDN DFGGTFHVNT KSSTGPGQL EGPELVADSN 41   ACCCAGATAC AGCATAATTA ATTTCAGGGA GATGGAATCC TGGCTGAGG GGCAATGCCT TATATCATCA AGCATGGGTGAGCCCCCCATGGT	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG  51   GCTGGGAACC GCATCATCAT GACACTCCAT TGAGCTGCAC AAGGTGTTTT ATGAAATGTT CTTTGCGGCT CTTCTAAAGG AAGTGAATGT TCCCCCAGCC	120 180 240 300 360 420 600 650 720 60 120 180 240 360 420 420 540
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	Protein Acci    MVPDTACVLL PLENTYMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE  Seq ID NO: Nucleic Ac Coding seq 1   GAGTCACCAA TTCCCCAGCC TATTCTGGCT CACAGTCACT TTTGAACCT CAGAGGCCGG GAAAAACGTG CAAGGGCAGG GAAAACGTG CAAGTGGTC CACAGTGATAT CACAGTGGTC CACAGTGTC CACAGTGGTC CACAGTGTC CACAGTGGTC CACAGTGGTC CACAGTGGTC CACAGTGTC CACAGTGTC CACAGTGTC CACAGTGTC CACAGTGTC CACAGTGTC CACAGTGTC CACAGTGTC CACAGTGTC CAC	cession #: 1  LTLAALGASG ACGMQSVRT CNAHPCFPRY CVPNSVCINT RSCVCRVGWA ACDPDADEDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKDMK NIIWANLRYR  71 DNA seq id Accessio uence: 71 11    GGAAGGCAGC GGAGGCAATTG GACATCAAAC CATGAGTTTC CACTCACAG GCTAACCTTG GCAGCTGG TGGCCATCAG TGGCCATCAG TGGCATCCC TGGCATCAG TGGCATCCC TGGCATCAG TGGCCATCCCC TGGCATCAG TGGCCATCCCC TGGCATCAG TGGCCATCCCC TGGCATCAG TGGCCATCCCC	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPL HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANFFRAV SYRWPLQHRP CNDTIPEDYE 1 GGCAGCTCCA TGGGGCAGAT TGCTGGCAA ATGCTGGCAC AGACCTTGCG AGACCTTGCG AGACCTTGCG AGACTTGACCA	GPOMLRELQE GPOMLRELQE CAPGPCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAPNGV AEFGIQLKAV QVGYIRVRFY THQLRQA  626 31   CTCAGCCAGT CCTCTTCTGG CGTGTTAGTA AGATGAGCTG AGTGATAGTT CTACAAATGT TGGAGCCTTC GGGGAGCCAAC	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP ECHEMORY ECHO ECHEMORY ECHEMORY ECHEMORY ECHEMORY ECHEMORY ECHEMORY ECHEMORY	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG  51   GCTGGGAACC GCATCATCAT GACACTCCAT TGAGCTGCAC AAGGTGTTTT ATGAAATGTT CTTTGCGGCT CTTCTAAAGG AAGTGAATGT TCCCCCAGCC	120 180 360 420 540 600 720 60 120 180 240 300 420 480 540
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	Protein Acci      MVPDTACVLL   PLENTVMECD     NGSHCTDVNE     NGSHCTDVNE     INECETGQHN     ADCVLERDGS     EDVDRDGIGD     DTDQDGGGDA     VDHDFVGDAC     RDNCRLVPNP     PEGDAQIDPN     FGYQDSSFY     ESQVRLLWKD     RLGVFCFSQE     Coding seq     GAGTCACCAA     TTTTCGCT     CACGTCACT     TTTTGAACCT     AGGCTTGGTC     CAGGGGCCGG     GAAAACGTG     CAAGGGGAAT     GAGTTTTAGTC     CAAGGGGAAT     CACGTTTTAGTC     CAGGTTTTAGTC     CAGGTTTAGTC     CAGGTTTTAGTC     CAGGTTTTAGTC     CAGGTTTAGTC     CAGGTTTAGTC     CAGGTTTAGTC     CAGGTTTAGTC     CAGGTTTAGTC     CAGGTTTAGTC     CAGGTTTTAGTC     CAGGTTTAGTC     CAGGTTTTAGTC     CAGGTTTAGTC     CAGGTTTTAGTC     CAGGTTTTAGTC     CAGGTTTAGTC     CAGGTTTTAGTC     CAGGTTTTAGTC     CAGGTTTAGTC     CAGGTTTAGTC     CAGGTTTAGTC     CAGGTTTAGTC     CAGGTTTTAGTC     CAGGTTTAGTC     CAGGTTTTAGTC     CAGGTTTTAGTC     CAGGTTTTAGTC     CAGGTTTTAGTC     CAGGTTTTAGTC     CAGGTTTTAGTC     CAGGTTTA	cession #: 1  LTLAALGASG ACGMQOSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDFDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMMKQMEQT PRNVGWKDKK NIIWANLRYR  71 DNA seq id Accessio uence: 71 11   ' GGAAGGCAGC ATGGCTTCCC GGAGCAATTG ACTGTCGCCT CAACTCAAAC CATGAGTTCA CAACTCACAG GCTAACCTTG GCCAGCTCGG TGGGCATCCG TGGCATCCCG TGGAACTCTCG	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPL ENQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANPFRAV SYRWFLQHRP CNDTIPEDYE  LUCIC GGCAGCTCCA TGGGGCAGAT CACTCATCAT CAGCTGGGAA TTTCTGATAT AAGAAGGCAA ATGCTGGCAC AGTATAAAAC AGGACTTGCG AAGTTGACGA AGGATTGACGA AAGATTGACGA	GPOMLRELQE GPOMLRELQE CAPGPCFPGV CEACPFGYSG PGFVGDQASG PGFVGDQASG PGFVGDQASG DLUGFPDEKL VRNPDQRNTD PNSDQKDSDG VVNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEPGIQLKAV OVGYIRVRFY THQLRQA  626 31   CTCAGCCAGT CCTCTTCTGG TGGCTTTGGT TGGTTTAGGAG CGTGATACAA AGATGATGGT CTCAAAATGT TGGAGCCATC GGGAGCCAAC GGAGGCCAAC CCATGAAGGTT CGAGAGGTAC CCATGAAGGTT	TMAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDD DGIGDACDNC HDGQGDACDD PENABVILTD DFESTFHVNT KSSTGPGEQL EGPELVADSN  41  ACCCAGATACT AGCATAATTA ATTICAGGGA TCGGAGCAGG GCCATGGCT TATATCATCA AGCATGCCGG CCCCCATGGT TTCTCGGAGG GTGTCTGTGG	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGG CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG  51   GCTGGGAACC GCATCATCAT GACACTCCAT TGAGCTGCAC AAGGTGTTTT ATGAAATGTT CTTTTGCGGCT CTTCTAAAGG AAGTGAATGT TCCCCCAGCC TCTCCAATAC TCTACAATGT	120 180 240 300 360 420 600 660 720 60 120 120 120 240 300 360 420 540 600 600 720
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	Protein Acci    MVPDTACVLL PLENTYMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Ac Coding seq 1   GAGTCACCAA TTCCCCAGCC TATTCTGGCT CACAGTCACT TTTTGAACCT AGGCTTGGTC CAGAGGGCAAT GGACTATAAT CACAGTGTGC CAGGGTTAGAC TACGGTTCACA TACGGTTTGGAC CAGGGTTAGAC TACGGTTTGGAC TACGGTTTGGAC TACGGTTTGAACT AGGCTTTGGAC TACGGTTGAG TACGATCAAC	cession #: 1  LTLAALGASG ACGMQOSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADEDG GDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMMKQMEQT PRNVGWKDKK NIIWANLRYR  71 DNA seq id Accessio uence: 71 11	NP_000086.1 21	GPOMLRELQE GPOMLRELQE CAPGPCFPGV CEACPFGYSG PGFVGDQASG DLDGFPDEKV VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEPGIQLKAV QVGYIRVRFY THQLRQA  626 31   CTCAGCCAGT CCTCATCGGG TGGCTTTGGT CATTGGGAG CGTGATACAA AGATGACTG TGGAGCCTTC GGGAGCCCAGT CTACAAATGT CTACAAATGT TGGAGGCTTC GGGAGCCCAGC CATGAAGGTT TGAAAATGAC	TMAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDD PENAEVILTD DFEGTFHVNT KSSTGPGEQL EGPELVADSN  41   ACCCAGATAC AGCATAATTA ATTTCAGGA GATGGAATGC TGGGTGAAGG TCGGAGCAGG GCAATGCT TATACATCA AGCATGCTG AGCATGCTG TTCTCGGAAGG CCCCGATGGT TTCTCGGAAGG CTGTCTGTGC ATTGCCAAAG	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG  51   GCTGGGAACC GCATCATCAT GACACTCCAT TGAGCTGCAC AAGGTGTTT ATGAAATGTT CTTCTAAAGG AAGTGAATGT TCCCCCAGCC TCTCCAATGC CAACAGGGGA	120 180 300 360 420 540 600 720 60 120 180 240 300 420 420 420 480 600 600 720
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	Protein Acci    MVPDTACVLL PLENTYMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE  Seq ID NO: Nucleic Ac Coding seq I GAGTCACCAA TTCCCCAGCC TATTCTGGCT CACAGTCACT TTTGAACCT CAGAGGCCGG GAAAAACGTG CAAGGGCAGA TCACAGTGTC CAGAGTGTC CAGATTGAAC TATCAAAGTGT TATCAAAGTGT TATCAAAGTGT	cession #: 1  LTLAALGASG ACGMQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADEDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR  71 DNA seq id Accessio uence: 71 11    GGAAGGCAGC GGAGGCAATTG ACTGTCGCCT GACATCAAAC CATGAGTTCA GCAGTCAAC GCTAACCTTG GCCAGCATGG TGGCATCACG TGGCATCACG TGGCATCACG TGGCAGCTCACG TGGCAGCTCACG TGGCAGCTCACG TGGCAGCTCACG TGGCAGCTCACG TGGCAGCTCACG TGGCAGCTCACG TGGCAGTCCC TGAACTCACG TACACATACT TACAGAATCCG TACAGAACT TACAGAATCCG TACAGAATCCCC TACAGAATCCCC TACAGAATCCCC TACAG	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPL HQDSRDNCPT GDVCQDDPDA YQTMNSDPGL YWQANFFRAV SYRWPLQHRP CNDTIPEDYE LUENCE N #: NM_024 919 QGCAGCTCCA TGGGCAGAT TTCTGATAT AAGAAGCAA ATTGCTGATCA ATGCTGGCAC AGTATAAAAC AGCTTGCG AAGATTGACCA AGACTTGCG AAGATTGACCA AGACTTGCG AAGATTGACCA CCTGTATGAT AGAATGTCAC CCTGTATGAT AGAATGTCAC	GPOMLRELQE GPOMLRELQE CAPGPCFPGV CEACPPGYSG PGFVGDQASG DLDGPPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAPNGV AEFGIQLKAV QVGYIRVRFY THQLRQA  626 31   CTCAGCCAGT CCTCTTCTGG CGTGTTAGGAGCTG AGTGATAGTT CTACAAATGT TGGAGCCTTC GGGAGCCAAC GGGAGAGTCAC GGGGAGTCAC GGGGAGTCAC	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPPQCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDNC HDGQGDACDNC EGPELVADSN  41 ACCCAGATAC AGCATAATTA ATTTCAGGA GATGAATCCT TATATCATCA AGCATGAGGT TCTCGGAAG CCCCCATGGT TTCTCGGAAG GTGTCTTGTCCAAG CATGCTGTCTTGCCAAG CATGCTGCTCAAG CCTACAGCTGCCT TTCTCCGAAG CCTCATGCT TTCTCCGAAG CTTCTTGCCAAG CTTCTTGCCAAG CTTCTTGCCAAG CTTCTTGCCAAG CTACAGCTGC	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG  51   GCTGGGAACC GCATCATCAT TGACCTCCAT TGAGCTGCAC AAGGTGTTTT ATGAAATGTT CTTTGCGGCT CTTCTAAAGG AAGTGAATGT TCCCCAGCC TCTCCAATAC TCTACAATGT TCACACGGGA TAAACTCAAA	120 180 240 360 420 540 600 600 720 60 120 180 240 300 480 540 660 720 780 840
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	Protein Acci    MVPDTACVLL PLKNTVMECD NGSHCTDVNE NIBCETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE  Seq ID NO: Nucleic Ac Coding seq    GAGTCACCAA TTCCCCAGCC TATTCTGGCT CACAGTCACT TTTTGAACCT AGGCTTGGTC CAGGGCAGA GGAGAAACGTG CAAGGGGAAT GGACTATAAT CACAGTCACT TATCAAAGTC TACCAGTCACT TATCAAAGTC CAGGTTCTCG GGCTTTCTCG GGCTTCTCTCG GGCTTCTCTCTC	Cession #: 1  LTLAALGASG ACGMQQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDFDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRGBV WVVLNQGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR  71 DNA seq id Accessio cuence: 71 11	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPL ENQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANPFRAV SYRWFLQHRP CNDTIPEDYE  LUCIC GGCAGCTCCA TGGGCAGAT CAGCTGGGAA TTTCTGATAT AAGAAGGCAA TTGCTGATCA AGTATAAAAC AGACTTGCG AGTATAAAAC AGAATGTCAC AGAATCAAAAC CCTTTCTTTGC	GPOMLRELQE   GPOMLRELQE   CAPGPCFPGVS   CEACPPGYSG   GFYGDQASG   DLDGFPDEKI   VRNPDQRNTD   PNSDQKDSDG   VPNSAQEDSD   DKVVDKIDVC   AVGYTAFNGV   AFEGIQLKAV   QVGYIRVRFY   THQLRQA   CTCAGCCAGT   CCTCTTCTGG   TGGCTTTGGT   CATTGGGGAG   CGTGATACAA   AGATGATGTT   CTGAGAGCTTC   CGGAGCCCAGT   CGGAGCCCAGC   CATGAAGGTT   TGAAAATGAC   CGGGGGGTCAC   CGCGGAGTCAC   CGCGGAGTCAC   CGTGGAGCCAGC   CATCAGCTGGCCACCCCCCCCCCCCCCCCCCCCCCCCCC	TMAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDD DFEMSEVILTD DFEGTFHVNT KSSTGPGEQL EGPELVADSN  41  ACCCAGATAC AGCATAATTA ATTTCAGGGA AGTGGAGAGG TCGGRGCAGG CCCCGATGGT TTTCTCGGAAG GTGTCTGTGC ATTGCCAAAG CTACACGCTGCAACGC CCCCATGGT CTTGCCAAGG CTACACGCC CCAACGT CTTGCCAAGG CTACACGCCC CCAACGT CTTCCCAAGG CTACACCCCCAACGT CTTCCCAAGG CTACACCCCCAACGT CTTCTCCCAAGG CTACACCCCCCAACGT CTTCCCAAGG CTACACCCCCCAACGT CTACACCCCCAACGT CTACACCCCCCAACGT CTTCTCCCAACGC CCCCATGGT CTACACCCCCCCAACGT CTACACCCCCCCCCC	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGG CRSQRNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG  51   GCTGGGAACC GCATCATCAT AGACATCCAT ATGAAATGTT CTTTGCGGCT CTTCTAAAGG AAGTGAATC TCTCCAATAC TCTACAATGT CAACAGGGGA TAAACTCAAA TCTACAAAT TTACAATGT CAACAGGGGA TAAACTCAAA TCTCAACCCC	120 180 240 300 360 420 600 650 720 60 120 300 360 420 480 540 600 720 780 840 900
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	Protein Acci      MVPDTACVLL   FLENTVMECD     NGSHCTDVNE     NGSHCTDVNE     INECETGQHN     ADCVLERDGS     EDVDRDGIGD     DTDQDGGRGDA     VDHDFVGDAC     RDMCRLVPNP     PEGDAQIDPN     FGYQDSSSFY     ESQVRLLWKD     RLGVFCFSQE     Seq ID NO:     Nucleic Ac     Coding seq     1	cession #: 1  LTLAALGASG ACGMQOSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADEDG GDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMMKQMEQT PRNVGWKDKK NIIWANLRYR  71 DNA seq id Accessio uence: 71 11    GGAAGGCAGC GGAGGCAGC CATGAGTTCA ACTGTCGCCT GACATCAAAC CAATGAATCG CATGAGTTCA CAACTCACAG GCTAACCTTG GCAACTCACG CCTGAACTCTG CCTGAACTCTG CCTGAACTCTG CCTGAACTCTG CTGACATCTG CTAAAATAAT	NP_000086.1 21 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPT ENQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANPFRAV SYRWFLQHRP CNDTIPEDYE USENCE H\$: NM_024 919 GGCAGCTCCA TGGGGCAGAT CACTCATCAT CAGCTGGGAA ATGCTGGGAA ATGCTGGACA ATGCTGGATCA AGACTTGCG AGATTAAAAC AGACTTGCG AGGTTGATCA AGACTTGCG AGGTTGATCA AGACTTGCG AGGTTGATCA CGCTGTATGAT AGAAGTCACA CCCTGTATGAT CCCTGTATGAT CAGTTCACA CCCTGTTATGAT CAGTTCACA CCCTGTTATGAT CCCTGTTATGAT CCCTGTTATGAT CCCTGTTATGAT CCCTGTTATGAT CCCTGTTATGAT CCCTGTTATGAT CCCTGTTATGAT CCCTGTTATGAT CCCTCTCCGGC CCTGTTCCTGCG CCTCCTCCGGC CCTCTCCGGC	GEGGAGCCAAC CATCAGCAGG CGTGAAAAAAAAAGC CAACAAAAAAAAAGC CAACACTAGCAGGC CATCAGCAGT CGTGAGCAGT CGAGAGCAGAGC	TMAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDD DGIGDACDNC HDGQGDACDD PENAEVILTD DFEGTFHVNT KSSTGPGEQL EGPELVADSN  41  ACCCAGATAC AGCATAATTA ATTICAGGAA GATGGAATGC TGGGTGAAGG TCGGAGGAGG GCCCCGATGGT TTCTCGGAG GTGTCTGTGG ATTGCCAAAG CTACAAGTAGCATCC CTACAGCTGC CCATGCTGC CCATGCTGC CCATGCTGC CCATGCAAAGT	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGG CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG  51   GCTGGGAACC GCATCATCAT GACACTCCAT TGAGCTGCAC AAGGTGTTT ATGAAATGTT CTTCTAAAGG AAGTGAATGT TCCCCCAGCC TCTCCAATTAC CAACAGGGGA TAAACTCAAA CTCTCAGCCC CATTGTTACA	120 180 240 360 420 540 660 720 60 120 180 240 300 420 420 420 420 480 540 600 600 720
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	Protein Acci    MVPDTACVLL FLKNTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Ac Coding seq 1   GAGTCACCAA TTCCCCAGCC TATTCTGGCT CACAGTCACT AGGCTTGGTC CAGAGGCCGG GAAAAACSTG GGACTATAAT CACAGTGTC CAGGCTTTAGACT TAGCATTAAA CAGGGGATCA TATCAAAGTG GGCTTCTCTG TACCTGTG TACCTGTGTC CAGGGGATCTG TATCAAAGTG GGCTTCTCTG TACCTGTGTC TTACCTGTGTC TTACCTGTC TTACCTC TTACCTC TTACCTC TTACCTC TTACCTC TTACCTC TTACCTC TTACCTC TTACCT TTACCTC TTACCTC TTACCTC TTACCTC TTACCT TTACCTC TTACCT TTACCT T	cession #: 1  LTLAALGASG ACGMQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR  71 DNA seq id Accessio uence: 71 11    GGAAGGCAGC ACTGACATCC GGAGCAATTG CATGACTTCC GGAGCTTCAAAC CATGACTTCAGC TGGCTTCCC TGCCATGACTTG CACAGACTCAG CACACACAGC CTGAACTCTG CACACACACC CACACACC CACACAC CACACACC CACACACC CACACACC CACACACC CACACAC CACAC CACACAC CACA	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPL HQDSRDNCPT GDVCQDDPDA VQTMNSDPGL YWQANPFRAV SYRWPLQHRP CNDTIPEDYE LUENCE I #: NM_024 919 21 I GGGCAGCTCCA TGGGGCAGAT CACTCATCAT CAGCTGGGAA TTTCTGATCA ATGCTGGCAC AGACCTTGCG AGACTTGACC AGACTTTACAC CCTGTAGAT AGAATGTAAAC AGACTTTGCC CCTGTAGAT AGAATGTAAAC CCTGTTGCC GGGCCACC	GPOMLRELQE GPOMLRELQE CAPEFCFFGV CEACPFGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEFGIQLKAV QVGYIRVFY THQLRQA  626  31   CTCAGCCAGT CCTCTTCTGG TGGCTTTGGT CATTCGGAGC CGTGATACAA AGATGAGCTT GGGAGCCTTC GGGGAGCCAAC CATGAAGGTT TGGAGCCTT CGGTGAGGCCT CGTGTGAGGCCT CGTGAGGCCT CGTGAGGCCC CATCAGCTGG CCACAAAAAC CGCGAGTCAC CACAAAAAAC CGATATGACCT CGGTATAGCT CCACAAAAAAC CGATATGACCT CGATTAGCT CGCGAGTCAC CACAAAAAAC CGATATGACCT CGATTAGCC CACAAAAAAC CGATATGACCT CGATTAGCT CCACAAAAAAC CGATATGACCT CACAAAAAAC CACAAAAAAC CACAAAAAAC CACAAAAAA	TNAALQDVRD ACIQTESGGR PTHQGVGLAP CQRGAQRFCP ECKEDEQCRED EDKWGDACDN DGIGDACDN DGIGDACDN DGIGDACND DFESTFHVNT KSSTGFGEQL EGPELVADSN  41  ACCCAGATAC AGCATAATTA ATTTCAGGA GATGGAATCC TGGGGAGAGG GGCAATGCCT TATATCATCA AGCATGCT TTCTCGGAAG CTCCCAGTGGT TTCTCGGAAG CTCCCAGTGGT TTCTCGGAAG CTACAGCTGCC CATGGCTAAG ATTTCATCA AGCATGCTAAG CTACAGCTGCC CATGCAAGT AGTTTTATAT	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG  51   GCTGGGAACC GCATCATCAT TGAGCTGCAC AAGGTGTTTT ATGAAATGTT CTCTGAGGCT CTTCTAAAGG AAGTGAATGT TCCCCAGCC TCTCCAATAC TCTACAATGT CAACAGGGA TAAACTCAAA CTCTACAAC TCTTCAGGCT CATTCTACAA CTCTCAGCCC CATTGTTACA TTCTGGGAGG	120 180 240 360 420 540 600 720 180 240 300 480 540 660 720 780 660 720 780 900 900 900 900 900
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	Protein Acci    MVPDTACVLL PLENTYMECD   NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSFY ESQVRLLWKD RLGVFCFSQE  Seq ID NO: Nucleic Ac Coding seq   GAGTCACCAA TTCCCCAGCC TATTCTGGCT CACAGTCACT CACAGTCACT CAGGCCAGC GAAAAACSTG GAAAAACSTG CAGGTTTGAG TACGATTCACA TATCAAAGTC GGCTTCTCG TTACCTGATC ACAGGACTCAT ACAGGATCTAAAT ACAGGATCTCTCAAATGAATTC AAATGAATTC AAATTC AAATGAATTC AAATTC AAATTC AAATGAATTC AAATTC AAA	Cession #: 1  LTLAALGASG ACGMQQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG GDDDIDGDRI DSDQDQDGDG GGEDADRGBV VVMWKQMEQT PRNVGWKDRK NIIWANLRYR  71 DNA seq id ACCESSIO CATGACTTCCC GGAAGCAATTG ACTGACGCT GACATCAAAC CATGACTCAC CATGA	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPL ENQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANPFRAV SYRWFLQHRP CNDTIPEDYE  LUCIC GGCAGCTCCA TGGGGCAGAT CACTCATCAT CAGCTGGGAA TTTCTGATAT AAGAAGGCAA ATGCTGGGAA TTGCTGATAC AGTATAAAAC AGACTTGCG AGTATAAAAC CCTTTACCAC CTTCACCAC TTCACCACCA CTTCACCACCACCACTCGGGAC TTCACCACCACCACTCGGGAC CTTCACCACCACCACTCGGAC TTCACCACCACCACTCGGAC TTCACCACCACCACTCGGAC TTCACCACCACCACTCGGAC TTCACCACCACCACTCGGAC TTCACCACCACCACTCGGACTCGGAC TTCACCACCACCACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTCGACTC	GPOMLRELQE GPOMLRELQE CABGPCFPGV CEACPPGYSG GFYGDQASG GFYGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AFEGIQLKAV QVGYIRVFFY THQLRQA  626 31   CTCAGCCAGT CCTCTTCTGG TGGCTTTGGT TGATAGATT CTACAAATGT TGGAGCCTTC GGGAGCCTAC GTGTGAGGTT GGTGAGGTT TGAAAATGAC GCGGAGTCAC CATCAGCTGG CATCAGAAAAAAC GGGAGTCAC GGGAGTCAC GACAAAAAAAC GGAAACAAC	TMAALQDVRD TMAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDD DGIGDACDNC HDGQGDACDD DFEMEVILTD DFESTFHVNT KSSTGFGEQL EGPELVADSN  41  ACCCAGATAC AGCATAATTA ATTTCAGGAA GGCATACTCA AGCATGCGG GGCATGCT TATATCATCA AGCATGCGG CCCGATGGT TTCTCGGAAG GTGTCTGTGC CATGCAAGT CTAGCAGAG CCTAGATTCACAAGT CATGCAAAGT CATGCAAAGT CATGCAAAGT CATGCAAAGT CATGCAAAGT AGCATACAAAGT AGCAAAGAAAA	WLRQQVREIT WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG  51   GCTGGGAACC GCATCATCAT TAGACTGCAC AAGGTGTTTT ATGAAATGTI TCTTGGGCT CTTCTAAAGG AAGTGAATC TCTACAATGTI CAACAGCGCC CATTGTTACA TTCACACAC TCTACAATGTI CAACAGCGCC CATTGTTACA TTCAGCCC CATTGTTACA TTCTGGGAGG AAAAAGAAGC	120 180 240 360 420 540 600 660 720 60 120 360 420 480 540 660 720 780 960 960 1020
50 55 60 65 70 75	Protein Acci    MVPDTACVLL PLENTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Ac Coding seq 1   GAGTCACCAA TTCCCCAGCC TATTCTGGCT CACAGTCACT TTTTGAACCT AGGGGGAAT GGACTATAAT CACAGTGGTC CAGGTTTGAG TACCAGTGTC CAGGGTTCACT TATCAAAGTGAC TATCAAAGTGAC TATCAAAGTGAT CACAGGGATTAAA ACAGGGATTT CAAAAGCAGA	cession #: 1  LTLAALGASG ACGMQOSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDFDADEDG GDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKDKK NIWANLRYR  71 DNA seq id Accessio uence: 71 11   ' GGAAGGCAGC GGAAGCAGC CATGAGTTCA ACAGCAGTGT CAACTCACAG GCTAACCTTG GCATCAAC CATGAGTTCA CAGGAATCG CAGGAATCG CAGGAATCG CAGGAACTCAG GCTAACCTTG CACACATGG CTGAACTTCAG GCAACTCAGG GCTAACCTTG CACAGAATCG CTGAACTCAG CTGAACTCAG CTGAACTCAG CTGAACTCTG CACAGAATCAG CAGGAATCG CTGAACTCTG CACAGAATCAG CAGGAATCG CTGAACTCTG CACAGAATCAG CAGGAATCG CTGAACTCTG CACAGAATCAG ACAGAATCAG AC	NP_000086.1 21 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPT ENQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANPFRAV SYRWPLQHRP CNDTIPEDYE USENCE GGCAGCTCCA TGGGGCAGAT CACTCATCAT AAGAAGACAAAAAA AGAATGTGACA AGAATTGACAA AGAATGTGACA CAGTTGATAT AAGAAGACAAAAAA CCTGTATAT AAGAAGACAAAAAA CCTGTATAT AGAACTTGACA CAGTTGATAT CAGTTGAT	GPOMLRELQE GPOMLRELQE CAPEPCFPGV CEACPFGYSG PGFVGDQASG DLDGFPDEKU VRNPDQRNTD PNSDQKDSDG DKVVDKIDVC AVGYTAFNGV AEPGIQLKAV OVGYIRVRFY THQLRQA  626 31   CTCAGCCAGT CCTCTTCTGG TGGCTTTGGT CATTGGGAG CGTGATACAA AGATGAAGTT TGGAGCCTTC GTGTGAGGCT CTGAGCCACC CATCAAATGT TGGAGCCTC CATCAAATGT TGAAAATGT TGAAAATGACC CATCAACTGT CACCAAAAAAAC CAACAACAAC TAAATGT AGCAACAAC TAAATGT AGCAACAAC TAAATGT AGCAACAAC TAAATGT TAGCACTIG CACCACACC CATCACCTIG CACCACACC CATCACCTIG CACCACACC CATCACCTIG CACCACACC CATCACCTIG CACCACACACACC CATCACCTIG CACCACACACACC CATCACCTIG CACCACACACACC CATCACCTIG CACCACACC CATCACCTIG CACCACACACC CATCACCTIG CACCACACACACC CATCACCTIG CACCACACACACC CATCACCTIG CACCACACACACC CATCACCTIG CACCACACACACC CATCACACACC CATCACACT CACCACACACA	TMAALQDVRD TMAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDD PENABVILTD DFGSTFHVNT KSSTGPGEQL EGPELVADSN  41    ACCCAGATACT AGCATAATTA ATTICAGGGA AGTGGAATCC TGGCTGAAGG TCGGAGCAGG GCCATGCT TTCTCGGAGG GTGTCTGTGC ATTGCCAAAGT ATTGCCAAAGT AGCATGAACT CATGCAAAGT AGCAAGAAAC TGGAGAAACC TCAAAGGT AGTTTTATAT AGCAAGAAAC TTCAAAGACA	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGG CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG  51   GCTGGGAACC GCATCATCAT GACACTCCAT TGAGCTGCAC AAGGTGTTTT ATGAAATGTT CTTCTAAAGG AAGTGAATGT TCCCCCAGCC TCTCCAATAC TCTACAATGT CAACAGGGGA TAAACTCAAA CTCTACAGCC CATTGTTACA TTCTGGGGG AAAAAGAAGC TATTTAGAAGT TATGAAAGG AAAAAGAAGC TATTTAGAAGT TATTTAGAAGT TATTTAGAAGT TATTTAGAAGT TATTTAGAAGT TATTTAGAAGT TATTTAGAAGT TATTTAGAAGT	120 180 240 360 420 600 660 720 60 120 180 240 300 420 480 540 660 720 780 660 720 780 900 900 900 900 900
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	Protein Acci    MVPDTACVLL PLENTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Ac Coding seq 1   GAGTCACCAA TTCCCCAGCC TATTCTGGCT CACAGTCACT TTTTGAACCT AGGGGGAAT GGACTATAAT CACAGTGGTC CAGGTTTGAG TACCAGTGTC CAGGGTTCACT TATCAAAGTGAC TATCAAAGTGAC TATCAAAGTGAT CACAGGGATTAAA ACAGGGATTT CAAAAGCAGA	cession #: 1  LTLAALGASG ACGMQOSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDFDADEDG GDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKDKK NIWANLRYR  71 DNA seq id Accessio uence: 71 11   ' GGAAGGCAGC GGAAGCAGC CATGAGTTCA ACAGCAGTGT CAACTCACAG GCTAACCTTG GCATCAAC CATGAGTTCA CAGGAATCG CAGGAATCG CAGGAATCG CAGGAACTCAG GCTAACCTTG CACACATGG CTGAACTTCAG GCAACTCAGG GCTAACCTTG CACAGAATCG CTGAACTCAG CTGAACTCAG CTGAACTCAG CTGAACTCTG CACAGAATCAG CAGGAATCG CTGAACTCTG CACAGAATCAG CAGGAATCG CTGAACTCTG CACAGAATCAG CAGGAATCG CTGAACTCTG CACAGAATCAG ACAGAATCAG AC	NP_000086.1 21 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPT ENQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANPFRAV SYRWPLQHRP CNDTIPEDYE USENCE GGCAGCTCCA TGGGGCAGAT CACTCATCAT AAGAAGACAAAAAA AGAATGTGACA AGAATTGACAA AGAATGTGACA CAGTTGATAT AAGAAGACAAAAAA CCTGTATAT AAGAAGACAAAAAA CCTGTATAT AGAACTTGACA CAGTTGATAT CAGTTGAT	GPOMLRELQE GPOMLRELQE CAPEPCFPGV CEACPFGYSG PGFVGDQASG DLDGFPDEKU VRNPDQRNTD PNSDQKDSDG DKVVDKIDVC AVGYTAFNGV AEPGIQLKAV OVGYIRVRFY THQLRQA  626 31   CTCAGCCAGT CCTCTTCTGG TGGCTTTGGT CATTGGGAG CGTGATACAA AGATGAAGTT TGGAGCCTTC GTGTGAGGCT CTGAGCCACC CATCAAATGT TGGAGCCTC CATCAAATGT TGAAAATGT TGAAAATGACC CATCAACTGT CACCAAAAAAAC CAACAACAAC TAAATGT AGCAACAAC TAAATGT AGCAACAAC TAAATGT AGCAACAAC TAAATGT TAGCACTIG CACCACACC CATCACCTIG CACCACACC CATCACCTIG CACCACACC CATCACCTIG CACCACACC CATCACCTIG CACCACACACACC CATCACCTIG CACCACACACACC CATCACCTIG CACCACACACACC CATCACCTIG CACCACACC CATCACCTIG CACCACACACC CATCACCTIG CACCACACACACC CATCACCTIG CACCACACACACC CATCACCTIG CACCACACACACC CATCACCTIG CACCACACACACC CATCACACACC CATCACACT CACCACACACA	TMAALQDVRD TMAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDD PENABVILTD DFGSTFHVNT KSSTGPGEQL EGPELVADSN  41    ACCCAGATACT AGCATAATTA ATTICAGGGA AGTGGAATCC TGGCTGAAGG TCGGAGCAGG GCCATGCT TTCTCGGAGG GTGTCTGTGC ATTGCCAAAGT ATTGCCAAAGT AGCATGAACT CATGCAAAGT AGCAAGAAAC TGGAGAAACC TCAAAGGT AGTTTTATAT AGCAAGAAAC TTCAAAGACA	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG  51   GCTGGGAACC GCATCATCAT TGAGCTGCAC AAGGTGTTTT ATGAAATGTT CTCTGAGGCT CTTCTAAAGG AAGTGAATGT TCCCCAGCC TCTCCAATAC TCTACAATGT CAACAGGGA TAAACTCAAA CTCTACAAC TCTTCAGGCT CATTCTACAA CTCTCAGCCC CATTGTTACA TTCTGGGAGG	120 180 240 360 420 540 600 660 720 60 120 360 420 480 540 660 720 780 960 960 1020

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	AGCTACGGCT GGGTGTG					120
	CAAGTGCGAG AGGCAAG					i80
	TCTGCAGCCG GCTCCCA					240
70	TTCAACCATG CCCCTGT					300
70						
	GCTGCTACTG CTGGCAT					360
	CGTGGTAACT GTGGTGC					420
	CGGCGAGCAA GTGGGGC					480
75	ACTAGOGCTA CTGCACT					540
75	GGAGCAGCCG CCGCCCC					600
	GCAGGCGGAT GAGGGCG	AGT ACGAGTGCCC	GGTCAGCACC	TTCCCCGCCG	GCAGCTTCCA	660
	GGCGCGGCTG CGGCTCC					720
	ACTAGAAGAG GGCCAGG					780
	CCCCAGCGTG ACCTGGG					840
80	CTCCCGCTCT GCTGCCG					900
00						960
	GCAGCCACTG ACTIGTG					
	CATCCTCCAC GTGTCCT					1020
	GTGGCACATT GGCAGAG					1080
0.5	CTCATACAAC TGGACAC					
85	CACTTTGGGC TTTCCCC	CAC TGACCACTG	A GCACAGCGGC	ATCTACGTC	GCCATGTCAG	1200

	CAATGAGTTC	TCCTCAAGGG	ATTCTCAGGT	CACTGTGGAT	GTTCTTGACC	CCCAGGAAGA	1260
	CTCTGGGAAG	CAGGTGGACC	TAGTGTCAGC	CTCGGTGGTG	GTGGTGGGTG	TGATCGCCGC	1320
				GGTGCTCATG			1380
_				GGAGCTGACC			1440
5	CCGGAGGCTG	CATTCCCATC	ACACGGACCC	CAGGAGCCAG	CCGGAGGAGA	GTGTAGGGCT	1500
				GGACAACAGT			1560
	AGAGCCCGAG	GGCCGCAGTT	ACTOCACGET	GACCACGGTG	MUGGAGATAG	AAACACAGAC	1620
	TGAACTGCTG	TCTCCAGGCT	CTGGGCGGGC	CGAGGAGGAG	GAAGATCAGG	ATGAAGGCAT	1680
				GAATGGGACC			1740
10							1800
10	CAATGGCATC	TACATCAATG	GGLGGGALA	CCTGGTCTGA	CCCMGGCC1G	CCICCCTICC	
	CTAGGCCTGG	CTCCTTCTGT	TGACATGGGA	GATTTTAGCT	CATCTTGGGG	GCCTCCTTAA	1860
	ACACCCCCAT	TTCTTCCCA	AGATGCTCCC	CATCCCACTG	ACTGCTTGAC	CTTTACCTCC	1920
	ACTOCCCC COTT	TTC1100001	CCCCCCCCCCC	AATTGAGTCT	CTCCCACCAT	CCATCCACCT	1980
				GTGTTGACTG			2040
15	TEACTETORS	TGGAGGGGTG	ACTGTGTCCG	TGGTGTGTAT	TATGCTGTCA	TATCAGAGTC	2100
10	1000011000	TOOMOTE TOO	CCCACCCAT	TTGAGTGGTT	COCTOCOCAA	CACTOTCACG	2160
	GTTTGGCGTG	TGTGTCATGT	GGCTGTGTGT	GACCTCTGCC	TGAAAAAGCA	GGTATTTTCT	2220
	CAGACCCCAG	AGCAGTATTA	ATGATGCAGA	GGTTGGAGGA	GAGAGGTGGA	GACTGTGGCT	2280
				TGGAATCTGC			2340
20	CAGACCCAGG	1010CGGGCW	INGCIGGAGE	IGGAAICIGC	CICCOGIGIG	AGGGAACCIG	
20	TCTCCTACCA	CTTCGGAGCC	ATGGGGGCAA	GTGTGAAGCA	GCCAGTCCCT	GGGTCAGCCA	2400
	GACCCTTGAA	CTGTTACAGA	AGCCCTCTGC	CCTCTGGTGG	CCTCTGGGCC	TGCTGCATGT	2460
			G100000000	GAGCTTCTTG	CACCAAMACT	CCTCCCAAATC	2520
	ACATATITIC	IGIAAAIAIA	CATGCGCCGG	GAGCIICIIG	CUOGNATUCE	GCTCCGAATC	
	ACTTTTAATT	TTTTTCTTTT	TTTTTTTCTTG	CCCTTTCCAT	TAGTTGTATT	TTTTATTTAT	2580
	TTTTATTTT	ATTTTTTTTT	AGAGTTTGAG	TCCAGCCTGG	ACGATATAGC	CAGACCCTGT	2640
25							
23	CIGIAAAAAA	ACCAAAACCC	AAAAAAAAA	44mmmm			
				•			
	Sea ID NO:	76 Protein	secuence				
		cession #: A					
	1	11	21	31	41	51	
30	1	1	1	1	1	. ]	
	MDI CI CADMW	CDEAWLLLL.	T.T.A CETTEDED	AGELETSDVV	TVVICODAKI	PCFVRGDSGR	60
	QVGQVAWARV	DAGEGAQELA	LLHSKYGLHV	SPAYEGRVEQ	PPPPRNPLDG	PAPPRNAAAW	120
	DEGEYECRVS	TFPAGSFOAR	LRLRVLVPPL	PSLNPGPALE	EGQGLTLAAS	CTAEGSPAPS	180
	THE PRESENCE	TOCHCOVUCD	CARIFFEEDIT	VPSRSMNGQP	T.TCANICHDCI.	LODOPITHII.	240
25							
35	HVSFLAEASV	RGLEDQNLWH	IGREGAMLKC	LSEGQPPPSY	NWTRLDGPLP	SGVRVDGDTL	300
	GEPPLTTERS	GIVVCHVSNE	<b>FSSRDSOVTV</b>	DVLDPQEDSG	KOVDLVSASV	VVVGVIAALL	360
				TLTRENSIRR			420
	<b>LCPDAAAAA</b>	MOKITAKAN	OUTOVIER	IDIKENSIKK	DESCRIPTION	OL DED AGENCY	
	eghpdslkdn	SSCSVMSEEP	EGRSYSTLTT	VREIETQTEL	LSPGSGRAEE	REDÖDEGIKÖ	480
	AMNHEVOENG	TLRAKPTGNG	IYINGRGHLV				
40							
70							
		77 DNA sequ					
	Nucleic Ac:	id Accession	1 #: NM 0034	174.2			
	Coding sequ	uence: 37	3036		41	<b>61</b>	
4.5				31	41	51	
45	Coding sequ	uence: 37	3036		41	51 	
45	Coding sequents	uence: 37 11 	3036 21 	31	1	1	60
45	Coding sequents 1   CACTAACGCT	uence: 37 11     CTTCCTAGTC	3036 21     CCCGGGCCAA	31   CTCGGACAGT	 TTGCTCATTT	 ATTGCAACGG	
45	Coding sequence 1     CACTAACGCT TCAAGGCTGG	uence: 37 11   CTTCCTAGTC CTTGTGCCAG	3036 21   CCCGGGCCAA AACGGCGCGC	31   CTCGGACAGT GCGCGACGCA	 TTGCTCATTT CGCACACACA	ATTGCAACGG CGGGGGAAA	120
45	Coding sequence 1     CACTAACGCT TCAAGGCTGG	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC	3036 21     CCCGGGCCAA AACGGCGCGC TAGAAGAGCT	31   CTCGGACAGT GCGCGACGCA CAGCGGCGGC	TTGCTCATTT CGCACACACA GCGGGCCGTG	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT	
45	Coding sequence 1     CACTAACGCT TCAAGGCTGG	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC	3036 21     CCCGGGCCAA AACGGCGCGC TAGAAGAGCT	31   CTCGGACAGT GCGCGACGCA CAGCGGCGGC	TTGCTCATTT CGCACACACA GCGGGCCGTG	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT	120
	Coding sequence of the control of the control of the control of the code of th	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG	3036 21   CCCGGGCCAA AACGGCGCGC TAGAAGAGCT CAGGAAATCC	31   CTCGGACAGT GCGCGACGCA CAGCGGCGGC CTCCGGTCGC	TTGCTCATTT CGCACACACA GCGGGCCGTG GACGCCCGGC	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC	120 180 240
45 50	Coding sequence of the control of th	uence: 37  11    CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG	3036 21   CCCGGGCCAA AACGCCGCGC TAGAAGAGCT CAGGAATCC CGCTCGCCGC	31 CTCGGACAGT GCGCGACGCA CAGCGGCGGC CTCCGGTCGC CGGGCCCGAG	TTGCTCATTT CGCACACACA GCGGGCCGTG GACGCCCGGC AGCTGCTGCA	ATTGCAACGG CGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG	120 180 240 300
	Coding sequence of the control of th	uence: 37  11  CTTCCTAGTC CTTGTGCAGG AATGAAAGGC CTCGCCGAGG GATGGTGCAG CAGCGCCCCC	21   CCCGGGCCAA AACGGCGGGC TAGAAGAGGCT CAGGAAATCC CGCTCGCCGG GCTGCCCGTG	31 CTCGGACAGT GCGCGACGCA CAGCGGCGGC CTCCGGTCGC CGGGCCCGAG TCCCCCGCCC	TTGCTCATTT CGCACACACA GCGGGCCGTG GACGCCCGGC AGCTGCTGCA GCGCCCTCCT	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCCTG	120 180 240 300 360
	Coding sequence of the control of th	uence: 37  11  CTTCCTAGTC CTTGTGCAGG AATGAAAGGC CTCGCCGAGG GATGGTGCAG CAGCGCCCCC	21   CCCGGGCCAA AACGGCGGGC TAGAAGAGGCT CAGGAAATCC CGCTCGCCGG GCTGCCCGTG	31 CTCGGACAGT GCGCGACGCA CAGCGGCGGC CTCCGGTCGC CGGGCCCGAG TCCCCCGCCC	TTGCTCATTT CGCACACACA GCGGGCCGTG GACGCCCGGC AGCTGCTGCA GCGCCCTCCT	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCCTG	120 180 240 300 360
	Coding sequence of the control of th	uence: 37  11	3036 21.	31   CTCGGACAGT GCGCGACGCA CAGCGGCGGC CTCCGGTCGC CGGGCCCGAG TCCCCCGCCC CGAGGGGTGA	TTGCTCATTT CGCACACACA GCGGGCCGTG GACGCCCGGC AGCTGCTGCA GCGCCCTCCT GCTTATGGAA	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCCTG CGAAGGAAGA	120 180 240 300 360 420
	Coding sequence of the control of th	uence: 37  11	3036 21    CCCGGGCCAA AACGCGCGC TAGAAGAGCT CAGGAAATCC CGCTGCCCGTG GCTGCCCGTG CTGCAGGGCC CTCTGTTCGG	31   CTCGGACAGT GCGCGACGCA CAGCGGCGGC CTCCGGTCGC CGGGCCCGAC CCAGGGGTGA AGTGGGGACC	TTGCTCATTT CGCACACACA GCGGCCCGGC GACGCCCGGC AGCTGCTGCA GCCCCCTCCT GCTTATGGAA TCTGGATCCC	ATTGCAACGG CGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCCTG CGAAGGAAGA AGTGAAGACC	120 180 240 300 360 420 480
50	Coding sequence of the control of th	uence: 37  11    CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG CAGCGCGCCC TGCTCAGGCC TTGTCAGTGC AGAATCATCC	3036 21.	31   CTCGGACAGT GCGCGACGCA CAGCGCCGCC CGGGCCCGAG TCCCCGCCC CGAGGGTGA AGTGGGGACC AATATTCGAC	TTGCTCATTT CGCACACACA GCGGGCCGTG GACGCCGGC AGCTGCTGCA GCTGCTATGGAA TCTGGATCCC TACAACGGGA	I ATTGCAACGG CGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCCTG CGAAGGAAGA AGTGAACGAAG AAGCAAAGAA	120 180 240 300 360 420
50	Coding sequence of the control of th	uence: 37  11    CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG CAGCGCGCCC TGCTCAGGCC TTGTCAGTGC AGAATCATCC	3036 21.	31   CTCGGACAGT GCGCGACGCA CAGCGCCGCC CGGGCCCGAG TCCCCGCCC CGAGGGTGA AGTGGGGACC AATATTCGAC	TTGCTCATTT CGCACACACA GCGGGCCGTG GACGCCGGC AGCTGCTGCA GCTGCTATGGAA TCTGGATCCC TACAACGGGA	I ATTGCAACGG CGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCCTG CGAAGGAAGA AGTGAACGAAG AAGCAAAGAA	120 180 240 300 360 420 480
	Coding sequence of the control of th	uence: 37  11	3036 21   CCCGGGCCAA AACGCGCGC TAGAAGAGCT CAGGAAATCC CGCTCGCCGC GCTGCCCGTG CTGCTGTCGC TGCGAGGCC CTCTGTTCG AGAAGTGCTG AAATGAAGGT	31   CTCGGACAGT GCGCGACGCA CAGCGGCGCG CTCCGGTCGC CGAGGGGTGA ACTCGGGACC AATTATCGAC CTCATTGCCA	TTGCTCATTT CGCACACACA GCGGGCCGTG GACGCCCGCC AGCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGGA GCAGTTTCAC	ATTGCAACGG CGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCCTG AGTGAAGAAA AGTGAAGAACA AGGAAACAA	120 180 240 300 360 420 480 540
50	Coding sequence of the control of th	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG CAGCGCGCC TTGTCAGTGC TTGTCAGTGC AGAATCATCC ATCTGGAAAG ACGGTACTGA	3036 21   CCCGGGCCAA AACGGCGGGC TAGAAGAGCT CAGGAAATCC CGCTCGCGGG CTGCCCGTG CTGCCAGGGCC CTCTGTTCGG AGAAGTGCTG AGAAGTGCTG TGTCTCCCTC	31 CTCGGACAGT GCGCGACGG CAGCGGGGC CTCCGGTCGC CGGGCCCGAG TCCCCCCC CAAGGGGTGA AGTCGGGACC AATATTCGAC CTCATTGCCA GCTCGAAATT	TTGCTCATTT CGCACACACA GCGGGCGTG GACGCCCGGC AGCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGGA GCAGTTTCAC ACACGGTAAT	ATTGCAACGG CGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG CGCAGGAAGA AGTGAAGAAGA AGTGAAGAAC AAGCAAAGAA TGGAACCCAC TCTGGGTCAC	120 180 240 300 360 420 480 540 600 660
50	Coding sequence of the control of th	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG CAGCGCGCC TTGTCAGTGC TTGTCAGTGC AGAATCATCC ATCTGGAAAG ACGGTACTGA	3036 21   CCCGGGCCAA AACGGCGGGC TAGAAGAGCT CAGGAAATCC CGCTCGCGGG CTGCCCGTG CTGCCAGGGCC CTCTGTTCGG AGAAGTGCTG AGAAGTGCTG TGTCTCCCTC	31   CTCGGACAGT GCGCGACGCA CAGCGGCGCG CTCCGGTCGC CGAGGGGTGA ACTCGGGACC AATTATCGAC CTCATTGCCA	TTGCTCATTT CGCACACACA GCGGGCGTG GACGCCCGGC AGCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGGA GCAGTTTCAC ACACGGTAAT	ATTGCAACGG CGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG CGCAGGAAGA AGTGAAGAAGA AGTGAAGAAC AAGCAAAGAA TGGAACCCAC TCTGGGTCAC	120 180 240 300 360 420 480 540
50	Coding sequence of the control of th	uence: 37  11	3036 21   CCCGGGCCAA AACGGGGGC TAGAAGAGCT CAGGAAATCC CGCTCGCCGC GCTGCCGGG CTCTGTTCGG AGAAGTGCTG AAATGAAGGT TGTCTCCCTC ACGGGGATAT	31 CTCGGACAGT GCGCGACGCC CACCGGCCGC CGGGCCCGAG TCCCCCGCCC CGAGGGGTGA AGTGGGGACC AATATTCGAC CTCATTGCAC GCTCGAAAAT TCTGATTCAG	TTGCTCATTT CGCACACACA GCGGCCGGG AGCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGGA ACACGGTAAT CAGTCAGTTAT	ATTGCAACGG CGGGGGGAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCCTG CGAAGGAAGA AGTGAAGAAGA AGTGAAGAACAA CGAAACCCAC TCTGGGTCAC CAGCACGTGT	120 180 240 300 360 420 480 540 600 660 720
50	Coding sequence of the control of th	uence: 37  11    CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG CAGCGCGCCC TGCTCAGGCC ATGTCAGTCC AGAATCATCC ATCTGGAAAG ACGGTACTGA ATGGACATGT	3036 21     CCCGGGCCAA AACGGCGGCC TAGAAGAGCT TAGGAAATCC CGCTCGCGG GCTGCCGTG CTGCGAGGCC CTCTGTTCGG AGAAGTGCTG AAATGAAGGT TGTCTCCCTC ACGGGGATAT	31   CTCGGACAGT GCGCGACGCA CAGCGGCGCC CGGGCCCGAG TCCCCCGCCC CGAGGGGTGC AATATCGAC CTCATTGCA GCTCGAAATT TCTGATTCAG AATAAAAGCT	TTGCTCATTT CGCACACACA GCGGGCCGTG GACGCCGGC GCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCC TACAACGGGA GCAGTTTCAC ACACGGTAAT CAGTCAGTCT	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCTG CGAAGGAAGA AGTGAAGACA AGGAAACCAC TCTGGGTCAC CAGCACGTGT ACCAATGAAA	120 180 240 300 360 420 480 540 600 660 720 780
50	Coding sequence of the control of th	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG CAGCGCGCC TTGTCAGTC ATGTAGTC ATCTGAAAG ACGTACTGA ATGGACATGT ACAGTACAA	3036 21 CCCGGGCCAA AACGGCGGC TAGAAGAGCT CAGGAAATCC GGCTGCCGTG CTGCCAGGCC CTCTGTTCGG AGAAGTGCTG AAATGAAGGT TGTCTCCCTC ACGGGGATAT TGTGTTTCGAA	31 CTCGGACAGT GCGCGACGGA CAGCGGCGGC CTCCGGTCGC CGAGGGGTGA AGTGGGGACC AATATTCGAC CTCATTGCA GCTCGAAATT TCTGATTCAG AATGAAAGGC	TTGCTCATTT CGCACACACA GCGGGCCGTG GACGCCCGGC AGCTGCTGCA TCTGGATCC TACAACGGCA GCAGTTTCAC ACACGGTAAT CAGTCAGTCA TCTGTCTTAGA TGAAAGGGT ATGTCTTAGA TGAAAAGGGT TGAAAAGGGT	ATTGCAACGG CGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG CGAAGGAAGA AGTGAAGAAGA AGTGAACAACGAA TCTGGGTCAC TCTGGGTCAC CAGCACGTGT ACCAATGAAA	120 180 240 300 360 420 480 540 600 660 720 780 840
50	Coding sequence of the control of th	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG CAGCGCGCCC TTGTCAGTGC ATGTAGAAC ATCGAAAC ATGACATATA ACAGATACAA	3036 21 CCCGGGCCAA AACGGGGGC TAGAAGAGCT CAGGAAATCC CGCTCGCCGC CTCTGTTCGG AGAAGTGCT AAATGAAGGT TGTCTCCCTC ACGGGGATAT TGTGTTTGAA ACTCTTCCCAA	31 CTCGGACAGT GCGCGACGCC CACCGGTCGC CGGGCCCAG TCCCCCGCC CGAGGGGTGA AGTGGGGAC AATATTCGAC CTCATTGCA GCTCGAAATT TCTGATTCAG AATGAAAGCT GCGAAGAAGC GCTCCAAAGA	TTGCTCATTT CGCACACACA GCGGCCGGGG AGCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGGA GCAGTTTCAC ACACGGTAAT CAGTCAGTCT ATGTCTTAGA TGAAAAGGT ATGTGTTCTC	ATTGCAACGG CGGGGGGAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCCTG CGAAGGAAGA AGTGAAGAAC AGGAAACCAA TCTGGGTCAC CAGCACGTCT ACCAATGAA ACCACCCTCT	120 180 240 300 360 420 480 540 600 720 780 840 900
50	Coding sequence of the control of th	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG CAGCGCGCCC TTGTCAGTGC ATGTAGAAC ATCGAAAC ATGACATATA ACAGATACAA	3036 21 CCCGGGCCAA AACGGGGGC TAGAAGAGCT CAGGAAATCC CGCTCGCCGC CTCTGTTCGG AGAAGTGCT AAATGAAGGT TGTCTCCCTC ACGGGGATAT TGTGTTTGAA ACTCTTCCCAA	31 CTCGGACAGT GCGCGACGCC CACCGGTCGC CGGGCCCAG TCCCCCGCC CGAGGGGTGA AGTGGGGAC AATATTCGAC CTCATTGCA GCTCGAAATT TCTGATTCAG AATGAAAGCT GCGAAGAAGC GCTCCAAAGA	TTGCTCATTT CGCACACACA GCGGCCGGGG AGCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGGA GCAGTTTCAC ACACGGTAAT CAGTCAGTCT ATGTCTTAGA TGAAAAGGT ATGTGTTCTC	ATTGCAACGG CGGGGGGAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCCTG CGAAGGAAGA AGTGAAGAAC AGGAAACCAA TCTGGGTCAC CAGCACGTCT ACCAATGAA ACCACCCTCT	120 180 240 300 360 420 480 540 600 720 780 840 900
50	Coding sequence of the control of th	uence: 37  11    CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCGAGG GATGGTGCAG CAGCGCGCC TTGTCAGTGC AGAATCATCC ATCTGGAAAG ACGGTACTGA ATGGACATGT ACAGATACAA ATCACACAC CAAGAAGGCA	3036 21   CCCGGGCCAA AACGGGGGC TAGAAGAGC CAGGAAATCC CGCTCGCCGG GCTGCCCGTG CTGCAGGGC CTCTGTTCGG AGAAGTGCTG AAATGAAGGT TGTCTCCCTC ACGGGGATAT TGTGTTTCAA ACTCTTCCAA ACCAAACCTC	31 CTCGGACAGT GCGCGACGCA CAGCGGCGG CTCCGGTCGC CGGGCCCGAG TCCCCCGCC CATATTCGAC ATATTCGAC TCTCATTGCA ACTCGAAATT TCTGATTCAG AATGAAAGCT GCGAAGAAGC GCTGCAAGAGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAA	TTGCTCATTT CGCACACACA GCGGGCCGTG GACGCCGGC GCTTATGGAA TCTGGATCCC TACAACGGGA GCAGTTTCAC ACACGGTAAT CAGTCAGTCT ATGTCATTAGA ATGTCTTAGA ATGTCTTAGA ATGTCTTAGA ATGTCTTAGA ATGTCTTAGA ATGTCTTAGA	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GGTCGCCTG CGAAGGAAGA AGTGAAGAGC AAGCAAAGAA GGAAACCCAC TCTGGGTCAC CAGCACGTGT ACCAATGAAA CCGGGGATCA ACCACCCTCT TCTGGAGCTG	120 180 240 300 360 420 480 540 660 720 780 840 900 960
50	Coding sequence of the control of th	uence: 37  11    CTTCCTAGTC CTTGTGCCAG ATGTGCAGG GATGGTGCAG GATGGTGCAG CAGCGCGCC TGCTCGCGCC TTGTCAGTGC ATGTGAAAC ACGGACTAT ACAGATACAA ATCACAACAC CAAGAAGGCA CAGAAACGCA	3036 21 CCCGGGCCAA AACGGCGGC CAGGAAATCC CGCTCGCGG CTGCCGTG CTGCAGGCC CTCTTTCGG AGAAGTGCT AAATGAAGGT TGTCTCCCTC ACGGGATAT TGTGTTTCAG ACTCATCCCA ACCAAACCTC TAAAAGAAG	31 CTCGGACAGT GCGCGACGGC CAGGGGGGC CTCCGGTCGC CGAGGGGTGA AGTGGGGAC AATATTCGA CTCAATATCGA GCTCGAAATT TCTGATTCAG GCTGAAGAG GCTGAAGAG GCTGCAAGGA ACCCTCAAGG ACCCTCAAGGA	TTGCTCATTT CGCACACACA GGGGCGTG GACGCCGGC GCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCCC ACACGGGA GCAGTTTCAC ACACGGTAAT CAGTCATTCTAGAA TGAAAAGGGT ATGTCTTAGA ATGACTATTA AAGATCTGGA	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCTG CGAAGGAAGA AGTGAAGAAG AGGAAACCAC TCTGGGTCAC TCTGGGTCAC ACCACCTCT TGTGGAGTCA ACCACCTCT TGTGGAGCTG AAAGGTAAG	120 180 240 360 420 480 540 660 720 780 840 900 960 1020
50	Coding sequence of the control of th	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTGCCGAGG GATGGTGCAG GATGTGCAG CAGCGCGCC TTGTCAGTC ATTGCAAAG ACGTACTGA ATGGAAAG ACGGTACTGA ATGGACATGT CAGAGAAGCA CAAGAAGACAC CAAGAAGCAC TAGACACCG TAGACATGC	21 CCCGGGCCAA AACGGCGGCC TAGAAGAGCT CAGGAAATCC CGCTCGCGG CTCGCAGGCC CTCTGTTCGG AGAAGTGCTG AAATGAAGGT TGTCTCCCTC ACGGGGATAT TGTGTTTGAA ACTCTTCCCA ACCAAACCTC TAAAAGAGA AGAGTTTCAG TAATCACGTT	31 CTCGGACAGT GCGCGACGCC CAGGGCGCC CTCGGTCGC CGGGCCCAA TCCCCCCCC CAATATTCGAC CTCATTGCA GCTCGAAATT TCTGATTCAG AATGAAAGC GCTGAAAGA ACCTCAAGA ACCTCAAGA ACCTCAAGA AGCAAGAGA	TTGCTCATTT CGCACACACA GCGGCCGTG GACGCCGGC AGCTGCTGCA GCTTATGGAA TCTGGATCCC TACAACGGGA GCAGTTTCAC ACACGGTAAT CAGTCATCTA ATGTCTTAGA TGAAAAGCGT ATGTGTTTCC AACTAAGTA AAGATCTGGA AAGATCACCACT	I ATTGCAACGG CGGGGGAAA CGCGCTCGGC CTGAAGGCAGAAGA AGTGAAGAAGA AGGAACCCAC TCTGGGTCAC CAGCACGTTA ACCACCTCT TGTGGGATCA ACCACCTCT TGTGGAGCTG AAAAAGTTAAG GAACATTAGG GAACATTAGG GAACATTCGG	120 180 240 300 420 480 540 600 720 780 840 900 960 1020
50 55 60	Coding sequence of the control of th	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTGCCGAGG GATGGTGCAG GATGTGCAG CAGCGCGCC TTGTCAGTC ATTGCAAAG ACGTACTGA ATGGAAAG ACGGTACTGA ATGGACATGT CAGAGAAGCA CAAGAAGACAC CAAGAAGCAC TAGACACCG TAGACATGC	21 CCCGGGCCAA AACGGCGGCC TAGAAGAGCT CAGGAAATCC CGCTCGCGG CTCGCAGGCC CTCTGTTCGG AGAAGTGCTG AAATGAAGGT TGTCTCCCTC ACGGGGATAT TGTGTTTGAA ACTCTTCCCA ACCAAACCTC TAAAAGAGA AGAGTTTCAG TAATCACGTT	31 CTCGGACAGT GCGCGACGCC CAGGGCGCC CTCGGTCGC CGGGCCCAA TCCCCCCCC CAATATTCGAC CTCATTGCA GCTCGAAATT TCTGATTCAG AATGAAAGC GCTGAAAGA ACCTCAAGA ACCTCAAGA ACCTCAAGA AGCAAGAGA	TTGCTCATTT CGCACACACA GCGGCCGTG GACGCCGGC AGCTGCTGCA GCTTATGGAA TCTGGATCCC TACAACGGGA GCAGTTTCAC ACACGGTAAT CAGTCATCTA ATGTCTTAGA TGAAAAGCGT ATGTGTTTCC AACTAAGTA AAGATCTGGA AAGATCACCACT	I ATTGCAACGG CGGGGGAAA CGCGCTCGGC CTGAAGGCAGAAGA AGTGAAGAAGA AGGAACCCAC TCTGGGTCAC CAGCACGTTA ACCACCTCT TGTGGGATCA ACCACCTCT TGTGGAGCTG AAAAAGTTAAG GAACATTAGG GAACATTAGG GAACATTCGG	120 180 240 360 420 480 540 660 720 780 840 900 960 1020
50 55 60	Coding sequence of the control of th	Lence: 37    CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCGAGG GATGGTGCAG GAGGTGCAG TGCTCAGTGC AGAATCATCC ATCTGAAAG ACGGACATGT GGGGACTTAT ACAGATACAA ATCACAACAC CAAGAAGGCA CAAGAAGGCA CAAGAAACAG CAAGACAACGG TAGAGATTGC	3036 21   CCCGGGCCAA AACGGGGGC TAGAAGAGCT CAGGAAATCC CGCTCGCCGC CTCTGCTCGG AGAAGTGCT AAATGAAGGT TGTCTCCGT ACGGGATAT TGTCTTCGT ACGGGGATAT TGTCTTCTTCAA ACTCTTCCAC TAAAAGAGAG AGAGTTTCAG TAAACAGAG TAATCACGTT AGTGTGAAAT	31 CTCGGACAGT GCGCGACGCC CACCGGCCCC CGGGCCCGAC CGACGGGTGA ACTGGGGACC AATATTCGAC CTCATTGCCA ACTGGAACAT TCTGATTCAG AATGAAAGCT GCGAAGAAG GCTCCAAGAA ACCCTCAAGA ACCCTCAAGA ACCACTCAAGGA AGCAAGTTTT GACAAGACAC	TTGCTCATTT CGCACACACA GCGGCCGGC AGCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGGA ACACGGTAAT CAGTCAGTTATA ACAGTCAGTTATA TGAAAAGGGT ATGTCTTAGA TGAAAAGGT ATGTCTTAGA AAGATCTGGA ACAGACCACT AATGCTCTGT	I ATTGCAACGG CGGGGGGAA CGCGAGGGCT CCGCTCGCCTGG GCTCGCCCTG GGAAGGAAGA AGTGAAGAA AGTGAAGAA CAGCACGTCTAGGGGTCAC CAGCACGTGT ACCAACGATAGAA ACCACCTCT TGTGGAGCTG AAAAGTTAAG AAAGTTAAG AAAGTTAAG AAAGTTAAG AAAGTTAAGAA AGTCAGACACCC	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1080 1140
50	Coding sequence of the control of th	uence: 37    CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG CAGCGCGCC TGCTCGCGCC AGAATCATCC AATCTGAAAG ACGGTACTGA ATGGACATGT ACAGATACAA ATCACAACAC CAGAAGGCA CAGACAACGG TAGACATCGC TAGGCATTGG TAGACATGGC TAGACATCGC TAGACATGGC TAGACATCGC TAGACATGGC TAGACATCGC TAGACATGGA	3036 21 CCCGGGCCAA AACGGCGGC TAGAAGAGCT CAGGAAATCC GCTCGCGGG CTCTGTTCGG AAATGAGGT TGTCTCCTC ACGGGATAT TGTCTTCAAA ACTCTTCCA ACCAAACCTC TAAAAGAGA TAATCACGT TAGTTTCAG TAATCACGTT AGTGTTCAA	31   CTCGGACAGT GCGCGACGCA CAGCGGCCCGAG TCCCGGCCC CGAGGGGTGA AGTGGGACC AATATTCGAC CTCATTGCA GCTCGAAATT TCTGATTCAG GCTGAAAAGCT GCGAAGAAGCA ACCCTCAAAGG ACCCTCAAAGG ACCCTCAAGG ACCACAGTTTT GACAAGGTA GACAAGTTTT GACAAGGAAAG TGGACGAAGA	TTGCTCATTT CGCACACACA GCGGCCGTG GACGCCGGC GCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC ACACGGTAAT CAGTCATTACAC TGAAAAGGGT ATGTCTTAGA TGAAAAGGGT ATGTCTTAGA ACACTCAGTCA ACACCCTAACT AAGACCACT AATGCTCTGA ACAGACCACT AATGCTCTT AAGACCACT TGAAGACCACT TGAAGACCTCT TGAAGCCTCTT	I ATTGCAACGG CGGGGGGAAA CGCGGTCGGC CTGAAGGCAGAAAA AGTGAAGAAA AGAAACCAC TCTGGGTCAC CAGCACCTTTTTGTGGAGTAAAAGTAA CCGGGGATCA ACCACCACCTTTTTTGTGGAGCTG AAAAGTTAAG AAAGTTAAG AACTTCAGAAAACTTCAGAAAAACTTCAGAAAAACTTCAGAAAAACTTAAG AAAAGTTAAAAAAATTCAGAAAAAAAAAA	120 180 240 300 360 420 680 660 660 720 780 840 900 1020 1020 1140 1200
50 55 60	Coding sequence of the control of th	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTGCCGAGG GATGGTGCAG CAGCGCGCC TTGTCAGTC ATGAAATCATCC ATCTGAAAG ACGATACTGA ATGGACATGT ACAGATACAA CAGACAACAC TAGACAACAC TAGACATGC	3036 21   CCCGGGCCAA AACGGCGGC TAGAAGAGCT CAGGAAATCC CGCTCGCGG CTCGCAGGCC CTCTGTTCGG AGAAGTGCT AATGAAGGT TGTCTCCTC ACGGGGATAT TGTGTTTCTGA ACCAAACCTC TAAAAGAGAG TAATCACGTT AGTGTTGGAA TGTGTTGGAA	31 CTCGGACAGT GCGCGACGG CAGCGGGGC CTCGGTCGC CGGGCCCGAG TCCCCCCC CAGGGGGTGA AGTCGGGAC ATTATTCGAC GCTCGAAATT TCTGATTCAG ATGAAAGGT GCGAAGAAG GCTCCAAGG ACCCTCAAGG ACCCTCAAGG AGCAAGGAA GACAAGTTTT GACATGGACA GTTATTCCC	TTGCTCATTT CGCACACACA GGGGGCGTG GACGCCGGC AGCTGCTGCA GCTTATGGAA TCTGGATCCC TACAACGGA ACACGGTAAT CAGTCATCA ACACGGTAAT CAGTCATCTAGA TGAAAAGCGT ATGTCTTAGA ATGATCTTCC CAACTAGTC AAGACCACT AATGCTCTGA ACAGACCACT AATGCTCTTGA ACAGACCACT AATGCTCTTCT AAGGCACCAC	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG CGAAGGAAGA AGTGAAGAAG AGGAAAGAA GGAAACCCAC TCTGGGTCAC CAGCACGTGT ACCAATGAAA ACCACCTCT TGTGGGGTCA TGTGAGCTG AAAGTTAAG AACACTGT AAAGTTAAG AACACTCT AAAAGTTAAG AAAATTAAG AAAATTAAG AACACTCTCGAAAA CACCGGCATG	120 180 240 360 420 480 660 660 720 780 840 900 1020 1080 1140 1200 1260
50 55 60	Coding sequence of the control of th	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTGCCGAGG GATGGTGCAG CAGCGCGCC TTGTCAGTC ATGAAATCATCC ATCTGAAAG ACGATACTGA ATGGACATGT ACAGATACAA CAGACAACAC TAGACAACAC TAGACATGC	3036 21   CCCGGGCCAA AACGGCGGC TAGAAGAGCT CAGGAAATCC CGCTCGCGG CTCGCAGGCC CTCTGTTCGG AGAAGTGCT AATGAAGGT TGTCTCCTC ACGGGGATAT TGTGTTTCTGA ACCAAACCTC TAAAAGAGAG TAATCACGTT AGTGTTGGAA TGTGTTGGAA	31 CTCGGACAGT GCGCGACGG CAGCGGGGC CTCGGTCGC CGGGCCCGAG TCCCCCCC CAGGGGGTGA AGTCGGGAC ATTATTCGAC GCTCGAAATT TCTGATTCAG ATGAAAGGT GCGAAGAAG GCTCCAAGG ACCCTCAAGG ACCCTCAAGG AGCAAGGAA GACAAGTTTT GACATGGACA GTTATTCCC	TTGCTCATTT CGCACACACA GGGGGCGTG GACGCCGGC AGCTGCTGCA GCTTATGGAA TCTGGATCCC TACAACGGA ACACGGTAAT CAGTCATCA ACACGGTAAT CAGTCATCTAGA TGAAAAGCGT ATGTCTTAGA ATGATCTTCC CAACTAGTC AAGACCACT AATGCTCTGA ACAGACCACT AATGCTCTTGA ACAGACCACT AATGCTCTTCT AAGGCACCAC	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG CGAAGGAAGA AGTGAAGAAG AGGAAAGAA GGAAACCCAC TCTGGGTCAC CAGCACGTGT ACCAATGAAA ACCACCTCT TGTGGGGTCA TGTGAGCTG AAAGTTAAG AACACTGT AAAGTTAAG AACACTCT AAAAGTTAAG AAAATTAAG AAAATTAAG AACACTCTCGAAAA CACCGGCATG	120 180 240 300 360 420 680 660 660 720 780 840 900 1020 1020 1140 1200
50 55 60	Coding sequence of the control of th	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG GATGGTGCAG CAGCGCCCC TTGTCAGTGC ATCTGGAAAG ATGACATCAT ACAGATACAA ATCACAACAG CAAGAAGGCA CAAGAAGGCA TAGGACAACGG TAGGACAACGG TAGGACAACGG TAGGACTACT ACAGATGCA CAGCACACGG TAGGACTACT TAGGCTTGGA ATGCCATGA TTAGGCTTGGA ATGCCATGA	3036 21 CCCGGGCCAA AACGGGGGC TAGAAGAGCT CAGGAAATCC CGCTCGCCGC CTCTGTTCGG AGAAGTGCT AAATGAAGGT TGTCTCCCT ACGGGATAT TGTGTTTGAA ACTCTTCCCA TAAAGAGAG AGAGTTTCAG TAATCACGT AGTGTGGAAT ATTCTGGAAT ATTCTGGAAT ATTCTGGAAT CTCAGTGGAAT TGTCAGTGGAAT CTCAGTGGAAT CTCAGTGGAAT CCCAGGGAAAC CCAGGCAGAC CCACGGCAGAC CCCGGGAGAC CCCGGGGAGAC CCCGGGGAGAC CCCGGGGAGAC CCCCGGGAGAC CCCCGGGAGAC CCCCGGGAGAC CCCCGGGAGAC CCCCGGGAGAC CCCCGGGAGAC CCCCGGGAGAC CCCCGGGAGAC CCCCGGGAGAC CCCCGGGGAGAC CCCCGGGGAGAC CCCCGGGGAGAC CCCCGGGGAGAC CCCCGGGAGAC CCCCGGGAGAC CCCCGGGAGAC CCCCGGGAGAC CCCCGGGAGAC CCCCGGGAGAC CCCCGGGCAGAC CCCCGGGCAGAC CCCCGGGCAGAC CCCCGGGCAGAC CCCCGGCAGAC CCCCGGGCAGAC CCCCGGCAGAC CCCCGCAGAC CCCCCGCAGAC CCCCCGCAGAC CCCCCCCC	31  CTCGGACAGT GCGCGCGCGC CTCCGGTCGC CGGGCCCAG TCCCCCGCC CGAGGGGGA AGTGGGGAC AATATTCAC AATATTCAC AATGAAAGCT TCGAAAAAGCT GCGAAGAAG ACCCTCAAAG ACCCTCAAGG AGCAAGAA ACCATTATTCGC CGGCAGAGAAG CGCTGCAAGAA CCTTCAAGG AGCAAGAAG CGTTGTAAGTTTTCCC CAGTTTTATTTCC CAGTCTTGGGG	TTGCTCATTT CGCACACACA GCGGCCGGG GACGCCCGGC GCTTATGGAA TCTGGATCCC TACAACGGGA ACACGGTAAT CAGTCATCA ACACGGTAAT CAGTCATCTA ATGTCTTAGA AAGATCTCA AAGACCACT AATGCTCTA AAGACCACT AATGCTCTTA AAGACCACT AATGCTCTTA AAGACCACT AATGCTCTT	ATTGCAACGG CGGGGGGAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG CGAAGGAAGA AGTGAAGAAC AGGAACCCAC TCTGGGTCAC CAGCACGTAT ACCAATGAA ACCACCTCT TGTGGAGCTG AAAGTTAAG GAACATTCAG ACCTCCCAATGAAA ACCACCTCT TGTGGAGCTG AAAGTTAAG CACCCCCCC AAGTCAGGAC ACCTCGCAAA ACTCGCACA ACCTCGCAAA ACTCGCACATCGCAAA ACATCGCACATCAGAC ACCTCGCAAA ACATCGCACATCA	120 180 240 300 360 420 540 660 720 780 900 960 1020 1080 1140 1200
50 55 60	Coding sequence of the control of th	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCGAGG GATGGTGCAG GATGGTGCAG TGCTCAGTGC AGAATCATCC ATCTGAAAG ACGTACTAA ACAGTACAA ATCACAACAC CAAGAAGGCA CAAGAACAC CAAGAACAC CAAGAATGCA CAAGATTGC TAGGCGTGGA TAGGCATGGA TAGGCATGGA TAGGCATGGA TAGGCATGGA TAGGCATGGA TAGGCATGGA TAGGCATGGA TAGGCATGGA TAGGCATGGA TTGGTGCAGC	21 CCCGGGCCAA AACGGGGGC TAGAAGAGCT CAGGAAATCC CGCTCGCCGC GCTGCCGGC CTCTGTTCGG AGAAGTGCTG AAATGAAGGT TGTCTCCCTC ACGGGGATAT TGTGTTCCGTC ACGAGACCTC TAAAAGAGAG TATTCTGGAC TATTCTGGAC TGTCTGGAAT TGTCTGGAAT CCTGAAGCTC CGTGACCCTG	31  CTCGGACAGT GCGCGCGCC CAGCGCCCC CAGCGCCCC AATATTCGAC AATATTCAA AATGAAAGCT GCGCAAGAAAA GCTCCAAAGA ACCCTCAAGG AGCAAGAAG ACCTCAAGG AGCAAGAAG CGTGCAAGAA CGCTCAAGG AGCAAGAAG CGTTCAAGG AGCAAGAAG CGCTCAAGG AGCAAGAAG CCTCAAGG CGCTCAAGG AGCAAGAAG CCTCAAGG AGCAAGAAG CCTCAAGG AGCAAGAGAAG CCTCAAGG AGCAAGAGAAG CCTCAAGG AGCAAGAAG CCCCCAGGCAAGA	TTGCTCATTT CGCACACAC GCGGCCGGC GACGCCGGC GCTTATGGAA TCTGGATCC TACAACGGGA GCAGTTTCAC ACACGGTAAT TCAGTCATACGTAA TCAGTCATACGATCC ATGTCTTAGA ACACTCATCA ACACACCACT ATGTCTTCAC ACACACCACT ATGTCTTCAC ACACACCACT AATGCTCTT TGAAGCTCT AATGCTCTT TGAAGCTCCACT TGAAGCTCCACT AAGGCTCCACT TGGGCCACAA	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GGACGAAGA AGTGAAGACA AGTGAAGACC TCTGGGTCAC TCTGGGTCAC ACCACGTCT TCTGGGACTC AAAAGTTAAA CCACCCTCT TCTGGAGCTG AAAAGTTAAG GAACATTCAC AACTTCAGGAC ACTCGCAAA CATCGGCATG ACTCGCAAA CATCGGCATG ACTTCGGCATG ACTTCGGGATCA CATCGGCATG AGCACTTCAC TTTCGGGATG CGACCATTCA CATCGGCATG GGACCATTCA TTTCGGGATG	120 180 240 300 360 420 600 660 660 720 780 840 900 960 1020 1140 1290 1140 1200 1320 1380
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	Coding sequilibrium control co	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG CAGCGCGCCC TTGTCAGTC ATGTCAGTC ATGTCAGTC ATGTCAGTC ATGGACATGT ACAGTACTA ATCACAACAC CAAGAAGGCA TAGAGATTGT TAGAGATTGC TAGAGATTGC TAGAGATGC TAGAGA	2036 21 CCCGGGCCAA AACGGCGGC CAGAAAACTCC CGCTCGCGGC CTCGCAGGCCCT CTGCTCGCGC CTCTGTTCGG AAATGACGT TGTCTCCCT ACGGGGATAT TGTCTTCCCA ACCAAACCTC TAAAAGAGA AGAGTTTCAG TAATCACGT AGTGTGGAGC CTCTGTTGGA CCAAACCTC TAAAAGAGA TGTCTTCCCA CCAAACCTC TAAAAGAGAC TGTCTGGACT CTGTCGGACCTC CGTGACCCTG GGGCTGACCCTG	31 CTCGGACAGT GCGCGACCGA GCGCCCGGCC CGAGGGGGA AGTGGGGACC AATATTCGAC GCTCGAAGT TCTGATTCAG GCTCGAAGAAG AATGAAAGCT GCGAAGAAGC GCTCCAAGG ACCTCCAAGG ACCTCCAAGG ACCATCGACA GCTCGAAGAAG CGTGCAAGAA CGCTGCAAGA CGCTAAGGA ACCTCAAGG ACCATCGACA GCAAGAAGATTTT CACATCGACA TGGAGGAAGA GCTTATTCCC CAGTCTGGGG GCACATGAGG TGTCAAATGG	TTGCTCATTT CGCACACACA GGGGCGTG GACGCCGGC GCTGCTGCA GCCCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGA GCAGTTTCAC ACACGGTAAT CAGTCATTCT ATGTCTTAGA TGAAAAGGGT ATGTGTTTCC ACAGACCACT AAGTCATCT AAGTCTCT AAGACCACT AATGCTCTGA ACAGACCACT AATGCTCTCT AAGGGCACAC GAATTGTCAA CGGTTGAGAA CGGTTGAGAA	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCTG CGAAGGAAGA AGTGAAGAAG AGGAAACCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC ACCACCTCT TGTGGAGCTG AAAGTTAAG GAACATTCAG AACTCAGCAC ACTCGGCATG AATCAGAA CCTGGCATG AACTCAGGAC TCTGGAAC TCTGGCATG AAGTCAGGAC TTTCGGCATG AAGTCAGGAC TTTCGGGATG AAGACCATTCG AAGTCAGGAC TTTTCGGGATG AAGACCATTCG AAGACCATTCG AAGACCATTCG AAGACCATTCG AAGAGGTTGC	120 180 240 300 360 420 540 660 720 780 900 960 1020 1080 1140 1200
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	Coding sequilibrium control co	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG CAGCGCGCCC TTGTCAGTC ATGTCAGTC ATGTCAGTC ATGTCAGTC ATGGACATGT ACAGTACTA ATCACAACAC CAAGAAGGCA TAGAGATTGT TAGAGATTGC TAGAGATTGC TAGAGATGC TAGAGA	2036 21 CCCGGGCCAA AACGGCGGC CAGAAAACTCC CGCTCGCGGC CTCGCAGGCCCT CTGCTCGCGC CTCTGTTCGG AAATGACGT TGTCTCCCT ACGGGGATAT TGTCTTCCCA ACCAAACCTC TAAAAGAGA AGAGTTTCAG TAATCACGT AGTGTGGAGC CTCTGTTGGA CCAAACCTC TAAAAGAGA TGTCTTCCCA CCAAACCTC TAAAAGAGAC TGTCTGGACT CTGTCGGACCTC CGTGACCCTG GGGCTGACCCTG	31 CTCGGACAGT GCGCGACCGA GCGCCCGGCC CGAGGGGGA AGTGGGGACC AATATTCGAC GCTCGAAGT TCTGATTCAG GCTCGAAGAAG AATGAAAGCT GCGAAGAAGC GCTCCAAGG ACCTCCAAGG ACCTCCAAGG ACCATCGACA GCTCGAAGAAG CGTGCAAGAA CGCTGCAAGA CGCTAAGGA ACCTCAAGG ACCATCGACA GCAAGAAGATTTT CACATCGACA TGGAGGAAGA GCTTATTCCC CAGTCTGGGG GCACATGAGG TGTCAAATGG	TTGCTCATTT CGCACACACA GGGGCGTG GACGCCGGC GCTGCTGCA GCCCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGA GCAGTTTCAC ACACGGTAAT CAGTCATTCT ATGTCTTAGA TGAAAAGGGT ATGTGTTTCC ACAGACCACT AAGTCATCT AAGTCTCT AAGACCACT AATGCTCTGA ACAGACCACT AATGCTCTCT AAGGGCACAC GAATTGTCAA CGGTTGAGAA CGGTTGAGAA	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCTG CGAAGGAAGA AGTGAAGAAG AGGAAACCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC ACCACCTCT TGTGGAGCTG AAAGTTAAG GAACATTCAG AACTCAGCAC ACTCGGCATG AATCAGAA CCTGGCATG AACTCAGGAC TCTGGAAC TCTGGCATG AAGTCAGGAC TTTCGGCATG AAGTCAGGAC TTTCGGGATG AAGACCATTCG AAGTCAGGAC TTTTCGGGATG AAGACCATTCG AAGACCATTCG AAGACCATTCG AAGACCATTCG AAGAGGTTGC	120 180 240 300 360 420 480 540 6600 6600 720 780 840 900 1020 1140 1200 1250 1320 1380 1440
50 55 60	Coding sequilibrium control co	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTGCCGAGG GATGGTGCAG GATGTGCAG CAGCGCGCC TTGTCAGTC ATCTGAAAG ACGTACTGA ATGAAAGA ATGACATGT CAAGAAGACAC CAAGAAGACAC TAGGCACTTAT TAGGCATGT ACAGATACAA ATCACAACAC TAGGCAGTG TAGGCAGTGGA ATGCCACCAGA CACCACCG TAGGCAGTGGA CTCCACCAGACAC CTCGCACCACGACACCG CTCGCACCACGACACCG CTCGCACCACGACACCG CTCCCACCACGACACCC CTCGCACCACGACACCCC CTCGCACCACGACACCCCCCCCCC	21 CCCGGGCCAA AACGGCGGC TAGAAGAGCT CAGGAAATCC CGCTCGCGG CTCGCGGG CTCGCAGGCC CTCTGTTCGG AGAAGTGCTG AAATGAAGGT TGTCTCCCTC ACGGGGATAT TGTCTTCCCA ACCAAACCTC TAAAAGAGAG AGAGTTTCAG AGAGTTTCAG TATTCAGGAT ATTTCTGGAAT ATTTCTGGAAT ATTTCTGGAAT ACTGTCAGTGGGACCCGG CAGGCCAGACCGGCAGACCGGCAGACCGGCAGACCGGCAGACCGGGGAGACCGGGGAGACGGGGGAGACGGCGG	31 CTCGGACAGT GCGCGACGCC CACGGCCGCC CGGGCCCGAC TCCCCCCCC CGAGGGGTGA AGTCGGGAC ATATTCGAC CTCATTGCA GCTCGAAATT TCTGATTCAG AATGAAGAC GCTCAAAGA ACCTCAAGA ACCTCAAGA AGCAAGATTT GACAAGACA GGTCTAAGACA TGGAGAAGA GGTTTATTCC CAGTCTGGGG GCACATGAGC TTGACAAGAC CTTCAATGGC CTGTCAATGGC CTGTCAATGGC CAGTCTGGGG GCACATGAGC TTGACATAGGC	TTGCTCATTT CGCACACACA GCGGGCGTG GACGCCGGC AGCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGA ACACGGTAAT CAGTCAGTCA ATGTCTTAGA ATGTCTTAGA ACAGTAGTC AACTAAGTA AAGATCTGGA ACAGACCACT AATGCTTTTC AAGGGACCACT AATGCTCTTAG ACAGACCACT CGAATTGTCAT TGGGCCACAA TCGGCCACAA TCAGCAGTTGAA TCAGCAGTTG	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG CGAAGGAAGA AGTGAAGAAGA AGGAAAGAA GGAAACCCAC TCTGGGTCAC CAGCACGTAT ACCAACTGAAA ACCACCTCT TCTGGGGTCAC AAAGTTAAG GAAACTTAG GAACATTCGG AAGTTAAG GAACATTCGG AAGTCAGGAT ACCACGATGT ACCACGAAA ACTTCGGAATG ACTTCGGAATG ACTTCGGAATG ACTTCGGAATG ACTTCGGAATG ACTTCGGAATG ACTTCGGAATG CATCGGAATA CATCGGCATG AGGAGGCTGC CAGCAGGAAG	120 180 240 300 360 420 540 660 720 780 960 1020 1140 1200 1320 1320 1340 1500
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	Coding sequilibrium control co	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG GATGGTGCAG CAGCGCCCC TTGTCAGTGC ATCTGGAAAG ATGAACATCATCA ATGACATACA ATGACAACAC CAAGATACAA CAAGATACAA CTAGCAACAC TAGGCATGGA ATGCCATGA ATGCCATGCA TAGGCATGGA CCAGCATGGA CCAGCATGGA CCAGCATGGA CCAGCATGGA CCTCCATGA CTGGCAGGC CTGGACAGG CTTCCACGG CCTCCATGA	3036 21 CCCGGGCCAA AACGGGGCC TAGAAGAGCT CAGGAAATCC CGCTCGCCGC CTCTGTTCGG AGAAGTGCT AGAAGAGT TGTCTCCCT ACGGGATTTCAGT AACTCTTCCA ACCAAACCTC TAAAAGAGAG AGAGTTTCAG TATTCTGGAG CCTGTTCGGAGGC CTGTGTTCGACGG CACGGCAGAC CGTGACCTG GGGCTGTAGC GGGCTGTAGC	31  CTCGGACAGT GCGCGCGCC CTCGGTCGC CGGGCCGAG ACTGGGACAC AATATTCGAC ATTATTCAC AATGAAAGCT TCTGAAAAGCT TCTGAAAAGCT GCGAAGAAGA ACCCTCAAGG AGCAAGAAG ACCATTATTCGAC CTCATTGCCC CTCATTGCCC CTCATTGCCC CTCATTGCAC AATTATTCAG AATTATTCAG AATTATTCAG ACTCAAAGA CCTCAAAGA ACCATTTATTTCC CAGTCTTGGGG GCACATGAGC TGGACAAGAA CTTATTTCCC CAGTCTTGGGG CCCATGTGT GCGAGTGTGCCC	TTGCTCATTT CGCACACAC GCGGCCGTG GACGCCGGC GCTTATGGAA TCTGGATCC TACAACGGGA GCAGTTTACAC ACACGGTAAT TAGGTCT ATGTCTTAGA ACAGTTAT AAGATCTGA ACAGTCTCT TGAACCGGA CCACTTATGA ACAGTCTCT TGAACGCACAC CGATTGCT TGAAGCTCT TGAAGCTCT TGAAGCTCT TGAAGCTCT TGAAGCTCT TGAAGCTCT TGAAGCTCT TGAAGCTTCT TGAGCACACAC CGGTTTAGAAA TCAGCAGTTG TGTTTAACCT TGTTTAACCT	I ATTIGCAACGG CGGGGGGAAA CGCGAGGGAAGAAAAAAAAAA	120 180 240 300 360 420 540 660 720 780 900 960 1020 1080 1140 1200 1260 1320 1380 1440 1500 1500
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	Coding sequilibrium control co	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGTGCAG CAGCGCGCC TGCTCGCGCC TGTCAGTC ATGTCAGTC ATGTCAGTC ATGTCAGTC ATGTCAGTC ATGGACATGT ACAGATACAA ATCACAACAC CAGACAACAC CAGACAACAC TAGACATC TAGACATGC TAGACATGC TAGACATGC TAGACATGC TAGACATCC TAGACATGC TAGACATCC TAGACATGC TAGACATGC CTAGACATGC CTAGACATCGC CTAGACATGC CTAGACATGC CTAGACATGC CTAGACATGC CTAGACATGC CTAGACATGTC CTAGACATGC CTCCACGG CTAGGCCTGGA CTCGCGGGGCCCA	3036 21 CCCGGGCCAA AACGGCGGC TAGAAGAGCT CAGGAAATCC CGCTCGCGGC CTCGTGCGG GTGCCCGTG CTGCTGGGGC TGTGTTCGG AAATGAGGT TGTCTCCTC ACGGGATAT TGTGTTTGAA ACTCTTCCCA ACCAAACCTC TAAAAGAGG TAATCAGGT TAGTGGGGCACAC CGTGGCCGGGGACAC CGTGACCCTG GGGCTGTAGC GGGCTGTAGC GGAGCCCTG GGGCTGTAGC GGAGCCCTG GAAGGAATC	TCGGACAGT CTCGGACAGT CAGGGCGCC CTCCGGTCGC CGAGGGGTGA AGTGGGGACC AATATTCGAC CTCATTGCAC GCTCGAAATT TCTGATTCAG GCTGAAAGAG ACCTCAAGG ACCACAGTTT GACAAGGAA GCACAGTTT GACATGACAC TGTGATAGC TGGAGAAGAT TGTGATAGC TGCAAAGAT TCTCATTGCAC TGCAAAGAT TCTCATTGCAC TGCAAAGATTTT GACATGACA TGCACAAGGAA TGCACAAGTTT GACATGTGC TGCAAATGG TGCATGTGC TGCAAATGG CCCATGTGT GGGGGTGTGC AACAGATTTG	TTGCTCATTT CGCACACAC GCGGCCGTG GACGCCGGC GCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC GCATTATGAA CAGCGTAAT CAGTCAGTCAT TGAAAAGGGT ATGTCTTAGA ACAGACCACT AATGCTCTT AAGGCACCACT AATGCTCTT AAGGCACCACT TGAAGACCACT TGAAGACCACT TGAAGACCACT TGAAGACACACT TGGACCACT TGGACCACT TGGACGACT TGGACAGACCACT TGGACGACT TGGAAGAAGAC TCTTTAACCT TGGAAGAAGAC TGGTTTAACCT TGGAAGAAGAC TGGTTTAACCT TGGAAGAAGAC TGGTTTAACCT TGGAAGAAGA	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCGCTCGGC CTGAAGGCCG GGAAGGAAGA AGTGAACGAC AGTGAACACAC TCTGGGTCAC CAGCACGTT ACCAATGAAA CCAGCACGTT TGTGGAGCTG AAAGTTAAG GAACATTCAG AACTTCGCAAA CATCGCACA TCTTGGAGCTG AAAGTTAAG GAACATTCGC AAGTCAGGAC ATTCGCAAA CATCGCATG AATGAACATTCGCAAA CATCGCATG AAGTTCAGGAC CATCGCAAA CATCGCAGAA CATCGCAGAC TTTTCGGGATG AGGAGGCTGC CAGCAGGAAG ACCACGAGAGG ACCACGAGAGG ACCAGGAAGTC AGGAGGAGTC AGAGGAGTTC AGAGGAGTTC AGAGGAGTTC	120 180 240 300 360 420 600 660 720 780 840 900 1020 1140 1200 1140 1320 1380 1440 1560 1620
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	Coding sequilibrium control co	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGTGCAG CAGCGCGCC TGCTCGCGCC TGTCAGTC ATGTCAGTC ATGTCAGTC ATGTCAGTC ATGTCAGTC ATGGACATGT ACAGATACAA ATCACAACAC CAGACAACAC CAGACAACAC TAGACATC TAGACATGC TAGACATGC TAGACATGC TAGACATGC TAGACATCC TAGACATGC TAGACATCC TAGACATGC TAGACATGC CTAGACATGC CTAGACATCGC CTAGACATGC CTAGACATGC CTAGACATGC CTAGACATGC CTAGACATGC CTAGACATGTC CTAGACATGC CTCCACGG CTAGGCCTGGA CTCGCGGGGCCCA	3036 21 CCCGGGCCAA AACGGCGGC TAGAAGAGCT CAGGAAATCC CGCTCGCGGC CTCGTGCGG GTGCCCGTG CTGCTGGGGC TGTGTTCGG AAATGAGGT TGTCTCCTC ACGGGATAT TGTGTTTGAA ACTCTTCCCA ACCAAACCTC TAAAAGAGG TAATCAGGT TAGTGGGGCACAC CGTGGCCGGGGACAC CGTGACCCTG GGGCTGTAGC GGGCTGTAGC GGAGCCCTG GGGCTGTAGC GGAGCCCTG GAAGGAATC	TCGGACAGT CTCGGACAGT CAGGGCGCC CTCCGGTCGC CGAGGGGTGA AGTGGGGACC AATATTCGAC CTCATTGCAC GCTCGAAATT TCTGATTCAG GCTGAAAGAG ACCTCAAGG ACCACAGTTT GACAAGGAA GCACAGTTT GACATGACAC TGTGATAGC TGGAGAAGAT TGTGATAGC TGCAAAGAT TCTCATTGCAC TGCAAAGAT TCTCATTGCAC TGCAAAGATTTT GACATGACA TGCACAAGGAA TGCACAAGTTT GACATGTGC TGCAAATGG TGCATGTGC TGCAAATGG CCCATGTGT GGGGGTGTGC AACAGATTTG	TTGCTCATTT CGCACACAC GCGGCCGTG GACGCCGGC GCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC GCATTATGAA CAGCGTAAT CAGTCAGTCAT TGAAAAGGGT ATGTCTTAGA ACAGACCACT AATGCTCTT AAGGCACCACT AATGCTCTT AAGGCACCACT TGAAGACCACT TGAAGACCACT TGAAGACCACT TGAAGACACACT TGGACCACT TGGACCACT TGGACGACT TGGACAGACCACT TGGACGACT TGGAAGAAGAC TCTTTAACCT TGGAAGAAGAC TGGTTTAACCT TGGAAGAAGAC TGGTTTAACCT TGGAAGAAGAC TGGTTTAACCT TGGAAGAAGA	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCGCTCGGC CTGAAGGCCG GGAAGGAAGA AGTGAACGAC AGTGAACACAC TCTGGGTCAC CAGCACGTT ACCAATGAAA CCAGCACGTT TGTGGAGCTG AAAGTTAAG GAACATTCAG AACTTCGCAAA CATCGCACA TCTTGGAGCTG AAAGTTAAG GAACATTCGC AAGTCAGGAC ATTCGCAAA CATCGCATG AATGAACATTCGCAAA CATCGCATG AAGTTCAGGAC CATCGCAAA CATCGCAGAA CATCGCAGAC TTTTCGGGATG AGGAGGCTGC CAGCAGGAAG ACCACGAGAGG ACCACGAGAGG ACCAGGAAGTC AGGAGGAGTC AGAGGAGTTC AGAGGAGTTC AGAGGAGTTC	120 180 240 300 360 420 600 660 720 780 840 900 1020 1140 1200 1140 1320 1380 1440 1560 1620
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	Coding sequilibrium control co	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG GATGGTGCAG CAGCGCGCC TTGTCAGTC ATGAAATCATCC ATCTGAAAG ACGTACTGA ATGACATGT ACAGATACAA ATCACAACAC TAGAGATGT GGGGACTTAT ACAGATACAA ATCACAACAC TAGAGATGC TAGAGATGC TAGAGATGC TAGAGATGC TAGAGATGC TAGAGATGC TTGGTGCAGC CACTGGACAGC CCACTGGACAG CTTCCACCGG CCAGCCTGGA TCGGGGGCCAG AGCCAGAGGGA TCGGGGGCCAG AGCCAGAGGGA	3036 21 CCCGGGCCAA AACGGCGGC CAGAAAACC CGCTCGCGG GCTCGCGGG CTCGCAGG CTCGCAGGC CTCTGTTCGG AGAACTGCT AAATCACGT TGTCTCCCT ACGGGGATAT TGTCTTCCCA ACCAAACCTC TAAAACAGAG TAATCACGT AGTGTGGAG CACGGCAGAC CGTGCCGTG CGTGCCCTG CGTACCCTG GGACTTTCAGGG GGACTGTTCAGGG GGACTGTAGCG GGACTGTAGCG GAAAGGATG GAAAGGATG GAAAGGATG GAAAGGATG GAAAGTGTGGG ATGTAGGAA	31   CTCGGACAGT GCGCGACGGC CAGGGCGCAC CAGGGGCCCAG TCCCCCCCCC CGAGGGGTGA AGTGGGGACC AATATTCGAC GCTCGAAATT TCTGATTCAG AATGAAAGCT GCGAAGAAG ACCCTCAAGG ACGCAAGAAG AGCAAGAAG GACAAGATTT GACATGGCA GCTCAAGG TGGAGAAGA GCTTATTCCC CAGTCTGGGG TGTCAAATG CCCATGGTGT CAACAGATTTCC CAGTCTGGGG CCCATGGTGT CGAACAGATTTG CAACAGATTTG CAACAGATTTG CAACAGATTTG CACAGATTGC AACAGATTTG CACGCTGCACA	TTGCTCATTT CGCACACACA GCGGCGGGG GACGCCGGC GCTTATGGAA TCTGGATCAC ACACGGGA GCAGTTTCAC ACACGGTAAT CAGTCATTTCAC ACACGGTAAT TGAAAAGGGT ATGTCTTTAG ACACTAAGTA AAGATCTGGA ACAGACCACT AATGCTCTGGA ACAGACCACT AATGCTCTGGA ACAGACCACT AATGCTCTGT TGAAGCTTCTGT TGAAGCTTCTGT TGAAGCTTCTGT TGAAGCTTCTGT TGAAGCTTCTGT TGAAGCTTCTTTTCACCTT TGGGCACAAT TCGGCACAAT TCGGCACAGA TCAGCAGTTGTTTAACCTT TGGAAGAAGG	ATTGCAACGG CGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG CGAAGGAAGA AGTGAAGAAGA AGGAAAGAA GGAAACCCAC TCTGGGTCAC CAGCACGTCT TGTGGAGCTC TGTGGAGTCA ACCACCTCT TGTGGAGCTG AAAGTTAAG GAACATTCAG CATCAGCATT ACTGCAATGAAA CCTGCAATGAAA CATCGGCATG AAAGTTAAG GAACATTCCG AAGTCAGGAT CATCGGCATG ACTCGGCAAA CATCGGCATG CAGCAGGATG CAGCAGGAAGTC CAGCAGGAAGTC CAGCAGGAAGTC CAGCAGGAAGTTC CAGCAGGAAGTC CAGCAGAGTC CAGCAGAGC CAGCAGAGTC CAGCAGAAGTC CAGCAGAGCT CAGCAGAGCT CAGCAGAGC CAGCAGAGC CAGCAGAGC CAGCAGA	120 180 240 360 420 480 660 660 720 780 840 900 1020 1140 1200 1260 1320 1440 1500 1500 1620 1680
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	Coding sequence of the control of th	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG GATGGTGCAG CAGGCGCCCC TTGTCAGTGC ATCTGGAAAG ACGGTACTGA ATGACATCAC ATCACAACAC CAAGAAGGCA CAAGAAGGCA CTGCCATGA ATCACAACAC CAGCATCCATGA ATCACAACAC CAGCATGCAG CTTGCACGG CTCCATGA CTTGGCAGGC CTTGCACGG CTTCCACGG CTTCGACGGGCCAA AGCCAGAGGAG CTTGTGGCGCCC CTTGGTGGCGCCCAAGCCAGGGGCCAAGCCAGGGGCCAAGCCTGGAGGCAGCCTGGAGCCAGGGGCCAAGCCAGGGGACCAAGCCAGGGGACCAAGCCAGGGGACCAACCAGGGGACCAAGCCAGGGGACCAAGCCAGGGGACCAAGCCAGGGGACCAAGCCAGGGGACCAAGCCAGGGGACCAAGCCAGGGGACCAAGCCAGGGGACCAAGCCAGGGGACCAAGCCAGGGACCACGTGTGTGCGCCC	3036 21 CCCGGGCCAA AACGGGGGC TAGAAGAGCT TAGAAGAGCT CAGGAAATCC CGCTGCCGG CTTGTTCGG AGAAGTGCT AAATGAAGGT TGTCTCCCTC ACGGGGATAT TGTGTTTGAA ACTCTTCCCA ACCAAACCTC TAAAAGAGA AGAGTTTCAG TAGTGTGGAAT ATTTCTGGAC CGTGCCCTG GGGCTGTACCTG GGACCTG GGACCTG GGACCTG GAAGGTTTCAG ACAGGAATCACGT AGAGTTTCAGTAGAT ATTTCTAGTAGAT ATTTCTAGTAGAT ATTTCTAGTAGAT AGAGTTTTGG AAAGGAATG	31   CTCGGACAGT GCGCGACGCA CAGCGGCGCCC CAGCGGCCCAGCA AGTCGGGCCC CGAGGGGTGA AGTCGGGACC AATATTCGAC GCTCGAAATT TCTGATTCAG AATGAAAGCT GCGAGAAGA ACCCTCAAGG AGGCAGAGA AGCAAGATTTT GACATGGCA TGGAGAAGAG CCTCAAGG AGGCAAGAG CCTCAAGG AGGCAAGAGA CCCTCAAGG AGGCAAGAGA TGGAGGAAGA TGCATGACA TGGAGGAAGA GCTTAATTTC CAGTCTGGGG GCACATGAGC TGTCAAATGG CCCATGGTGT GGGGTTGCC AACAGATTTG CGCTCCTCGAG TGCTGCTGCAA	TTGCTCATTT CGCACACACA GCGGCCGTG GACGCCGGC AGCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCCC ACACGGGA ACACGGTAAT CAGTCATCT ATGTCTTAGA ACAGTCATCT ATGTCTTAGA ACAGTCATCT AAGTCATCT TGAACTCATCT TGAACTCTTC AATGTCTTCA ACAGTCATCT TGAACTCTCT TGAAGTCTCT TGGACTCTCT TGGACACAC TGGACACACAC ACTCACACACACACACACACACACACACACA	ATTGCAACGG CGGGGGAAA CGCGGGGGCT CCCGCTCGCC CTGAAGGCCG CGAAGGAAGA AGTGAAGAAGA AGTGAACACCAC TCTGGGTCAC CAGCACGTAT ACCAACGAAT ACCACCTCT TGTGGGTCAC AACATGAAA ACCACCTCT TGTGGACTGA AAAAGTTAAG GAACATTAGG AACATTCGG AACTTCGGATG ACCTCGCAAA CATCGGCATG ACCTCGCAAG CATCGGAAG CATCGGAAG CATCGGAAG CATCGGAAG CATCGGAAG CATCGGAAG CATCGGAAG CATCGGAAG CATCGGAAG CAGGAGGATG AGGAGGCTGC AGGAGGCTGC AGGAGGATG CAGCAGGAAG CCTGCAAGAGG CCGGAAGTCC GAAGCCTGCA	120 180 240 300 360 420 540 660 720 780 900 960 1020 1140 1260 1320 1380 1440 1500 1560 1680 1740
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	Coding sequilibrium control co	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG GATGGTGCAG CAGCACCCC TTGTCAGTGC AGAATCATCC ATCTGAAAAG ATGACATACA ATGACATACA CAAGATACAA CAAGATACAA CTAGCATACAA CTAGCATGCAG TTGGCGCGC TTGGCGCGCC CTGTCAGCAG CTGGCAGGACACGG CTTCCACCGG CTGGCACGAGGAACACGC CTCCATGAA CTCGCAGGACAACGC CTCCATGAA CTCGCAGGACGAGGAACACGC CCAGCCTGGACAGGCACGAGGAACACGC CCAGCCTGGACCAG CCAGCCTGGACCAG CCAGCCTGGACCAG CCAGCCTGGACCAG CCAGCCTGGACCAG CCAGCCTGGACCAG CCAGCCTGGACCAG CCAGCCTGGACCAG CCAGCGGACCAC CCAGCGGACCAC CCAGCGGACCAC CCAGCGGACCAC CCAGCGGACCAC CCAGCGGGACCAC CCAGCGGACCAC CCAGCGGACCAC CCAGCGGGACCAC CCAGCGGGACCAC CCAGCGGACCAC CCAGCGGGACCAC CCACGGGGACCAC CCACGGGGACCAC CCACGGGGACCAC CCACGGGGACCAC CCACGGGACCAC CCACGGGACCAC CCACGGGACCAC CCACGGGACCAC CCACGCGGACCAC CCACGGGACCAC CCACGCGGACCAC CCACGCGGACCAC CCACGCGGACCAC CCACGCGACCAC CCACGCGACCAC CCACGCGACCAC CCACGCGACCAC CCACGCACCAC CCACCAC CCACCAC CCACCAC CCACCAC CCACCA	3036 21 CCCGGGCCAA AACGGGGCCAA AACGGGGGC TAGAAGAGCT CAGGAAATCC CGCTCGCGGC CTCTGTTCGG AGAAGTGCT AAATGAAGGT TGTCTCCCCA ACCGAGACT TAGAACACTC TAAAAGAGAG TAATCACGT AATCACGT AGTGTGGAAT ATTTCTGGAC CGCGCAGAC CGTGACCTG GGGCTGTAGC GGACCTG GGAACTTC GGAAGGTTAGA CATGGACATG CACATGGACCTG CAAAGCATC	31  CTCGGACAGT GCGCGCGCC CAGGGCCGAG ACTCGGCCC CAGGGCCGAG ACTCGGGACA ACTCGGACC AATATTCAC ACTCATTGCC GCTCCAAAGA ACCCTCAAAGA ACCCTCAAGG AGCAAGAAGC GCTGCAAAGA CCTCAAAGAC CTCATTGCC GCTGCAAAGA CCTCAAGG ACCAAGTTT GACATGGAGAAG CCAGTTTATTCC CAGTCTGGGG CCAACAGTTT CACATGGGG CCAACAGTTT CACATGGGG CCAGTCTGGGG CCCATGGTGT CGCGCTGCC AACAGTTTT CGCTGCTGCA TGCGCGCTGCAACAGTTTT CGCTGCTGCAG TGCTGCTGCAG TGCTGCTGCAG TGCTGCTGCAG TGCTGCTGCAG TGCTGCTGCAG TGCTGCTGCAG TGTGAACTCCC	TTGCTCATTT TGGCTCATTT CGCACACACA GCGGGCCGTG GACGCCGGC GCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCCC ACACGGTAAT TCAGCTCATTCACA ACACGGTAAT TCAGTCATCTTAGA ACATCATCTTAGA ACACACCACT TGAACACCACT TGAACCACT TGAACTCTT AATGCTCTT AATGCTCTT AAGGCTTCT AAGGCTCTCT TGAAGCTTCT TGGGCCACAA CGGTTGAGAA TCAGCAGTT TGGGACAAC CGTTTAACCT TGGAAGAACG ATTGCCACCAC ACTGCCAGCT CAGAGTTCTC CAGAGTTCTC CAGAGTTCTC CAGAGTTCTC	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCTG CGAAGGAAGA AGTGAAGACA AGGAAACCCAC TCTGGGTCAC CAGCACGTGT ACCAATGAAA CCAGCCTCT TGTGGGCTG AAAGTTAAG GAACATTCGG AACATTCGGAAC TCTCGGACGAC ACCTCCTCT TCTTGGAGCTG AAAGTTAAG CAACACTTCT TTTGGAGCTG AACATTCGGAAA CATCGGCATG ACCACGAGAAC CATCGGCATG CGACCAGGAGC TCTTCGGATG AGGAGGCTGC CGCCAGGAGGT CCTGCAGAGAC CCTCGCAGAGC CCTCTGCACAC CCTCGCAGGAGCTGC CCGCAGGAGTC CCTTACCCTG GAAGGCTGCA CACAGGGGCCC	120 180 240 360 420 480 660 660 720 780 840 900 1020 1140 1200 1260 1320 1440 1500 1500 1620 1680
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	Coding sequilibrium control co	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG GATGGTGCAG CAGCACCCC TTGTCAGTGC AGAATCATCC ATCTGAAAAG ATGACATACA ATGACATACA CAAGATACAA CAAGATACAA CTAGCATACAA CTAGCATGCAG TTGGCGCGC TTGGCGCGCC CTGTCAGCAG CTGGCAGGACACGG CTTCCACCGG CTGGCACGAGGAACACGC CTCCATGAA CTCGCAGGACAACGC CTCCATGAA CTCGCAGGACGAGGAACACGC CCAGCCTGGACAGGCACGAGGAACACGC CCAGCCTGGACCAG CCAGCCTGGACCAG CCAGCCTGGACCAG CCAGCCTGGACCAG CCAGCCTGGACCAG CCAGCCTGGACCAG CCAGCCTGGACCAG CCAGCCTGGACCAG CCAGCGGACCAC CCAGCGGACCAC CCAGCGGACCAC CCAGCGGACCAC CCAGCGGACCAC CCAGCGGGACCAC CCAGCGGACCAC CCAGCGGACCAC CCAGCGGGACCAC CCAGCGGGACCAC CCAGCGGACCAC CCAGCGGGACCAC CCACGGGGACCAC CCACGGGGACCAC CCACGGGGACCAC CCACGGGGACCAC CCACGGGACCAC CCACGGGACCAC CCACGGGACCAC CCACGGGACCAC CCACGCGGACCAC CCACGGGACCAC CCACGCGGACCAC CCACGCGGACCAC CCACGCGGACCAC CCACGCGACCAC CCACGCGACCAC CCACGCGACCAC CCACGCGACCAC CCACGCACCAC CCACCAC CCACCAC CCACCAC CCACCAC CCACCA	3036 21 CCCGGGCCAA AACGGGGCCAA AACGGGGGC TAGAAGAGCT CAGGAAATCC CGCTCGCGGC CTCTGTTCGG AGAAGTGCT AAATGAAGGT TGTCTCCCCA ACCGAGACT TAGAACACTC TAAAAGAGAG TAATCACGT AATCACGT AGTGTGGAAT ATTTCTGGAC CGCGCAGAC CGTGACCTG GGGCTGTAGC GGACCTG GGAACTTC GGAAGGTTAGA CATGGACATG CACATGGACCTG CAAAGCATC	31  CTCGGACAGT GCGCGCGCC CAGGGCCGAG ACTCGGCCC CAGGGCCGAG ACTCGGGACA ACTCGGACC AATATTCAC ACTCATTGCC GCTCCAAAGA ACCCTCAAAGA ACCCTCAAGG AGCAAGAAGC GCTGCAAAGA CCTCAAAGAC CTCATTGCC GCTGCAAAGA CCTCAAGG ACCAAGTTT GACATGGAGAAG CCAGTTTATTCC CAGTCTGGGG CCCATGGTGT GGGGTGTGCC AACAGTTTT CGCTGCTGCA ACCAGTTTT CGCTGCTGCA CGCTGCTGCAC CGCTGCTGCC CAGTCTTCCACGTGT CGCTGCTGCAC CGCTGCTGCAC CGCTGCTGCAC CTCTGTGAG CTGTGAAGC TGTGAACCTCCC	TTGCTCATTT TGGCTCATTT CGCACACACA GCGGGCCGTG GACGCCGGC GCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCCC ACACGGTAAT TCAGCTCATTCACA ACACGGTAAT TCAGTCATCTTAGA ACATCATCTTAGA ACACACCACT TGAACACCACT TGAACCACT TGAACTCTT AATGCTCTT AATGCTCTT AAGGCTTCT AAGGCTCTCT TGAAGCTTCT TGGGCCACAA CGGTTGAGAA TCAGCAGTT TGGGACAAC CGTTTAACCT TGGAAGAACG ATTGCCACCAC ACTGCCAGCT CAGAGTTCTC CAGAGTTCTC CAGAGTTCTC CAGAGTTCTC	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCTG CGAAGGAAGA AGTGAAGACA AGGAAACCCAC TCTGGGTCAC CAGCACGTGT ACCAATGAAA CCAGCCTCT TGTGGGCTG AAAGTTAAG GAACATTCGG AACATTCGGAAC TCTCGGACGAC ACCTCCTCT TCTTGGAGCTG AAAGTTAAG CAACACTTCT TTTGGAGCTG AACATTCGGAAA CATCGGCATG ACCACGAGAAC CATCGGCATG CGACCAGGAGC TCTTCGGATG AGGAGGCTGC CGCCAGGAGGT CCTGCAGAGAC CCTCGCAGAGC CCTCTGCACAC CCTCGCAGGAGCTGC CCGCAGGAGTC CCTTACCCTG GAAGGCTGCA CACAGGGGCCC	120 180 240 300 360 420 540 660 720 780 900 960 1020 1140 1260 1320 1380 1440 1500 1560 1680 1740
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	Coding sequilibrium control co	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGTGCAG GATGTGCAG CAGCGCGCC TTGTCAGTC ATGTCAGTC ATGTCAGTC ATGTCAGTC ATGGACATGT ACAGTACTA ATGACATACAA CAAGAAGGC TAGGACATGT TAGGCTGGA CTGCCATGA CTTCCACGG CAGCCTGGA CTTCCACGG CTCGCAGGA CTTCCACGG CTCGCCTGGA CTTCGACGG CTCGCCTGGA CTCGGCCCG CGCGGGCCCA	2036 21 CCCGGGCCAA AACGGCGGC CTAGAAGAGCT CAGGAAATCC CGCTCGCGG CTCGCAGGC CTCTGTTCGG AGAAGTGCTG AAATGAAGGT TGTCTCCCTC ACGAGGATAT TGTGTTTCAA ACTCTTCCCAA ACCAAACCTC TAAAAGAGA TATTCAGGT TATTCAGGT TGTCTGGAAGCC CGTGGCGGGCAGAC CGTGACCCTG GGGCTGTAGCG GAAGTGTGG ATGTAGGG ATGTAGGG ATGTAGGGCAGAC CGTACCCTG CGAGAGCTCCCCCCCCCC	31 CTCGGACAGT GCGCGACGGC CTCCGGTCGC CGGGCCCGAC GCGCCCCGCCC	TTGCTCATTT CGCACACACA GCGGCGTG GACGCCGGC GCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGA GCAGTTTCAC ACACGGTAAT CAGTCAGTCT ATGTCTTTAGA ACATAAGGT AAGACCACT AATGCTCTG AAGACCACT AATGCTCTC AAGGCACCACT AATGCTCTC AAGGCACCAC TGGAAGAAG CGTTGAGAA CGGTTGAGAA CGGTTCACCACCAC TGGAAGAAGG ATGCCACCAC ACTGCCACCAC ACTGCCACCAC ACTGCCAGCTTCA	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GGAAGGAAGA AGTGAAGAGA AGTGAAGAGA AGGAAACCCAC TCTGGGTCAC CAGCACGTCT TGTGGAGTCA ACCACCTCT TGTGGAGCTG AAAGTTAAG AACATTCAG AACATCACAC TCTGGAGTCA ACCACCTCT TGTGGAGCTG AAAGTTAAG GAACATTCGG AAGTCAGGAC TCTTCGGAAT CCTCGCAAA ACTCGGCATG ACGCAGTGT ACGACGATTCGG CAGCAGGAGT CTTTCGGGATG CAGCAGGAGT CCTGCAAA CCTCGGAAG CCTCGCAAA CCTCGGAAG CCTCGCAAG CCTGCAGAGGCTGC CAGGGAGTGT CCTGTACCCTG GAAGCCTTGCA CACAGGGGCC CACAGGGGCC CACAGGGGCC CACAGGGGCC CACAGGGGCC CACAGGGGCC CACAGGGCC CACAGGGGCC CACAGGGGCC CACAGGGGCC CACAGGGGCC CACAGGGGCC CACAGGGCC CACAGGGGCC CACAGGGCC CACAGGGGCC CACAGGGCC CACAGGCC CACAGGGCC CACAGGGCC CACAGGCC CACAGCC CACAGGCC CACAGCC CACAGGCC CACAGGCC CACAGGCC CACAGGCC CACAGCC CACAGGCC CACAGCC CACAGC	120 180 240 360 420 480 540 660 660 720 780 840 900 1020 1140 1200 1320 1380 1440 1500 1560 1620 1680 1740 1800
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	Coding sequilibrium control co	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTGCCGAGG GATGTGCAG GATGTGCAG CAGCGCGCC TTGTCAGTC ATTGCAGTG ATGAAAGA ATGGACATGT ACAGATACAA ATCACAACAC CAAGAAGGCA TAGGCAGTTAT ACAGATACAA CAGACATGC TAGGCAGTACTGA ATCACAACAC CAAGAAGGCA CAGCAGCAGCA CAGCAGCAGCA CTCGCAGCA CTCGCAGCA CTCGCAGCA CTCGCAGCA CTCGCAGCA CTCGCAGCA CTCGCAGCAG CTCCAGCAG CTCCAGCAG CTCCAGCAG CTCCAGCAG CTCCAGCAG CTCGCAGCAG CTCGCAGCAG CCGCCAGCAGAC CCGCCAGCCAA CCGCCCAGCCAA CCGCCCCAGCCAA CCGCCCCAGCCAA CCGCCCCAGCCCAA CCGCCCCAGCCCAA CCGCCCCAGCCCAA CCACGCCCAA CCGCCCCAGCCCAA CCGCCCCAGCCCAA CCGCCCCAGCCCAA CCCCCCCC	3036 21 CCCGGGCCAA AACGGGGGC TAGAAGAGCT TAGAAGAGCT CAGGAAATCC GCTCGCGGG CTCTGTTCGG AGAAGTGCT AAATGAAGGT TGTCTCCCTC ACGGGGATAT TGTCTTCCCA ACCAAACCTC TAAAAGAGA AGAGTTTCAG AGAGTTTCAG CAGGGCTGTAGCG CAGGCAGAC CGTGACCTG GAAGGTTTCAG CAGGCAGAC CGTGACCCTG AAATGAAGT ATTTCTGGAA ACTATTCAGGT AATGAAGT CAGGCAGAC CGTGACCCTG AAAGGAATCC CGTGACCTG CGAGCAACTCC CGTGTACCTG CGGCAACTCC CGTGTACCTG CGGCAACTCC CGTGTACCTG CGTGTACCTG CGGCAACTCC CGTGTACCTG CGTGCAGACT	31   CTCGGACAGT GCGCGACGCA CAGCGGCGCCC CAGGGGCGCACCA ATATTCGAC CTCATTGCA GCTCGAAATT TCTGATTCAG AATATCAAGC GCTCAAAGA ACCCTCAAGA ACCCTCAAGA ACCATCAAGA ACCATCAAGA CGTTCAAAGA ACCATCAAGA CGTTCAAAGA CGTTCAAAGA CGTCTAAGA CGCTAAAGA CGCTCAAGGA CGCTCAAGGA CGCTCAAGGA CGCTCAAGGA CGCTAAGACAC TGGACAAGA TGGACAAGA CTTTATTCCC CAGTCTGGG CCCATGGTGT CGCGCTGCAAA TGGACAATTTG CCCATGGTGT CGCTGCTGCA TGTGACCTCCC CACGATGGCG CCACGAGGGC CCACGAGGCGC CCACGAGGCGGC CACGAGGCGGC	TTGCTCATTT CGCACACACA GCGGCCGTG GACGCCGGC AGCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGA ACACGGTAAT CAGTCATCTAGAA TGAAAAGCGT ATGTCTTAGA ACACTAAGTA ACACTAAGTA TGAACACGT AATGCTCTTAGA ACAGACCACT AATGCTCTGGA ACAGACCACT TGAGCACTCAT TGGACAAGC CGATTGTAGAA TCAGCACTTCG TGTTAACCT TGGACAAGC ACTGCCACAA ACTGCCACCA ACTGCCACCA ACTGCCACCA ACTGCCACCA ACTGCCACCA ACTGCCACCA ACTGCCACCA ACTGCCACCA ACTGCCACCAC ACTCATGTCA	ATTGCAACGG CGGGGGGAAA CGCGGGGGCT CCCGCTCGGC CTGAAGGCCG CGAAGGAAGA AGTGAAGAAGA AGGAAACCCAC TCTGGGTCAC CAGCACGTGT ACCAATGAAA ACCAATGAAA ACCACCTCT TGTGGGGTCAC AAAGCAAGAA ACCACCTCT TGTGGAGTCA ACCACCTCT AAAAGTTAAG GAACATTCGG AAGTCAGGAC ACTCGCAAA ACTCGGCATG CAGCAGGATG CGGACGGATG CAGCAGGATG CAGCAGGATG CAGCAGGATG CAGCAGGATG CAGCAGGAGTG CAGCAGGAGTG CAGCAGGAGTG CAGCAGGAGG CCTGCAGAGGACG CACAGGGGCC CAGCAGGGGCC CGGATGTGGAC CACCTGGGACG CGGATGTGGAC CGGATGTGGAC CACCTGGGAC CACCTGGGAC CACCTGGGAC CACCTGGGAC CGGATGTGGAC CGGATGTGGAC CACCTGGGAC CACCTGGAC CACCTGGAC CACCTGGAC CACCTGGAC CACCTGGGAC CACCTGCAC CACCTGGAC CACCTGCAC CACCTGGAC CACCTGCAC CACCTGGAC CACCTGCAC CACCTGGAC CACCTGCAC CACCTGGAC CACCTGCAC CA	120 180 240 360 420 540 660 720 780 960 1020 1140 1200 1320 1380 1440 1500 1680 1740 1880 1860 1920
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	Coding sequilibrium control co	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTGCCGAGG GATGTGCAG GATGTGCAG CAGCGCGCC TTGTCAGTC ATTGCAGTG ATGAAAGA ATGGACATGT ACAGATACAA ATCACAACAC CAAGAAGGCA TAGGCAGTTAT ACAGATACAA CAGACATGC TAGGCAGTACTGA ATCACAACAC CAAGAAGGCA CAGCAGCAGCA CAGCAGCAGCA CTCGCAGCA CTCGCAGCA CTCGCAGCA CTCGCAGCA CTCGCAGCA CTCGCAGCA CTCGCAGCAG CTCCAGCAG CTCCAGCAG CTCCAGCAG CTCCAGCAG CTCCAGCAG CTCGCAGCAG CTCGCAGCAG CCGCCAGCAGAC CCGCCAGCCAA CCGCCCAGCCAA CCGCCCCAGCCAA CCGCCCCAGCCAA CCGCCCCAGCCCAA CCGCCCCAGCCCAA CCGCCCCAGCCCAA CCACGCCCAA CCGCCCCAGCCCAA CCGCCCCAGCCCAA CCGCCCCAGCCCAA CCCCCCCC	3036 21 CCCGGGCCAA AACGGGGGC TAGAAGAGCT TAGAAGAGCT CAGGAAATCC GCTCGCGGG CTCTGTTCGG AGAAGTGCT AAATGAAGGT TGTCTCCCTC ACGGGGATAT TGTCTTCCCA ACCAAACCTC TAAAAGAGA AGAGTTTCAG AGAGTTTCAG CAGGGCTGTAGCG CAGGCAGAC CGTGACCTG GAAGGTTTCAG CAGGCAGAC CGTGACCCTG AAATGAAGT ATTTCTGGAA ACTATTCAGGT AATGAAGT CAGGCAGAC CGTGACCCTG AAAGGAATCC CGTGACCTG CGAGCAACTCC CGTGTACCTG CGGCAACTCC CGTGTACCTG CGGCAACTCC CGTGTACCTG CGTGTACCTG CGGCAACTCC CGTGTACCTG CGTGCAGACT	31   CTCGGACAGT GCGCGACGCA CAGCGGCGCCC CAGGGGCGCACCA ATATTCGAC CTCATTGCA GCTCGAAATT TCTGATTCAG AATATCAAGC GCTCAAAGA ACCCTCAAGA ACCCTCAAGA ACCATCAAGA ACCATCAAGA CGTTCAAAGA ACCATCAAGA CGTTCAAAGA CGTTCAAAGA CGTCTAAGA CGCTAAAGA CGCTCAAGGA CGCTCAAGGA CGCTCAAGGA CGCTCAAGGA CGCTAAGACAC TGGACAAGA TGGACAAGA CTTTATTCCC CAGTCTGGG CCCATGGTGT CGCGCTGCAAA TGGACAATTTG CCCATGGTGT CGCTGCTGCA TGTGACCTCCC CACGATGGCG CCACGAGGGC CCACGAGGCGC CCACGAGGCGGC CACGAGGCGGC	TTGCTCATTT CGCACACACA GCGGCCGTG GACGCCGGC AGCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGA ACACGGTAAT CAGTCATCTAGAA TGAAAAGCGT ATGTCTTAGA ACACTAAGTA ACACTAAGTA TGAACACGT AATGCTCTTAGA ACAGACCACT AATGCTCTGGA ACAGACCACT TGAGCACTCAT TGGACAAGC CGATTGTAGAA TCAGCACTTCG TGTTAACCT TGGACAAGC ACTGCCACAA ACTGCCACCA ACTGCCACCA ACTGCCACCA ACTGCCACCA ACTGCCACCA ACTGCCACCA ACTGCCACCA ACTGCCACCA ACTGCCACCAC ACTCATGTCA	ATTGCAACGG CGGGGGGAAA CGCGGGGGCT CCCGCTCGGC CTGAAGGCCG CGAAGGAAGA AGTGAAGAAGA AGGAAACCCAC TCTGGGTCAC CAGCACGTGT ACCAATGAAA ACCAATGAAA ACCACCTCT TGTGGGGTCAC AAAGCAAGAA ACCACCTCT TGTGGAGTCA ACCACCTCT AAAAGTTAAG GAACATTCGG AAGTCAGGAC ACTCGCAAA ACTCGGCATG CAGCAGGATG CGGACGGATG CAGCAGGATG CAGCAGGATG CAGCAGGATG CAGCAGGATG CAGCAGGAGTG CAGCAGGAGTG CAGCAGGAGTG CAGCAGGAGG CCTGCAGAGGACG CACAGGGGCC CAGCAGGGGCC CGGATGTGGAC CACCTGGGACG CGGATGTGGAC CGGATGTGGAC CACCTGGGAC CACCTGGGAC CACCTGGGAC CACCTGGGAC CGGATGTGGAC CGGATGTGGAC CACCTGGGAC CACCTGGAC CACCTGGAC CACCTGGAC CACCTGGAC CACCTGGGAC CACCTGCAC CACCTGGAC CACCTGCAC CACCTGGAC CACCTGCAC CACCTGGAC CACCTGCAC CACCTGGAC CACCTGCAC CACCTGGAC CACCTGCAC CA	120 180 240 360 420 480 540 660 660 720 780 840 900 1020 1140 1200 1320 1380 1440 1500 1560 1620 1680 1740 1800
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	Coding sequence of the control of th	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGTGCAG GATGTGCAG CAGCGCCCC ATCTGGAAAG ACGGTACTGA ATGACATCA ATGACAACAC CAGATACAA CCAGACACCG TTGGCAGGC TTGGGAGGC ATCTGGAAAG ACGCTACTAT ACAGATACAA CCAGACAACG TAGGCATGCA CAGCACACG TAGGCATGCA CAGCATGCA CCAGCCAGGC CCAGCCTGGA CCTCCCAGGCAAG CCAGCCAGGC CCAGCCAGCCAGC CGCAGGCACAC CGCCAGCCA	3036 21 CCCGGGCCAA AACGGGGGC TAGAAGAGCT CAGGAAATCC CGCTCGCCGC CTCTGTTCGG AGAAGTGCT AAATGAAGGT TGTCTCCCT ACGGGGATAT TGTCTTCCCA ACCAAACCTC TAAAAGAGA ACTCTTCCCA AGAGTTTCAG TAATCACGT AGTGTGGAAT ATTTCTGGAC CGTGCCATG GGACTTTGG GAAGTTTCGC GAAGTTTCGC CAGGCATACCTC GAAGCTTCGC CGTGCCATT GAAGGAATC CGTACCTC CAGGCATCC CGTGTACCTC CGGCAACTCC CGTGCACTCC CTGCCAGACT CTGCAGACT CTGGCAGACT CTGCAGACT	TCTCGGACAGT GCGCGACGCA CACGGCGGGCCCAGG ACTCGGCCCGCCC CACGGGCCCAGG ACTCGGACAT TCTGATTCAG AATGAAAGCT TCTGATTCAG AATGAAAGC GCTCCAAAGA ACCCTCAAGG AGCAAGAAGA CCCTCAAGG AGCAAGAAGC TGTATTTCGC CAGTCTGAGG GCTGCAAAGA TCTCAAGG AGCAAGAAGTTTT GACATGACA TGGAGGAAGA TTTATTTCC CAGTCTGGGG GCACATGAGC TGTCAAATGG TGTGAAGATTTG CACGACAGCAGC TTTTAAGAAGAG TTTTAAGAAGAG TTTTAAGAAGAG TTTTAAGAAGAG TTTTAAGAAGAG	TTGCTCATTT CGCACACAC GCGGCCGTG GACGCCGGC AGCTGCTGCAC AGCTGCTGCACACAC ACACGCCACAC GCTTATGGAA TCTGGATCCC TACAACGGAA CAGCGTATT CAGTCAGTCA ATGTCTTAGA ATGTCTTAGA ACAGTCAGTA AAGATCTGGA ACAGACCACT TGAAGACCACT TGAAGACCACT TGAAGCTTCT TGGACCACAC CGATTGTCAC AGATTGTAGAA TCAGCACTTC TGGACGACAC CGATTTACCT TGGACGACT CACTCCACC ACTGCACGCT CAGAGTTCTC ACTGCACGCT ACTGCACGCT ACTCCACGCT ACTGCACGCT ACTCCACTCC	ATTGCAACGG CGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCTG CGAAGGAAGA AGTGAAGACC ACTCTGGGTCAC TCTGGGTCAC AGCAATGAAA CCACCACTCT TCTGGGACTG AAAAGTTAAG GAACATTCGA ACTCGCATA ACTCGGCATG AACTCAGCATG ATTCGGGATG ACTCGGCATG CGACCATTCA CTTCGGGAGC ACCTCGCAAA CATCGGCATG AGGAGGCTGC CGCAGGAGGTG AGGAGCTTCC CAGCAGGAG GCCGGAAGTC CAGCAGGGAC CACCAGGAGCTGC CAGCAGGAGC CACCAGGAGCTGC CAGCAGGAGC CACCAGGAGC CACCAGGACGC CACCAGGAGC CACTGGGAC ACTCTGGGAC ACTCTGGGAC ACTCTGGGAC CACTGGACCT	120 180 240 360 420 540 660 720 780 900 960 1020 1140 1200 1380 1440 1500 1560 1620 1680 1740 1800 1800 1920
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	Coding sequilibrium control co	uence: 37  11  CTTCCTAGTC CTTGTGCCAG ATGAAAGGC CTCGCCGAGG GATGTGCAG GATGTGCAG CAGCGCGCC TGCTCGCGCC TGCTCGCGCC ATCTGGAAAG ACGTACTGA ATGGACATGT ACAGATACAA ATCACAACAC CAGACAGCG TAGGCAGTTT TAGGCTGGA CTTCCACGG CTTCCACCGG CTCCAGCCTGGA CTCCAGCAGGGCC CGCAGGGACTC CGCAGCTGGA CTCGCAGCCAG CGCAGCCCAG CGCAGCCCAG CGCAGCCCAG CGCAGCCCAG CGCAGCCCAG CGCAGCCCAG CGCAGCCCAG CGCAGCCCAG CGCAGCCCAG CACTGGCCCAC CGCAGCCCAG CGCAGCCCAG CGCAGCCCAA CACATGGCCCA CGCAGCCCAG CGCAGCCCAA CCGCACCCCAG CGCAGCCCAA CCGCAGCCCAA CCGCAGCCCAA CCGCACCCAA CCGCAGCCCAA CCGCCAGCCCAA CCGCAGCCCAA CCGCAGCCCAA CCGCAGCCCAA CCGCAGCCCAA CCGCCCCAGCCCAA CCGCAGCCCAA CCGCAGCCAA CCGCCAGCCCAA CCGCCAGCCCAA CCGCAGCCCAA CCGCAGCCCAA CCGCAGCCCAA CCGCCAGCCCAA CCGCAGCCCAA CCGCAGCCCAA CCGCAGCCCAA CCGCAGCCCAA CCGCAGCCAA CCGCAGCCCAA CCGCAGCCAA CCGCAGCCAA CCGCCAGCCA	2036 21 CCCGGGCCAA AACGGCGGC CAGAAAACCT CAGGAAATCC CGCTCGCGGC CTCGTGCGG CTGCCGGG CTGCCGGG CTGCTGTTCGG AAATGAGGT TGTCTCCCA ACCAAACCTC TAAAACAAC TGTATTCAG TAATCACGT AATCACGT AATCACGT TGTGTTGGAAT ACTCTTCCCA ACCAAACCTC TAAAACAGG CACGAACCTC GGGCTGTACCTG GGGCTGTAGCG GGGCTGTAGC GGAGTGTGGG ATGTACCAT CGTGCACACC CCGGGACCCC CGGGACCCC CGGGACCCC CGGGACCCC CGGGACCCC CGGGACCCC CGGGACCCC CCGGGACCCC CCGGCACACCC CCGGCACCCC CCGGCACCCC CCGCCACCC CCCCACCC CCCCACCC CCCCACCC CCCCCC	TCCATGACAGA  GCACAAGAT  GCACAGAGA  CTCGGACGAC  CAGGGCGCC  CGAGGGGGC  CTCCGGTCGC  CGAGGGGTGA  AGTGGGACC  AATATTCGAC  GCTCGAAATT  TCTGATTCAG  GCTGCAAGAAG  ACCCTCAAGG  ACCATGAGAA  GCAAGATTT  GACAAGAAGAC  GTTAATTCCC  CAGTCTGGGG  GCACAAGAAG  GTTAATTCCC  CAGTCTGGGG  TGTCAAATG  CCATGTGTG  CGCATGTGT  CGCTGCTGCAC  TGCTGTAATGG  CACAGATTTG  CGCTGCTGCAC  CACAGATTGC  CACAGATTGC  CACAGACAGC  CACAGACAGC  CACAGACAGC  CACAGACAG	TTGCTCATTT CGCACACACA GCGGCGTG GACGCCGGC GCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC GCACACACACA GCACCCTCACACACACACACACACACACACACACACACAC	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GGAAGGAAGA AGTGAAGAGA AGTGAACGAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC ACCACCTCT TGTGGAGCTG AAAGTTAAG GAACATTCAG AACTTCGGAAC CATCGCAAA CATCGCATC TTTTCGGATC ACCACGTCT TGGGGAGCTCC CACGCAGGAGC CATCGCAAA CATCGCATC TTTCGGGATC AGGAGGCTGC CACGCAGGAGC CACGCAGGAGC CACGCAGGAGC CACGGAAGTC CACAGGGCCC CACGGAAGTC CACAGGGGCC CACGGGACC CACTCGCAC CACAGGGGCC CACAGGGCC CACAGGGCC CACAGGGGCC CACAGGGGCC CACAGGGGCC CACAGGGGCC CACAGGGGCC CACAGGGCC CACAGGC CACAGGGCC CACAGGGCC CACAGGGCC CACAGGGCC CACAGGGCC CACAGGGCC CACAGGCC CACAGGCC CACAGGGCC CACAGGGCC CACAGGGCC CACAGGCC CACAGGCC CACAGGCC CACAGGCC CACAGGCC CACAGGCC CACAGGCC CACAGGCC CACAGGCC CA	120 180 240 360 420 480 540 660 660 720 780 840 900 1020 1140 1200 1140 1500 1620 1680 1740 1680 1740 1860 1980 2040
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	Coding sequilibrium control co	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTGCCGAGG GATGTGCAG GATGTGCAG CAGCGCGCC TTGTCAGTC TTGTCAGTGC ATGTAGAAG ACGATACTGA ATGGACATGT GGGGACTATT ACAGATACAA CAGACAACAG TAGGACATGT TAGGCTGAAG CAGCACACGC TAGGACATGC TAGGCTGAAG CTTCCACCGG CTCCATGA CTTCCACCGG CTCCATGA CTTCGACCAG CTCCATGA CTTCGACCAG CTCCATGA CTTCGACCAG CTCCATGA CTTCGACCAG CTCCATGA CTTCCACCGG CCAGCCTGAA CTCGACCAG CCAGCCTGAA CTCGACCAG CTCCACCGG CCAGCCTGAA CTCGACCAG CTCCACCGG CCAGCCTGAA CTCGACCAG CCAGCCTGAA CTCGACCAG CCAGCCCAA CACATGCCCC CTCGCCCAAAG CCGCCAAAG CCGCCCAAAG CCGCCCAAAG CCGCCCAAAG CAAATGCCAG CAAATGCCAG CTGCCCAGACG CAAATGCCAG CAAATGCCAG CAAATGCCAG CAAATGCCAG CAAATCCAGCC CAAAATCCAGCC CAAAAATCCAGCC CAAAATCCAGCC CAAAATCCAAACCC CAAAATCCAAACCC CAAAATCCAAACCC CAAAAATCCAAACCC CAAAATCCAAACCC CAAAATCCAAACCC CAAAAATCCAAACCC CAAAATCCAAACCC CAAAATCCAAAACCC CAAAATCCAAAACCC CAAAATCCAAAACCCAAAACCC CAAAAATCCAAAACCCAAAACCCAAAACCCAAAACCCAAAACCC	3036 21 CCCGGGCCAA AACGGCGGC CTAGAAGAGCT CAGGAAATCC CGCTCGCGG CTCGCAGGC CTCTGTTCGG AGAAGTGCT AATCAAGT TGTCTCCCT ACGGGGTAT TGTGTTTCGA ACCAAACCTC TAAAAGAGA TGATGTTGGAA TGTGTTCGAA CGGGGTTTCAG TGATGTTGGAA TGTGTTCGGA CGTGCCGT CACGGCAGC CGTGACCCT GAAAGGAT GGAAGTTCAG GGAAGTTGGG ATGTACCAT CGAGAACTC CGTGACCCT CCGGCAGAC CTGCAGACT CCGGCAGACT CCGGCAGACT CTGCAGAGT CTGCAGAGT TTGAAGGAGT TTGAAGAGGT TCGAAGAGGT TCGAAGAGGT TCGAAGAGGT TCGAAGAGGT TCGAAGAGGT TCGAAGAGGT TCAAGGAGGT TCAAGGAGGT TCAAGGAGGT TCAAGGAGGT TCAAGGAGGT TCAAGGAGGT TCAAGGAGGT TCAAGGAGGT TCAAGGAGT TCAAGGAGGT TCAAGGAGT TCAAGGAG	TCCGGACAGT CCCGGCCCCCCCCCCCCCCCCCCCCCCCC	TTGCTCATTT CGCACACACA GGGGCGTG GACGCCGGC AGCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGA GCAGTTTCAC ACACGGTAAT TGAAAAGGGT ATGTCTTAGA ACAGTAATT AAGATAAGA ACAGTAATT AAGATCTGGA ACAGACCACT AATGCTCTGA TGAAACGGCACAC TGAATTCTCGA ACAGCTTCTGA TGAAGACTCTCT TGAAGCTTCTCT TGGAAGAAG TCAGCCACAC ACTGCCACAC ACTGCCACAC ACTGCCACAC ACTGCCACAC ACTGCCACAC ACTGCCACAC ACTGCCAGCT CAGAGTTCTCC ACTCATTCTCC ACTCATTCTCC ACTCATTCTCC ACTCATTCTCC AATGCGAGAT CAGAGTTCTCC ACTCATTCTCC AATGCGAGAT CAGTCATTCTCC AATGCGAGAT CAGTCATTCCC AATGCGAGAT CAGTCATTCTCC AATGCGAGAT CAGTCATTCTCC AATGCGAGAT CAGTCATTCTCC CAGTCTCTCC CAGTCTCTCC CAGTCTCTCC CAGTCTCTCC CAGTCTCC CAGTCTCTCC CAGTCTCC CAGTCTCC CAGTCTCC CAGTCTCC CAGTCTCC CAGTC	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG CGAAGGAAGA AGTGAAGACGA AGTGAAGACCAC TCTGGGTCAC CAGCACGTCT TGTGGGATCA ACCAATGAAA CCGGGGATCA ACCACCTCT TGTGGAGCTG AAAGTTAAG GAACATTCAG CATCGCAAT ACTACGCATT CGGGATCA CATCGGCATG ACTCGGCATG CAGCAGGGTG CAGCAGGAGG CCCGGAAGT CAGCAGGAGT CAGCAGGAGG CCCGGAAGT CAGCAGGAGT CCCTGCAGAGG CCCGGAAGT CCCTGCGGA CACTCTGCGGA CACTCTGCGGA CACTCTGGGGA CACTCTGGGA CACTCTGGGGA CACTCTGGGGA CACTCTGGAGATCT CACTCTGGGGA CACTCTGGAGATCT CACTCTGGGGA CACTCTGGAGATCT CACTCTGGGGA CACTCTGGAGATCT CACTCTGGGAA CACTCTGCAATGCC CACTCTTGCAA	120 180 240 360 420 540 660 720 780 960 1080 1140 1200 1320 1380 1560 1680 1740 1880 1740 1880 1920 1980 2040 2100
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	Coding sequilibrium control co	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTGCCGAGG GATGTGCAG GATGTGCAG CAGCGCGCC TTGTCAGTC TTGTCAGTGC ATGTAGAAG ACGATACTGA ATGGACATGT GGGGACTATT ACAGATACAA CAGACAACAG TAGGACATGT TAGGCTGAAG CAGCACACGC TAGGACATGC TAGGCTGAAG CTTCCACCGG CTCCATGA CTTCCACCGG CTCCATGA CTTCGACCAG CTCCATGA CTTCGACCAG CTCCATGA CTTCGACCAG CTCCATGA CTTCGACCAG CTCCATGA CTTCCACCGG CCAGCCTGAA CTCGACCAG CCAGCCTGAA CTCGACCAG CTCCACCGG CCAGCCTGAA CTCGACCAG CTCCACCGG CCAGCCTGAA CTCGACCAG CCAGCCTGAA CTCGACCAG CCAGCCCAA CACATGCCCC CTCGCCCAAAG CCGCCAAAG CCGCCCAAAG CCGCCCAAAG CCGCCCAAAG CAAATGCCAG CAAATGCCAG CTGCCCAGACG CAAATGCCAG CAAATGCCAG CAAATGCCAG CAAATGCCAG CAAATCCAGCC CAAAATCCAGCC CAAAAATCCAGCC CAAAATCCAGCC CAAAATCCAAACCC CAAAATCCAAACCC CAAAATCCAAACCC CAAAAATCCAAACCC CAAAATCCAAACCC CAAAATCCAAACCC CAAAAATCCAAACCC CAAAATCCAAACCC CAAAATCCAAAACCC CAAAATCCAAAACCC CAAAATCCAAAACCCAAAACCC CAAAAATCCAAAACCCAAAACCCAAAACCCAAAACCCAAAACCC	3036 21 CCCGGGCCAA AACGGCGGC CTAGAAGAGCT CAGGAAATCC CGCTCGCGG CTCGCAGGC CTCTGTTCGG AGAAGTGCT AATCAAGT TGTCTCCCT ACGGGGTAT TGTGTTTCGA ACCAAACCTC TAAAAGAGA TGATGTTGGAA TGTGTTCGAA CGGGGTTTCAG TGATGTTGGAA TGTGTTCGGA CGTGCCGT CACGGCAGC CGTGACCCT GAAAGGAT GGAAGTTCAG GGAAGTTGGG ATGTACCAT CGAGAACTC CGTGACCCT CCGGCAGAC CTGCAGACT CCGGCAGACT CCGGCAGACT CTGCAGAGT CTGCAGAGT TTGAAGGAGT TTGAAGAGGT TCGAAGAGGT TCGAAGAGGT TCGAAGAGGT TCGAAGAGGT TCGAAGAGGT TCGAAGAGGT TCAAGGAGGT TCAAGGAGGT TCAAGGAGGT TCAAGGAGGT TCAAGGAGGT TCAAGGAGGT TCAAGGAGGT TCAAGGAGGT TCAAGGAGT TCAAGGAGGT TCAAGGAGT TCAAGGAG	TCCGGACAGT CCCGGCCCCCCCCCCCCCCCCCCCCCCCC	TTGCTCATTT CGCACACACA GGGGCGTG GACGCCGGC AGCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGA GCAGTTTCAC ACACGGTAAT TGAAAAGGGT ATGTCTTAGA ACAGTAATT AAGATAAGA ACAGTAATT AAGATCTGGA ACAGACCACT AATGCTCTGA TGAAACGGCACAC TGAATTCTCGA ACAGCTTCTGA TGAAGACTCTCT TGAAGCTTCTCT TGGAAGAAG TCAGCCACAC ACTGCCACAC ACTGCCACAC ACTGCCACAC ACTGCCACAC ACTGCCACAC ACTGCCACAC ACTGCCAGCT CAGAGTTCTCC ACTCATTCTCC ACTCATTCTCC ACTCATTCTCC ACTCATTCTCC AATGCGAGAT CAGAGTTCTCC ACTCATTCTCC AATGCGAGAT CAGTCATTCTCC AATGCGAGAT CAGTCATTCCC AATGCGAGAT CAGTCATTCTCC AATGCGAGAT CAGTCATTCTCC AATGCGAGAT CAGTCATTCTCC CAGTCTCTCC CAGTCTCTCC CAGTCTCTCC CAGTCTCTCC CAGTCTCC CAGTCTCTCC CAGTCTCC CAGTCTCC CAGTCTCC CAGTCTCC CAGTCTCC CAGTC	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG CGAAGGAAGA AGTGAAGACGA AGTGAAGACCAC TCTGGGTCAC CAGCACGTCT TGTGGGATCA ACCAATGAAA CCGGGGATCA ACCACCTCT TGTGGAGCTG AAAGTTAAG GAACATTCAG CATCGCAAT ACTACGCATT CGGGATCA CATCGGCATG ACTCGGCATG CAGCAGGGTG CAGCAGGAGG CCCGGAAGT CAGCAGGAGT CAGCAGGAGG CCCGGAAGT CAGCAGGAGT CCCTGCAGAGG CCCGGAAGT CCCTGCGGA CACTCTGCGGA CACTCTGCGGA CACTCTGGGGA CACTCTGGGA CACTCTGGGGA CACTCTGGGGA CACTCTGGAGATCT CACTCTGGGGA CACTCTGGAGATCT CACTCTGGGGA CACTCTGGAGATCT CACTCTGGGGA CACTCTGGAGATCT CACTCTGGGAA CACTCTGCAATGCC CACTCTTGCAA	120 180 240 360 420 480 540 660 660 720 780 840 900 1020 1140 1200 1140 1500 1620 1680 1740 1680 1740 1860 1980 2040
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	Coding sequilibrium control co	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG GATGGTGCAG CAGGCGCCC TTGTCAGTGC ATCTGGAAAG ACGGTACTGA ATGACATACAA ATCACAACAC CAAGAAGGCA TAGGCAGTGT TAGGCAGTGT GGGGACTTAT ACAGATACAA ATCACAACAC TAGGCAGTGGA CAGGCAGCAGCA CAGGCAGCAGCAC CAGGCAGCAGCAC CTCGCAGCAGCAC CTCGCAGCAGCAC CTCGCAGCAGCAC CTCGCAGCACCCGGACCACCCAGCACACCCGACCACCCAGCACACCCGGACCACC	3036 21 CCCGGGCCAA AACGGGGGC TAGAAGAGCT TAGAAGAGCT CAGGAAATCC CGCTGGCGGG CTCTGTTCGG AGAAGTGCT AAAGAGGT TGTCTCCCTC ACGGGGATAT TGTCTTCCCA ACCAAACCTC TAAAAGAGA AGAGTTTGA AGAGTATCAGGT AGTGTGGAAT ATTTCTGGAA CCATCCTG GGAGTCTGG GGAGTTGGGAT ATTTCTGGAA CCTGTAGCGG GGACCCTG GGAAGTGGG GTACCCTG CAGGAGAC CGTGACCTG CAGGAGAC CGTGACCTG CTGCAAGACT CCCCCTGCAC	TCCGGACAGT GCGGGCGCC CAGGGCGCCC CAGGGGCGCC CAGGGGCGCC CAGGGGCCC CAGAGGGGCC CAGAGGAC CATCATTGCA GCTCGAAATT TCTGATTCAG AATGAAAGCT TCCAAAGA ACCCTCAAGG AGGAGAAGA ACCCTCAAGG AGGAGAAGA CCCTCAAGG AGCAAGAAGTTTT GACATGGCA GCTGAAATT GACATGGACA TGGAGAAGAC CAGTCTGGGG GCACATGGGC TGTCAAATGG CCCATGGTGT GGGGGTGCC TGTCAAATGG CCCATGGTGC CACGATGGC CACGAGCGGC CTTTGGAGAGAG CCACGAGCGGC CACGAGCGGC CACGAGCGGC CACGAGCGGC CACGAGCGGC CCACGAGCGGC CCACGAGCAGC CCAAGGAGGCC CCACGAGCAGC CCAAGGAGGCC CCACGAGCAGC CCAAGGAGGGCC CCACGAGCAGC CCAAGGAGGGCC CCACGGCCGGC	TTGCTCATTT CGCACACAC GCGGCCGGC GACGCCGGC AGCTGCTGCACACAC GCGGCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGGA GCAGTTTCAC ACACGGTAAT TAGGTCAT ATGTCTTAGA ACAGTCAT AATGTCTCGA TGAACAGGA ACAGCCACT TGAAGCTCT TGAAGCTCT TGAAGCTCT TGAAGCTTCT TGAGCATTCT TGGGCCACAA CGGTTTAGAA TCAGCAGTTC TGATCTCTCACACGGATTTTAACCT TGGAAGACACAC CGATTTTACCT TGGAGGAACGA ACTCCACCACAC ACTCCACGCT CAGAGTTCTC ACTCCAGCT ACTCCAGCT ACTCACTCCC ACTCACTCCC ACTCACTCCC ACTCACTC	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCTG CGAAGGAAGA AGTGAAGAGC AGGCAAGCAAGA AGGAACCCAC TCTGGGTCAC CAGCACGTT ACCAATGAAA CCAGCCTCT TCTGGAGCTG AAAAGTTAAG GAACATTCAG AACTCAGCAT TTTCGGAAC TTTCGGGATCA CATCAGCATT ACCACGCTTC TTTCGGAAC CACCCCTCT TTTCGGAAC CACCACGCATC ACCTCGCAAA CATCGGCATG AGGAGGTTCA CAGCAGGAAG CACCAGGGAC CACCAGGGGCC CACCAGGGCC CACCAGGGCC CACCAGGGGCC CACCAGGGCC CACCAGGGCC CACCAGGGGCC CACCAGGGGCC CACCAGGGGCC CACCAGGGGCC CACCAGGGGCC CACCAGGGGCC CACCAGGGGCC CACCAGGGCC CACCAGGGGCC CACCAGGGGCC CACCAGGGCC CACCAGGCC CACCAGGGCC CACCAGGGCC CACCAGGGCC CACCAGGGCC CACCAGGGCC CACCAGGGCC CACCAGGGCC CACCAGGGCC CACCAGGGCC CACCAGGCC CACCAGGGCC CACCAGGGCC CACCAGGGCC CACCAGGGCC CACCAGGGCC CACCAGGGCC CACCAGGGCC CACCAGGGCC CACCAGGGCC CACCAGGCC CACCAGGCC CACCAGGGCC CACCAGGGCC CACCAGGGCC CACCAGGGCC CACCAGGGCC CACCAGGGCC CACCAGGCC CACCAGGCC CACCAGGCC CACCAGGCC CACCAGGCC CACCAGGCC CACCAGGCC CACCAGGCC CAC	120 180 240 360 420 540 660 720 780 960 1020 1080 1140 1200 1380 1440 1500 1680 1680 1740 1800 1980 2040 2160
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	Coding sequilibrium control co	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGTGCAG CAGCGCGCC TGCTCGCGCC TGTCAGTC ATCTGAAAG ACGATACTAA ATCACAACAC CAGACAACAC CAGACAACAC TAGACATGC TTCCACCGG CTCGCTGGACC CCGCTGGACCC CCGCCTGGACCC CCGCCCGGACCC CCGCCCGC	3036 21 CCCGGGCCAA AACGGCGGC TAGAAGAGCT CAGGAAATCC CGCTCGCAGGC CTCTGTTCGG AGAAGTGCTG AAATGAGGT TGTCTCCCT ACGGGATAT TGTCTTCCCA ACCAAACCTC TAAAAGAGG TAATCAAGGT TAGTCTTGAA AGTTTCAG AGAGTTTCAG TAATCAAGTT AGTCTGAAGAG TAATCAGTT AGTCTGGAA CGTGACCCTG GGACTGTAGC GGAGTGTAGC CGTGACCATT CGAAGAATC CTGCAAGATC CTGCAAGATC CTGCAAGATC CTGCAAGATC CTGCAAGATC CTGCAAGAGT CCCCCTGCAC CCTGCAAGAGT CCCCCCTGCAAC CCATGCAGAGGT CCCCCCTGCAAC CCATGCAGGAGGT CCCCCCTGCAAC CCATGCAAGAGGT CCCCCCTGCAAC CCATGCAGGAGGT CCCCCCTGCAAC CCATGCAGGAGGT CCCCCCTGCAAC CCATGCAGGAGGT CCCCCCTGCAAC CCATGCAGGAGGT CCCCCCTGCAAC CATGCCCGGAAC CATGCCCGGAAC CCATGCAGCAC CCATGCAACAC CCCCCTGCAACAC CATGCCCGGAAC CATGCCGGAAC CATGCCCGGAAC CATGCCGGAAC CATGCCGAAC CATGCCGCAC CATGCCGCAC CATGCCGCAC CATGCCCTCGCAC CATGCCCTCGCAC CATGCCCTCCCTCCCCTC	TCCGGACAGT CCCGGCCCCCCCCCCCCCCCCCCCCCCCC	TTGCTCATTT CGCACACAC GCGGCCGTG GACGCCGGC GACGCCTCCT GCTTATGGAA TCTGGATCCC GCTATGGAA GCACTTATCAC ACACGGTAAT TCAGCACTACAC ACACGGTAAT TCAGCACTACAC ACACGCTAAT TCAGAAAAGGT ATGTCTTAGA ACACACTACT AATGCTCTT AATGCTCTT AAGGCTCAC TGAAGCCACT TGGACCACAC CGGTTGAGAA CGGTTGAGAA CGGTTGAGAA CGGTTGAGAA CGGTTCAC ACTCCACT CAGCACTTCC ACTCCACC ACTCCACC ACTCCACC ACTCCACC ACTCCACC CCAGCTTCC ACTCATTCC ACTCATCCC ACTCATCCC ACTCATCCC ACTCATCCC ACTCATTCCC ACTCATTCCC ACTCATCCC ACTCATTCCC ACTCATTCC ACTCATTCCC ACTCATTCC ACTCATTCCC ACTCATTCC AC	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCTG CGAAGGAACA AGTGAACACCAC TCTGGGTCAC ACCACCTCT ACCAATGAAA CCAGCACTTC TGTGGGTCAC ACCACCTCT AAAGTTAAG AACATCGCAA ACTCGCAAA CATCGCAAA CATCGGATA ACCACCTCT ACCACTCT ACCACTCT ACCACCTCT ACCACCTCC ACCACGAGAG CATCGCAGAA CATCGCAGAA CATCGCAGAAG CCACAGGAGC CCACAAGCCTCC GCACAGGACC CACAGGGCCC CCACAAGTCC CCCGGGGACC CCCCGGGGCC CCCCGGGGCCC CCCGGGGCCC CCCGGGGCCC CCCGGGGCCC CCCGGGGCCC CCCGGGGCCC CCCGGGGCCC CCCGGGGCCC CCCGCGGGCCC CCCGGGGCCC CCCCGGGGCCC CCCCGCGCGCCC CCCCGCGGCCC CCCCGCGCGCCC CCCCGCGGCCC CCCCCC	120 180 240 360 420 660 660 720 780 840 900 1020 1140 1200 1320 1380 1440 1560 1620 1680 1740 1860 1980 2040 2160 2160 2220
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	Coding sequilibrium control co	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGTGCAG GATGTGCAG CAGCGCGCC TTGTCAGTC TTGTCAGTGC ATGTGAAAG ACGGTACTGA ATGACATACTA ATGACATACAA CAAGAACAG TAGAGATTGC TAGGCTGAAG CAGCACACG TAGGCATGT TAGGCTGGA CTTCCACCGG CTCCATGA CTTCCACCGG CTCCATGA CTTCCACCGG CTCCATGA CTTCCACCGG CTCCATGA CTTCCACCGG CTCCATGA CTCCATGACAG CTCCATGACAG CTCCATGACAG CTCCATGACAG CTCCATGACAG CTCCATGACGC CTCGGCCAG CTCCAGCCTGAA CTCCAGCCTGAA CTCCAGCCTGAA CTCGCCCAGCCTGAA CTCGGCCCAG CTGGCCCAGCCTGAA AAACTGCCCAG AAAACCAGCCAA AAACTGCCCAG AAAACCAGCCAA AAATCCAGTC AAAATCCAGTC AAAAATCCAGTC AAAATCCAGTC AAATCCAGTC AAAATCCAGTC AAATCCAGTC AACCTGCACC AAATCCAGTC AATCCAGTC AAATCCAGTC AATCCAGTC AAATCCAGTC AAATCCAGTC AAATCCAGTC AAT	3036 21 CCCGGGCCAA AACGGCGGC CTAGAAGAGCT CAGGAAATCCT CGCTCGCGG GCTGCCGTG CTGCTGCGG AGAAGTGCT AATGAAGGT TGTCTCCCTC ACGGGGATAT TGTGTTTCACT AACGAAGACTC TAAAAGAACTC TAAAAGAGT TATTCTCCCA ACCAAACCTC TAAAAGAGT TGTGTTCAGT AGTGTGGAAT AGTGTGGAAT ATTCTCGAACTC GGGCTGTAGC GAAGGATCG CACGGCAGC CCTGCAGACTC CTGCAGACTC CTGCAGACTC CTGCAGACTC CTGCAGACGC CCCCCTGCAG CCCCCTGCAG CATGCCGGGC CCCCTGCAGCT CCAAGCACCC CCTCGAAGAGGT CCCCCTTGCAAGAGGT CCCCCCTGCAGCT CCCCCTGCAGCT CCAAGCACCC CCTGCAAGAGGT CCCCCTGCAGCT CCAAGCACCC CCTGCAAGGGT CCCCCTGCAGCT CCAAGCACCC CCTGCAGCGC CCCCTGCAGCGT CCAAGCACCC CCTGCAGCGCT CCCCCTGCAGCGT CCAAGCACCC CCTGCAACGGCT CCCCCTGCAGCGT CCAAGCACCC CCTGCAACGGCT CCCCCTGCAGCT CCAAGCACCC CCTGCAACGCT CCAAGCACCC CCTGCAACGCT CCAAGCACCC CCAACACCC CCAAGCACCC CCAAGCACC CCAAGCACCC CCAAGCCACC CCAACCC CCA	TCCGGACAGT CCCGGCCCCCCCCCCCCCCCCCCCCCCCC	TTGCTCATTT CGCACACACA GCGGCGTG GACGCCGGC GCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGA GCAGTTTCAC ACACGGTAAT CAGTCATTTCAC ACACGGTAAT TGAAAAGGGT ATGTCTTTAGA ACATAAGTA AAGATCTGGA ACAGACCACT AATGCTCTT AAGGCACCAC TGAAAAGCTCT TGAAAGCTACT TGAAAGCTACT TGAAAGCTACT TGAAGACCACT TGAAGCTACT TGAAGCTCCT AAGGCACAC CAGTTGAGAA CCGTTGAGAA CCGTTGAGAA CCGTTGAGAA CCGTTGAGAA CCGTTCACAC ACTGCCACAC ACTGCCACAC ACTGCCACAC CAGAGTTCTCA AGTGCTACTC AATGCGAGAT CAGATTCTCC CAGAGTTCTCC AATGCGAGAT CAGTCTTCCC CAGTTCTCC CAGTTCC CAGTTCTCC CAGTTCC CAGTTCTCC CAGTTCC CAGTTCTCC CAGTTCC CAGTTCTCC CAGTTCTCC CAGTTCTCC CAGTTCTCC CAGTTCC CAGTTCTCC CAGTTCCC CAGTTCTCC CA	ATTGCAACGG CGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG CTGAAGGAGA AGTGAAGAGA AGTGAAGAGA AGGAAACCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC ACCACCTCT TGTGGAGCTG AAAGTTAAG AACATCGGAT ACCACCTCT TGTGGAGCTG AAAGTTAAG GAACATTCGG AAGTCAGGAC TCTTCGGAAT CCTCGCAAA CCTCGGCAAG CATCGGCATG AGGAGGTTCC CAGCAGGAGG CCTGCAAA CCTCGGCAGAG CCTCTGCAAA CATCGGCATG AGGAGGTTCC CAGAGGAGTCT CTGACCTGCA ACTCTGGGAA CCTCTGCAAA CCTCGGAAGTCT CTGACCTGCA CCCGGGAAGTC CCCGGGAGTCT CCCGGGAGTCT CCCGGGGAGCC CCCCAGAGGCCC CCCCAGGGGCCC CCCCAGGGGCCC CCCCAGAGCCCC CCCCAGGGGCCC CCCCAGAGGCCC CCCCAGGGGCCC CCCCAGAGGCCC CCCCAGAGGCCC CCCCAGAGGCCC CCCCAGGGGCCC CCCCAGGGGCCC CCCCAGGGGCCC CCCCAGAGGCCC CCCCAGGGGCCC CCCCAGGGGCCC CCCCAGGGGCCC CCCCAGGGGCCC CCCCAGGGGCCC CCCCAGGGGCCC CCCCAGGGGCCC CCCCAGGGGCCC CCCCAGGGGCCC CCCAGGGGCCC CCCCAGGGGCCC CCCCAGGGGCCC CCCCAGGGGCCC CCCCAGGGGCCC CCCAGGGGCCC CCCCAGGGCCC CCCCAGGGCCC CCCCAGGGCCC CCCCAGGGCCC CCCCACAAGGCCT CCCCCCC CCCCAGGGCCC CCCCCCC CCCCCCCC CCCCCCCC	120 180 240 360 420 540 660 720 780 960 1020 1080 1140 1200 1380 1440 1500 1680 1680 1740 1800 1980 2040 2160
50 55 60 65 70 75	Coding sequilibrium control co	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGTGCAG GATGTGCAG CAGCGCGCC TTGTCAGTC TTGTCAGTGC ATGTGAAAG ACGGTACTGA ATGACATACTA ATGACATACAA CAAGAACAG TAGAGATTGC TAGGCTGAAG CAGCACACG TAGGCATGT TAGGCTGGA CTTCCACCGG CTCCATGA CTTCCACCGG CTCCATGA CTTCCACCGG CTCCATGA CTTCCACCGG CTCCATGA CTTCCACCGG CTCCATGA CTCCATGACAG CTCCATGACAG CTCCATGACAG CTCCATGACAG CTCCATGACAG CTCCATGACGC CTCGGCCAG CTCCAGCCTGAA CTCCAGCCTGAA CTCCAGCCTGAA CTCGCCCAGCCTGAA CTCGGCCCAG CTGGCCCAGCCTGAA AAACTGCCCAG AAAACCAGCCAA AAACTGCCCAG AAAACCAGCCAA AAATCCAGTC AAAATCCAGTC AAAAATCCAGTC AAAATCCAGTC AAATCCAGTC AAAATCCAGTC AAATCCAGTC AACCTGCACC AAATCCAGTC AATCCAGTC AAATCCAGTC AATCCAGTC AAATCCAGTC AAATCCAGTC AAATCCAGTC AAT	3036 21 CCCGGGCCAA AACGGCGGC CTAGAAGAGCT CAGGAAATCCT CGCTCGCGG GCTGCCGTG CTGCTGCGG AGAAGTGCT AATGAAGGT TGTCTCCCTC ACGGGGATAT TGTGTTTCACT AACGAAGACTC TAAAAGAACTC TAAAAGAGT TATTCTCCCA ACCAAACCTC TAAAAGAGT TGTGTTCAGT AGTGTGGAAT AGTGTGGAAT ATTCTCGAACTC GGGCTGTAGC GAAGGATCG CACGGCAGC CCTGCAGACTC CTGCAGACTC CTGCAGACTC CTGCAGACTC CTGCAGACGC CCCCCTGCAG CCCCCTGCAG CATGCCGGGC CCCCTGCAGCT CCAAGCACCC CCTCGAAGAGGT CCCCCTTGCAAGAGGT CCCCCCTGCAGCT CCCCCTGCAGCT CCAAGCACCC CCTGCAAGAGGT CCCCCTGCAGCT CCAAGCACCC CCTGCAAGGGT CCCCCTGCAGCT CCAAGCACCC CCTGCAGCGC CCCCTGCAGCGT CCAAGCACCC CCTGCAGCGCT CCCCCTGCAGCGT CCAAGCACCC CCTGCAACGGCT CCCCCTGCAGCGT CCAAGCACCC CCTGCAACGGCT CCCCCTGCAGCT CCAAGCACCC CCTGCAACGCT CCAAGCACCC CCTGCAACGCT CCAAGCACCC CCAACACCC CCAAGCACCC CCAAGCACC CCAAGCACCC CCAAGCCACC CCAACCC CCA	TCCGGACAGT CCCGGCCCCCCCCCCCCCCCCCCCCCCCC	TTGCTCATTT CGCACACACA GCGGCGTG GACGCCGGC GCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGA GCAGTTTCAC ACACGGTAAT CAGTCATTTCAC ACACGGTAAT TGAAAAGGGT ATGTCTTTAGA ACATAAGTA AAGATCTGGA ACAGACCACT AATGCTCTT AAGGCACCAC TGAAAAGCTCT TGAAAGCTACT TGAAAGCTACT TGAAAGCTACT TGAAGACCACT TGAAGCTACT TGAAGCTCCT AAGGCACAC CAGTTGAGAA CCGTTGAGAA CCGTTGAGAA CCGTTGAGAA CCGTTGAGAA CCGTTCACAC ACTGCCACAC ACTGCCACAC ACTGCCACAC CAGAGTTCTCA AGTGCTACTC AATGCGAGAT CAGATTCTCC CAGAGTTCTCC AATGCGAGAT CAGTCTTCCC CAGTTCTCC CAGTTCC CAGTTCTCC CAGTTCC CAGTTCTCC CAGTTCC CAGTTCTCC CAGTTCC CAGTTCTCC CAGTTCTCC CAGTTCTCC CAGTTCTCC CAGTTCC CAGTTCTCC CAGTTCCC CAGTTCTCC CA	ATTGCAACGG CGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG CTGAAGGAGA AGTGAAGAGA AGTGAAGAGA AGGAAACCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC ACCACCTCT TGTGGAGCTG AAAGTTAAG AACATCGGAT ACCACCTCT TGTGGAGCTG AAAGTTAAG GAACATTCGG AAGTCAGGAC TCTTCGGAAT CCTCGCAAA CCTCGGCAAG CATCGGCATG AGGAGGTTCC CAGCAGGAGG CCTGCAAA CCTCGGCAGAG CCTCTGCAAA CATCGGCATG AGGAGGTTCC CAGAGGAGTCT CTGACCTGCA ACTCTGGGAA CCTCTGCAAA CCTCGGAAGTCT CTGACCTGCA CCCGGGAAGTC CCCGGGAGTCT CCCGGGAGTCT CCCGGGGAGCC CCCCAGAGGCCC CCCCAGGGGCCC CCCCAGGGGCCC CCCCAGAGCCCC CCCCAGGGGCCC CCCCAGAGGCCC CCCCAGGGGCCC CCCCAGAGGCCC CCCCAGAGGCCC CCCCAGAGGCCC CCCCAGGGGCCC CCCCAGGGGCCC CCCCAGGGGCCC CCCCAGAGGCCC CCCCAGGGGCCC CCCCAGGGGCCC CCCCAGGGGCCC CCCCAGGGGCCC CCCCAGGGGCCC CCCCAGGGGCCC CCCCAGGGGCCC CCCCAGGGGCCC CCCCAGGGGCCC CCCAGGGGCCC CCCCAGGGGCCC CCCCAGGGGCCC CCCCAGGGGCCC CCCCAGGGGCCC CCCAGGGGCCC CCCCAGGGCCC CCCCAGGGCCC CCCCAGGGCCC CCCCAGGGCCC CCCCACAAGGCCT CCCCCCC CCCCAGGGCCC CCCCCCC CCCCCCCC CCCCCCCC	120 180 240 360 420 540 660 720 780 840 900 1080 1140 1200 1320 1380 1440 1560 1620 1680 1740 1860 1980 2040 2160 2220
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	Coding sequilibrium control co	uence: 37  11  CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTGCCGAGG GATGTGCAG GATGTGCAG CAGCGCGCC ATCTGGAAAG ACGATACTAA ATGACATGC ATGACAACAC CAAGAAGGCA CAGACACCG TAGGCATTAT ACAGATACAA CAGACAACCG TAGGCAGAG CAGCAGCAGC TAGGCAGAGCA CAGCAGCAGC CAGCCTGCAC CTGGCAGCAC CTGGCAACGC CTGGCAAACGC CTGGCAAACCAC CTGCAGCAC CTGCAGCAC CTGCAGCAC CTGCAGCAC CTGCACAC CTGCACC CTGCCACC CTGCCACC CTGCCACC CTGC	3036 21 CCCGGGCCAA AACGGGGGC TAGAAGAGCT TAGAAGAGCT TAGAAGAGCT CAGGAAATCC CGCTCGCAGG CTCGCAGGCC CTCTGTTCGG AAATGAAGGT TGTCTCCTC ACGGGGATAT TGTCTTCCCA ACCAAACCTC TAAAAGAGAG AGAGTTTCAG TAATCACGTT AGTGTGGAAT ATTTCTGGAA CCGTGACCTG CAGGGCTGTAGC CGTGACCTG GAAGGTATCAG TGTAATCAGTT AGTGTGGAAT CTGTCAGTGGG CACGGCAGAC CGTGACCTG CGAGAACTCC CTGCAGAGCT CCTGCAGAGCT CCTGCAGAGCT CCTGCAGAGCT CCCCCTGCAG CATGCCCGGA CATGCCGGA CATGCCGGAG CCCCCTGCAG CCGCCAGAGGG CCCCCTGCAG CCGCCAGAGGGG CCCCCTGCAG CCCCCCCCCC	TCTCGGACAGT GCGCGCCCCCCCCCCCCCCCCCCCCCCC	TTGCTCATTT CGCACACACA GCGGCGGGG GACGCCGGC GCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCTC TACACGGA ACACGGTAAT ACACGGTAAT TGAAAAGGGT ATGTGTTTCAC CAACTAAGT AAGATCTGGA ACAGACCACT AATGCTCTGT TGAAGACCACT AATGCTCTGT TGAAGACT TGAGCACTAC CGATTGTAAC CGGTTGAGAA TCAGCCACT AATGCTCTGT TGAAGACTACT TGGACAACG ACTGCCACC ACTGCCACC ACTGCCACC ACTGCCACC ACTGCCACC TCAGAGTTCTCC TGGAAGAACG ACTGCCACC ACTGCCACC TCAATTCTCC TCAGTCATCC TCAGTCATCC TCAGTCATCC TCAGTCTTCC TCAGTCTTCC TCAGTCTTCC TCAGTCTTCC TCAGGAAGAACA TTAGGGAAGAA TCAGGGAAGAA TCAGGGAAGAA TCAGGGAAGAA TCAGGGAAGAA TCAGGGAAGAA TCAGGGAAGAA TCAGGGAAGAA TCAGGGAAGAA TCAGGGAAGAA TTAGGGAAGAA TCAGGGAAGAA TCAGGGAAGAA	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCTG CGAAGGAACA AGTGAACACCAC TCTGGGTCAC ACCACCTCT ACCAATGAAA CCAGCACTTC TGTGGGTCAC ACCACCTCT AAAGTTAAG AACATCGCAA ACTCGCAAA CATCGCAAA CATCGGATA ACCACCTCT ACCACTCT ACCACTCT ACCACCTCT ACCACCTCC ACCACGAGAG CATCGCAGAA CATCGCAGAA CATCGCAGAAG CCACAGGAGC CCACAAGCCTCC GCACAGGACC CACAGGGCCC CCACAAGTCC CCCGGGGACC CCCCGGGGCC CCCCGGGGCCC CCCGGGGCCC CCCGGGGCCC CCCGGGGCCC CCCGGGGCCC CCCGGGGCCC CCCGGGGCCC CCCGGGGCCC CCCGCGGGCCC CCCGGGGCCC CCCCGGGGCCC CCCCGCGCGCCC CCCCGCGGCCC CCCCGCGCGCCC CCCCGCGGCCC CCCCCC	120 180 240 360 420 540 660 720 780 960 1020 1080 1140 1250 1380 1440 1500 1680 1740 1860 1920 1980 2040 2160 2220 2280 2340

	000000111100	0001100101	TAACCAAGGT	TTAACCATAG	CAATTCTCCT	CACCATOCTC	2460
	GGCCCCATCC	GGCAAGCAGA	TGTGGTTTAT	CTCARACCAIAG	OWITTCION.	PUCCULCUIG	2520
	TGICIICIIG	CIGCCGGATT	CATTGAAAAA	CTA ACCTCTC	ACCCLICAT	CCCCC ACCC	2580
	TITACAAATA	AGAAGACCAC	GGCTCACCTC	CCCCACCTTG	CANANCCCCT	CONTERCORNE	2640
5	COLOGUITATION	AACCCIGICA	GAAGGACAAT	CCCACCACA	TOTOTO CTC	TO TO A TOTAL	2700
,	CCGCCAGATT	CULACCCACC	CGGCCTGAAT	CCCAGGAGAI	CCCACTCAAC	TCAGAATGII	2760
	GACATCAGCA	BOCK COCCO	CCCACGTGCA	CCENCCETCC	CCCAGICACC	CCACCCACCC	2820
	*************	TCCACCGGGC	CCAGGGGACC	TCTANCCCA	DIGCOMMICE.	CARCCTCTC	2880
	AAGCC1GCAC	TIAGGCAGGC	AACAACTCGG	CTCACTCATG	CCTCCCCC	GAMOCCICIO	2940
10	CCTGCAGATC	CTCTGGCCAG	CCTGGCACCC	CICACICATO	CTCCACAAAA	TOCACA COA	3000
10			CECCTATATT				3060
	GTGCCCAGAT	CCACCCACAC	ATCTTTCAGC	MAGIGAGAAG	CCGACACCII	CCARCOMOTA	3120
	TGAAGACAGA	AGTTTGCACT	ATCTTTCAGC	CCAGIIGGA	GIIIIIIGIA	TCCAACIIIIA	3180
	GGATTTTTT	TAATGITTAA	AACATCATTA	CTATAAGAAC	TITGAGCIAC	A DEL A DEL AGI	3240
15	GCTGTGCTGT	GCTATGGTGC	TCTGTCTACT	TGCACAGGIA	CIIGIAAAII	ATTAATTAT	3300
13	GCAGAATGTT	GATTACAGTG	CAGTGCGCTG	TAGTAGGCAT	TITIMCCATC	WC1GWG1111	3360
	CCATGGCAGG	AAGGCTTGTT	GTGCTTTTAG	TATTTTAGIG	AACTIGAAA1	AICCIGCIIG	3420
	ATGGGATTCT	GGACAGGATG	TGTTTGCTTT	CIGATCAAGG	CCTTATTGGA	AAGCAGTCCC	
			TTATGGTACC				3480
20	CTCAGTTGAT	TTTCTGGATT	CCCCATCTCA	GGCCAGAGCC	AAGGGGCTTC	AGGTCCAGGC	3540
20	TGTGTTTGGC	TTTCAGGGAG	GCCCTGTGCC	CCTTGACAAC	TGGCAGGCAG	GCTCCCAGGG	3600
			TTCTGGCCAG				3660
			ACACCAGGAT				3720
			GTGAGCATGT				3780
25			AGCACTTCTT				3840
25	CCAGTAGGTT	ATTTAGCTTG	GGAAAGGTGG	TGTTTCTGTA	AGAAACCTAC	TGCCCAGGCA	3900
	CTGCAAACCG	CCACCTCCCT	ATACTGCTTG	GAGCTGAGCA	AATCACCACA	AACTGTAATA	3960
	CAATGATCCT	GTATTCAGAC	AGATGAGGAC	TTTCCATGGG	ACCACAACTA	TTTTCAGATG	4020
			GTCAATCAAG				4080
20			CTTGCAAAAA				4140
30			ATTATTCGTA				4200
			GCTGCAGGAA				4260
			CAACCTACCT				4320
			TATATAAAT				4380
25	CTCTTCACTC	TTCAAATGCC	TGACTAGGGA	GCCATGTTTC	ACAAGGTCTT	TAAAGTGACT	4440
35	AATGGCATGA	GAAATACAAA	AATACTCAGA	TAAGGTAAAA	TGCCATGATG	CCTCTGTCTT	4500
	CTGGACTGGT	TTTCACATTA	GAAGACAATT	GACAACAGTT	ACATAATTCA	CTCTGAGTGT	4560
			TGGGGTCAAC				4620
			GCCTTCCAGA				4680
40			CATAGTATTC				4740
40	AAACACACAC	AAAAGGGAAC	CCAGCTCTAA	TACATTCCAA	CTCGTATAGC	ATGCATCTGT	4800
			TCTTTAAAAT				4860
	AGATACATAC	AGAATTACTG	TAACTGATTA	CACTTGGTAA	TTGTACTAAA	GCCAAACATA	4920
	TATATACTAT	TAAAAAGGTT	TACAGAATTT	TATGGTGCAT	TACGTGGGCA	TTGTCTTTTT	4980
4.5	AGATGCCCAA	ATCCTTAGAT	CTGGCATGTT	TATGGTGCAT AGCCCTTCCT	TACGTGGGCA CCAATTATAA	TTGTCTTTTT GAGGATATGA	4980 5040
45	AGATGCCCAA	TAAAAAGGTT ATCCTTAGAT AAAAAAAAA	CTGGCATGTT	TATGGTGCAT AGCCCTTCCT	TACGTGGGCA CCAATTATAA	TTGTCTTTTT GAGGATATGA	
45	AGATGCCCAA ACCAAAAAAA	ATCCTTAGAT AAAAAAAAAA	CTGGCATGTT AA	TATGGTGCAT AGCCCTTCCT	TACGTGGGCA CCAATTATAA	TTGTCTTTTT GAGGATATGA	
45	AGATGCCCAA ACCAAAAAAA Seq ID NO:	ATCCTTAGAT AAAAAAAAA 78 Protein	CTGGCATGTT AA sequence	TATGGTGCAT	TACGTGGGCA CCAATTATAA	TTGTCTTTT GAGGATATGA	
45	AGATGCCCAA ACCAAAAAAA Seq ID NO:	ATCCTTAGAT AAAAAAAAAA 78 Protein cession #: 1	CTGGCATGTT AA sequence NP_003465	AGCCCTTCCT	CCAATTATAA	GAGGATATGA	
	AGATGCCCAA ACCAAAAAAA Seq ID NO:	ATCCTTAGAT AAAAAAAAA 78 Protein	CTGGCATGTT AA sequence	TATGGTGCAT AGCCCTTCCT	TACGTGGCA CCAATTATAA	TTGTCTTTTT GAGGATATGA	
45 50	AGATGCCCAA ACCAAAAAA Seq ID NO: Protein Acc 1	ATCCTTAGAT AAAAAAAAA 78 Protein cession #: 1 11	CTGGCATGTT AA sequence NP_003465 21	AGCCCTTCCT	CCAATTATAA 41	GAGGATATGA 51	5040
	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1       MAARPLPVSP	ATCCTTAGAT AAAAAAAAA 78 Protein cession #: 1 11   ARALLLALAG	CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG	31   VSLWNEGRAD	CCAATTATAA 41   EVVSASVRSG	GAGGATATGA 51   DLWIPVKSPD	5040
	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1           MAARPLPVSP SKNHPEVLNI	ATCCTTAGAT AAAAAAAAA 78 Protein cession #: 1 11   ARALLLALAG RLQRESKELI	CTGGCATGTT AA sequence NP_003465 21 i ALLAPCEARG INLERNEGLI	31   VSLWNEGRAD ASSFTETHYL	CCAATTATAA 41   EVVSASVRSG QDGTDVSLAR	GAGGATATGA 51   DLWIPVKSFD NYTVILGHCY	5040 60 120
	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1       MAARPLPVSP   SKNHPEVLNI   YHGHVRGYSD	ATCCTTAGAT AAAAAAAAA 78 Protein cession #: 1 11   ARALLLALAG RLQRESKELI SAVSLSTCSG	CTGGCATGTT AA sequence UP_003465 21 ALLAPCEARG INLERNEGLI LRGLIVFENE	31   VSLWNEGRAD ASSFTETHYL SYVLEPMKSA	41     EVVSASVRSG QDGTDVSLAR TNRYKLFPAK	GAGGATATGA 51   DLWIPVKSPD NYTVILGHCY KLKSVRGSCG	5040 60 120 180
50	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1   MAARPLPVSP SKNHPEVLNI YHGHVRGYSD SHHNTPNLAA	ATCCTTAGAT AAAAAAAAA  78 Protein cession #: 1 11   ARAILLALAG RLQRESKELI SAVELSTCSG KNVFPPPSQT	CTGGCATGTT AA sequence UP_003465 21 ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL	31   VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI	41   EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ	51   DLWIPVKSPD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR	5040 60 120 180 240
	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1       MAARPLPVSP SKNHPEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK	ATCCTTAGAT AAAAAAAAA  78 Protein cession #: 1 11 ARAILLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV	CTGGCATGTT AA sequence NP_003465 21   ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGVEVWNDM	31   VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF	41     EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ TSLHEFLDWR	S1   DLWIPVKSFD NYTVILGHCY KLKSVRGSG GKDLEKVKQR KMKLLPRKSH	5040 60 120 180 240 300
50	AGATGCCCAA ACCAAAAAAA Seġ ID NO: Protein Acc 1       MAARPLPVSP SKNHPEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY	ATCCTTAGAT AAAAAAAAA  78 Protein cession #: 1 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV FQGTTIGMAP	CTGGCATGTT AA sequence NP_003465 21   ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADQS	31   VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN	41     EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ TSLHEFLDWR PLGAAVTLAH	S1     DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH	60 120 180 240 300 360
50	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1     MAARPLPVSP SKNHPEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ	ATCCTTAGAT AAAAAAAAA  78 Protein cession #: 1 11   ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV FQGTTIGMAP MAVEKGGCIM	CTGGCATGTT AA  sequence 1P_003465 21    ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADQS NASTGYPFPM	31   VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSCSRKDL	41   EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV	51     DLWIPVKSPD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVRE	5040 60 120 180 240 300 360 420
50	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1     MAARPLPVSP SKNNPEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCY DTLDRGCSCO SFGGGKCGNR	ATCCTTAGAT ANAAAAAAA  78 Protein cession #: 1 1   ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV FQGTTIGMAP FVEGGCIM FVEGGECDC	CTGGCATGTT AA sequence NP_003465 21   ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADQS NASTGYPFPM GEFEECMNRC	31   VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSSCSRKDL CNATTCTLKP	41   EVVSASVRSG QDGTDVSLAR VADNREFQRQ TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV DAVCAHGLCC	51   DLWIPVKSPD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLPNLPEVRE EDCQLKPAGT	60 120 180 240 300 360 420 480
50 55	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1     MAARPLPVSP SKNHPEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGGQKCGNR ACRDSSNSCD	ATCCTTAGAT AAAAAAAAA  78 Protein cession #: 1 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV FQGTTIGMAP MAVEKGGCIM MAVEKGGCIM MAVEKGGCIM EVEEGECCDC LPEECTGASP	CTGGCATGTT AA  sequence NP_003465 21    ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADQS NASTGYPFPM NASTGYPFM GEPEECMNRC HCPANYYLHD	31   VSLWNEGRAD ASSFTETHYL SYVLEPMKS KATKYVELVI DKCSVSQDPF GGIVMDHSDN VPSSCSRKDI CNATTCTLKP GHSCQDVDGY	41	51   DLWIPVKSPD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVTLWGPG	60 120 180 240 300 360 420 480 540
50	AGATGCCCAA ACCAAAAAA  Seq ID NO: Protein Acc	ATCCTTAGAT ARAAAAAAA  78 Protein cession #: 1 11   ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV FQGTIIGMAP MAVEKGGCIM FVEEGEECDC LPEFCTGASP RVNSAGDPYG	CTGGCATGTT AA  sequence tp_003465 21     ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADQS NASTGYPFPM GEPEECMNRC HCPANYYLHD NCGKVSKSSF	31   VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPI GGIVMDHSDN VFSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC	41   EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV DAVCAHGLCC CYNGICQTHE GKIQCQGGAS	51     DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLPRKSH ELIGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVTLWGFG QPVIGTNAVS	60 120 180 240 300 360 420 480 540 600
50 55	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc I   MAARPLPVSP SKNHPEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGQQKCGNR ACRDSSNSCD AKPAPGICFE IETNIFLQQG	ATCCTTAGAT ANAAAAAAA  78 Protein cession #: 1 11	SEQUENCE SEQ	31   VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSODPF GGIVMDHSDN VPSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD	41	51     DLWIPVKSPD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC	60 120 180 240 300 360 420 480 540 600 660
50 55	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc I   MAARPLPVSP SKNNPEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSGV SFGGGKCGNR ACRDSSNSCD AKPAPGICFE IETNIPLQQG AMQCHGRGVC	ATCCTTAGAT ANAAAAAAA  78 Protein cession #: 1 1   ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV FQGTTIGMAP MAVEKGGCIM FVEEGECDC LPEFCTGASP RVMSAGDPYG GRILCRGTHV NNRNCHCEA	SEQUENCE SEQ	31   VSLWNEGRAD ASSFTETHYL EYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP	41	51   DLWIPVKSPD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLPNLPEVRE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS ITSVFGVHEC IGILVTILCL	5040 60 120 180 240 300 420 480 540 600 660 720
50 55	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1   MAARPLPVSP SKNHPEVLNI YHGHURGYSD SHHNTPNLAA LIEIANHUDK DNAQLVSGVY DTLDRGCSCQ SFGGGKCGNR ACRDSNSCD AKPAPGICFE IETNIPLQQG AMQCHGRGVC LAAGFVYYLK	ATCCTTAGAT AAAAAAAAA  78 Protein cession #: 1 11   ARAILLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV FQGTIIGMAP MAVEKGGCIM FVEEGEECDC LPEFCTGASP RVMSAGDPYG GRILCRGTHV NNRKNCHCEA RKTIIRLLFT	CTGGCATGTT AA  sequence tp_003465 21    ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGVEVWNDH IMSMCTADQS NASTGYPFPM GEFEECMARC HCPANYLHD NCGKVSKSSF YLGDDMPDPG HWAPPFCDKF NKKTTIEKLR	31   VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDF GGIVMDHSDN VFSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG	41   EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ TSLHEFLDW PLGAAVTLAH ETSLEKGMGV DAVCAHGLCC CYNGICQTHE GKIQCQGGAS GKICLNRQCQ IRQADNQGLT FQPCQAHLGH	51    DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVTLWGFG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP	60 120 180 240 300 360 420 480 540 600 660 720 780
50 55 60	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc I   MAARPLPVSP SKNHPEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGGOKCGNR ACRDSSNSCU AKPAPGICFE IETNIPLQQG AMQCHGRGVC LAAGFVVYLK DSYPPKDNPR	ATCCTTAGAT ARAAAAAAA  78 Protein cession #: 1 11   ARAILLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV FQGTTIGMAP MAVEKGGCIM FVESGEECDC LPEFCTGASP GRILCRGTHV NNRNCHCEA RKTLIRLLFT RLLQCQNVDI	SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  ALLAPCEARG INLERNEGLI LUGLIVFENE WARRHKRETL LUGVEVWNDM IMSMCTADQS NASTGYPFPM GEPECMNRC HCPANYYHD NCGKVSKSSF YLGDDMPDPG HWAPPFCDKF NKKTTIEKLR SRPLNGLNVP	31   VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VPSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQRVLP	41	51    DLWIPVKSPD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELIGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAKP	60 120 180 240 300 420 480 540 660 720 780 840
50 55	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc I   MAARPLPVSP SKNHPEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGQQKCGNR ACRDSSNSCD AKPAPGICFE IETNIFLQQG AMQCHGRGVC LAAGFVVVLL DSYPPKDNPR ALRQAQGTCK	ATCCTTAGAT ARAAAAAAA  78 Protein cession #: 1 11   ARAILLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV FQGTTIGMAP MAVEKGGCIM FVESGEECDC LPEFCTGASP GRILCRGTHV NNRNCHCEA RKTLIRLLFT RLLQCQNVDI	CTGGCATGTT AA  sequence tp_003465 21    ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGVEVWNDH IMSMCTADQS NASTGYPFPM GEFEECMARC HCPANYLHD NCGKVSKSSF YLGDDMPDPG HWAPPFCDKF NKKTTIEKLR	31   VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VPSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQRVLP	41	51    DLWIPVKSPD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELIGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAKP	60 120 180 240 300 360 420 480 540 600 660 720 780
50 55 60	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc I   MAARPLPVSP SKNHPEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGGOKCGNR ACRDSSNSCU AKPAPGICFE IETNIPLQQG AMQCHGRGVC LAAGFVVYLK DSYPPKDNPR	ATCCTTAGAT ARAAAAAAA  78 Protein cession #: 1 11   ARAILLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV FQGTTIGMAP MAVEKGGCIM FVESGEECDC LPEFCTGASP GRILCRGTHV NNRNCHCEA RKTLIRLLFT RLLQCQNVDI	SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  ALLAPCEARG INLERNEGLI LUGLIVFENE WARRHKRETL LUGVEVWNDM IMSMCTADQS NASTGYPFPM GEPECMNRC HCPANYYHD NCGKVSKSSF YLGDDMPDPG HWAPPFCDKF NKKTTIEKLR SRPLNGLNVP	31   VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VPSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQRVLP	41	51    DLWIPVKSPD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELIGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAKP	60 120 180 240 300 420 480 540 660 720 780 840
50 55 60	AGATGCCCAA ACCAAAAAA  Seq ID NO: Protein Acc      MAARPLPVSP SKNHPEVLNI YHGHURGYSD SHHNTPNLAA LIEIANHUDK DNAQLVSGVY DTLDRGCSCQ SFGGGKCGNR ACRDSNSCD AKPAPGICFE IETNIPLQG AMQCHGRGVO LAAGFVVYLK DSYPPKDNPR ALRQAQGTCK RSTHTAYIK	ATCCTTAGAT ARAAAAAAA  78 Protein cession #: 1 11   ARAILLALAG RILQESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV FQGTIIGMAP MAVEKGGCIM FVEEGEECDC LPEFCTGASP GRILCRGTHV NNRKNCHCE RKTLIRLLFT RLLQCQNVDI PNPPQKPLPA	SEQUENCE  SEQUENCE  P_003465  I  ALLAPCEARG INLERNEGLI LUGLIVFENE WARRHKRETL LUGVEVWNDD NASTGYPFPM GEFEECMNRC HCPANVYLHD NCGKVSKSSF YLGDDMPDPG HWAPPFCDK NKKTIEKLR SRPLNGLNVP DPLARTTRLT	31   VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VPSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQRVLP	41	51    DLWIPVKSPD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELIGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAKP	60 120 180 240 300 420 480 540 660 720 780 840
50 55 60	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc I   MAARPLPVSP SKNHPEVLNI JHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGGQKCGNR ACRDSNSCD AKPAPGICFE IETNIPLQG AMQCHGRGVC LAAGFVVVL LAAGFVVVL LAAGFVVVL CSYPPKDNPR ALRQAQGTCK RSTHTAYIK Seq ID NO:	ATCCTTAGAT ANAAAAAAA  78 Protein cession #: 1 11   ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV FQGTTIGMAP MAVEKGGCIM FVEEGEECDC LPEECTGASP GRILCRGTHV NNRNCHCEA RKTLIRLLFT RLLQCQNVDI PNPPQKPLPA	CTGGCATGTT AA  sequence 1P_003465 21    ALLAPCEARG INLERNEGLI LKGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADQS NASTGYPFPM GEPECMNRC HCPANYYLHD NCGKVSKSF YLGDDMPDPG HWAPPFCDKF NKKTTIEKLE SRPLNGLNVP DPLARTTRLT	31   VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VPSSCSRKDL CNATTCTLKP GHSCQDVDGF AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPR QPQSTQRVLP HALARTPGQW	41	51    DLWIPVKSPD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELIGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAKP	60 120 180 240 300 420 480 540 660 720 780 840
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc I   MAARPLPVSP SKNHPEVINI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVV STGGQKCGNR ACRDSSNSCD AKPAPGICFE IETNIPLQG AMQCHGRGVC LAAGFVVYLK DSYPPKDNPR ALRQAQGTCK RSTHTAYIK Seq ID NO: Nucleic Ac	ATCCTTAGAT ANAAAAAAA  78 Protein cession #: 1 11   ARALLLALAG RIQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV FQGTTIGMAP MAVEKGGCIM FVEEGEECDC LPEFCTGASP RVNSAGDPYG GRILCRGTHV NNRKNCHCEA RKTLIRLLFT RLLQCQNVDI PNPPQKPLPA 79 DNA sequid Accession	SEQUENCE SEQ	31   VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VPSSCSRKDL CNATTCTLKP GHSCQDVDGF AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPR QPQSTQRVLP HALARTPGQW	41	51    DLWIPVKSPD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELIGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAKP	60 120 180 240 300 420 480 540 660 720 780 840
50 55 60	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc      MAARPLPVSP SKNHPPVINI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGGGKCGNR ACRDSSNSCD AKPAPGICFE IETNIPLQQG IETNIPLQQG CLAAGFVVYLK DSYPPKDNPR ALRQAGGTCC RSTHTAYIK Seq ID NO: Nucleic Ac Coding seq	ATCCTTAGAT AAAAAAAAA  78 Protein cession #: 1 11	SEQUENCE  F 003465  21  ALLAPCEARG INLERNEGLI LUGUEVENDM IMSMCTADQS NASTGYPFPM GEPECMNRC HCPANYUHD NCGKVSKSF YLGDDMPDPG HWAPPFCDKF NKKTIEKLR SRPLNGLNVP DPLARTTRLT  UENCE  ##: NM_003.1043	31.   VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDP GGIVMDHSDN VPSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQRVLP HALARTPGQW	41   EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ TSLHEFLDW PLGAAVTLAH ETSLEKGMGV DAVCAHGLCC CYNGICQTHE GKIQCQGGAS GKICLNRQCQ IRQADNQGLT FQPCQAHLGH PLERAPRAPS ETGLRLAPLR	GAGGATATGA  51    DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVTLWGFG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAKP PAPQYPHQVP	60 120 180 240 300 420 480 540 660 720 780 840
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc I   MAARPLPVSP SKNHPEVINI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVV STGGQKCGNR ACRDSSNSCD AKPAPGICFE IETNIPLQG AMQCHGRGVC LAAGFVVYLK DSYPPKDNPR ALRQAQGTCK RSTHTAYIK Seq ID NO: Nucleic Ac	ATCCTTAGAT ANAAAAAAA  78 Protein cession #: 1 11   ARALLLALAG RIQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV FQGTTIGMAP MAVEKGGCIM FVEEGEECDC LPEFCTGASP RVNSAGDPYG GRILCRGTHV NNRKNCHCEA RKTLIRLLFT RLLQCQNVDI PNPPQKPLPA 79 DNA sequid Accession	SEQUENCE SEQ	31   VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VPSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQRVLP HALARTPGQW  714 31	41	51    DLWIPVKSPD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELIGHNFGMNH CLFNLPEVRE EDCOLKPAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILLE LGKGLMRKPP VPARPLPAKP PAPQYPHQVP	60 120 180 240 300 420 480 540 660 720 780 840
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1   MAARPLPVSP SKNHPEVINI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVV DTLDRGCSQQ SFGGQKCGNR ACRDSSNSCD AKPAPGICFE IETNIPLQQG AMQCHGRGVC LAAGFVVYLK DSYPPKDNPR ALRQAQGTCK RSTHTAYIK Seq ID NO: Nucleic Ac Coding seq 1	ATCCTTAGAT ANAAAAAAA  78 Protein cession #: 1 11	SEQUENCE SEQ	31   VSLWNEGRAD ASSFTETHYL EXYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VPSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQRVLP HALARTPGQW  714 31	41	51   DLWIPVKSPD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAKP PAPQYPHQVP	5040 60 120 180 240 300 360 420 480 540 660 720 780 900
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc      MAARPLPVSP SKNHPLPVSP SKNHPLPVSN SHHNTPNLAA LIEIANHOUD DTLDRGCSCQ SFGGGKCGNR ACRDSSNSCD AKPAPGICFE IETNIPLQGG AMQCHGRGVC LAAGFVVYLK DSYPPKDNPR ALRQAGGTCK RSTHTAYIK Seq ID NO: Nucleic Ac Coding seq 1	ATCCTTAGAT AAAAAAAAA  78 Protein cession #: 1 11   ARAILLALAG RIQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV FQGTTIGMAP MAVEKGGCIM FVEEGEECDC LPEFCTGASP RVMSAGDPYG GRILCRGTHV NNRKNCHCEA RKTLIRLLFT RLLQCQNVDI PNPPQKPLPA  79 DNA seq id Accessio vence: 135. 11   GGAAAAGGCGA	SEQUENCE  FOOS 465  INLERNEGLI LUGUEVENE WARRHKRETL LUGUEVEND MIMMCTADQS NASTGYPFPM GEFEECMNRC HCPANYLHD NCGKVSKSSF YLGDDMPDPG HWAPPFCDKF NKKTIEKLR SRPLNGLNVP DPLARTTRLT  UENCE  #: NM_003 .1043 21	31   VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDP GGIVMDHSDN VPSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQRVLP HALARTPGQW  714 31   AGAGTGGGAG	41   EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFORQ TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV DAVCAHGLCC CYNGICQTHE GKIQCQGGAS GKICLNRQCQ IRQADNQGLT FOPCQAHLGH PLERAPRAPS ETGLRLAPLR  41   GAGGAGGGGGA	GAGGATATGA  51    DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCQLKPAGT OQCVTLWGFG RPVIGTNAVS NISVFGVHEC LGKGLMRKPP VPARPLPAKP PAPQYPHQVP	60 120 120 240 300 360 420 480 540 600 720 780 840 900
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc	ATCCTTAGAT ANAAAAAAA  78 Protein cession #: 1 11   ARALLIALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV FQGTTIGMAP MAVEKGGCIM FVEEGEECDC LPEFCTGASP GRILCRGTHV NNRNCHCEA RKTLIRLLFT RLLQCQNVDI PNPPQKPLPA  79 DNA seq id Accessio uence: 135. 11   GAAAAGGCGA	SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  ALLAPCEARG INLERNEGLI LUGUVEVWNDM IMSMCTADQS NASTGYPFPM GEPECMNCT HCANVYHD NCGKVSKSSF YLGDDMPDPG HWAPPFCDKF NKKTTIEKLM SRPLNGLNVP DPLARTTRLT  UERICE  # : NM_003 .1043 21	31   VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VPSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQRVLP HALARTPGQW  714 31   AGAGTGGGAG ACAAAGGATC	41	51     DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KKKLPRKSH ELIGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAKP PAPQYPHQVP	60 120 120 300 360 420 480 540 660 720 780 900
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1   MAARPLPVSP SKNHPEVINI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGQQKCGNR ACRDSSNSCD AKPAPGICFE IETNIFLQQG AMQCHGRGVC LAAGFVVYLK DSYPPKDNPR ALRQAQGTCK RSTHTAYIK Seq ID NO: Nucleic Ac Coding seq 1   GAGGAGGAGGG GAGGAGGAGGG GAGGAGGAGGG GAGGAG	ATCCTTAGAT ANAAAAAAA  78 Protein Cession #: 1 11   ARALLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV FQGTTIGMAP MAVEKGGCIM FVEEGEECDC LPEFCTGASP GRILCRGTHV NNRNCHCEA RKTLIRLFT TRLLQCQNVDI PNPPQKPLPA  79 DNA seq id Accessio vence: 135. 11   GAAAAAGGCGAA AGGAGGAAGGAG AACCATGTGT	SEQUENCE UP 003465 21   ALLAPCEARG INLERNEGLI LUGUVEVENDE WARRHKRETL LUGUEVWNDE IMSMCTADQS NASTGYPFPM GEPECMNRC HCPANYYLHD NCGKVSKSF YLEDDMPDPG HWAPPFCDKF NKKTTIEKL UENCE n #: NM_003 .1043 21   GCAAAAAGGA AGGGGGAGC GCCGAGGGGG	31   VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSODPF GGIVMDHSDN VPSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPFRG QPOSTQRVLP HALARTPGQW  714  31   AGAGTGGGAG ACAAAGGATC TGGGCCAGTT	41	GAGGATATGA  51      MIPVKSPD NYTVILGHCY KLKSVRGSGG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP PAPQYPHQVP  51    AGCGGCGAAG GACCGGAGGT GGCTTTGGTGT	60 120 180 240 300 360 420 480 540 660 720 780 900
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc      AARPLPVSP SKNHPPVINI YHGHVRGYSD SHHNTPNLAA LIEIANHOUD DTLDRGCSCQ SFGGGKCGNR ACRDSSNSCD AKPAPGICFE IETNIPLQQG AMQCHGRGVC LAAGFVVYLK DSYPPKDNPR ALRQAGGTCK RSTHTAYIK Seq ID NO: Nucleic Ac Coding seq 1     GAGGAGGAGG GAGGAAGAGG GAGGAAGAGG TAATACCAAG TGGCCACCTT	ATCCTTAGAT AAAAAAAAA  78 Protein cession #: 1 11	SEQUENCE  F 003465  I 003465  I 1  ALLAPCEARG INLERNEGLI LUGUEVENDE MARRHKRETL LUGVEVWNDM IMSMCTADQS NASTGYPFPM GEPECMNRC HCPANYLHD NCGKVSKSF YLGDDMPDPG HWAPPFCDKF NKKTTIEKLR SRPLNGLNVP DPLARTTRLT  UENCE  #: NM_003 .1043  21  GCAAAAAAGGA AGAGGGGAGCC GCGGGGGGCCCG	31   VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VPSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPFRG QPQSTQRVLP HALARTPGQW  714 31   AGAGTGGGAG ACAAAGGATC TGGGCCACCAA	41   EVVSASVRSG QDGTDVSLAR TMRYKLFPAK VADNREFORQ PLGAAVTLAH ETSLEKGMGV DAVCAHGLCC CYNGICQTHE GKIQCQGGAS GKICLNRQCQ IRQADNQGLT FOPCOAHLGH PLERAPRAPS ETGLRLAPLR  41   GAGGAGGGGA CAGGTCTCCC CATGACCCTG CCCACCCGAG	GAGGATATGA  51    DLWIPVKSFD	60 120 180 240 300 360 420 480 540 660 720 780 840 900
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc        AGATGCCAA ACCAAAAAAA Seq ID NO: Protein Acc     AGATGCAAAAAAA     AGATGCAAAAAA     AGATGCAAAAAAA     AGATGCAAAAAAA     AGATGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	ATCCTTAGAT ARAAAAAAA  78 Protein cession #: 1 11   ARALLIALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV FQGTIIGMAP MAVEKGGCIM FVEEGEECDC LPEFCTGASP RVNSAGDPYG GRILCRGTHV NNRKNCHCEA ARKTLIRLLFT RLLQCQNVDI PNPPQKPLPA  79 DNA seq cid Accessio Lid Access	SEQUENCE  SEQUEN	31   VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPI GGIVMDHSDN VFSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPFRG QPQSTQRVLP HALARTPGQW  714 31   AGAGTGGGAG ACAAAGGATC TGGGCCACTA ACGCCACCAA	41	51    DLWIPVKSFD DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVTLWGFG RPVIGTNAVS NISVFGVHEC LGKILMTKPP VPARPLPAKP PAPQYPHQVP  51    AGCGGCGAAG GGCGCGAAG GGCCCAAG ATCCAGCACT	60 120 180 240 300 420 480 660 720 840 900
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc        MAARPLPVSP SKNHPEVLNI     MAARPLPVSP SKNHPEVLNI LIEIANHUDK DNAQLVSGVY DTLDRGCSCQ SFGGQKCGNR ACRDSSNSCD AKPAPGICFE LIETNIFLQQG AMQCHGRGVC LAAGFVVVLK DSYPPKDNPR ALRQAQGTCK RSTHTAYIK Seq ID NO: Nucleic Acc Coding seq 1     GAGGAGGAGG GAGGAGGAGG GAGGAAGAGG TAATACCAAG TGGCCACCTTI ACAGGAGCTCA	ATCCTTAGAT ANAAAAAAA  78 Protein cession #: 1 11   ARALLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV FQGTTIGMAP MAVEKGGCIM FVEEGEECDC LPEFCTGASP GRILCRGTHV NNRNCHCEA RKTLIRLLF TRLLQCNVDI PNPPQKPLPA  79 DNA seq id Accessio uence: 135. 11   GAAAAGGCGAA AGCAGGAGGAA AACCATGTGT TGACCCGGCC CCAGCAGAAA CGCTGGCGAA	SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  ALLAPCEARG INLERNEGLI LUGLIVFENE WARRHKRETL LUGVEVWNDM IMSMCTADQS NASTGYPFPM GEPECMNRC HCPANYYLHD NCGKVSKSF YLGDDMPDPG HWAPPFCDKF NKKTTIEKF SRPINGLNVP DPLARTTRLT  UENCE  SEQUENCE  GCAAAAAGGA AGGGGAGGC GCGCGCGGGGCCGCC GGGGGGCCCCTGT GTGGGGGTCTG	31   VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VPSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEWRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQRVLP HALARTPGQW  714 31   AGAGTGGGAG ACAAAGGATC TGGGCCAGTT ACGCCACCAA GCGTGTTTGA	41	51     UMIPVKSPD NYTVILGHCY KIKSVRGSGG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVTLWSPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP PAPQYPHQVP  51   AGCGGCGAAG GCTCCCCAAG GCTCCCCAAG ATCCAGCACT AACAACTCTT	60 120 180 240 300 420 480 540 660 720 780 900
50 55 60 65 70 75	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc      AARPLPVSP SKNHPFVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGGGKCGNR ACRDSSNSCD AKPAPGICFE IETNIPLQQG IETNIPLQQG CLAAGFVVYLK DSYPPKDNPR ALRQAGGTCK RSTHTAYIK Seq ID NO: Nucleic Ac Coding seq 1     GAGGAGGAGG GAGGAAGAGG TAATACCAAG TGGCCACCTT ACAGGAGTTCG GTTTGGTTCAR GTGAGGATTCC	ATCCTTAGAT AAAAAAAAA  78 Protein cession #: 1 11 11 ARAILLALAG RIQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV FQGTTIGMAP MAVEKGGCIM FVEGGECDC LIPECTGASP RVNSAGDPYG GRILCRGTHV NNRKNCHCEA RKTLIRLLFT RLLQCQNVDI PNPPQKPLPA 79 DNA seq id Accessio Lence: 135. 11 GGAAAAGGCGA AGGAGGAGGAA AACCATGTGI TGACCCGGCG CCAGCAGAAAA CCGCTGGCGAT GGGCTTACAT	SEQUENCE  F 003465  I 003465  I 1  ALLAPCEARG INLERNEGLI LUGUEVENDE MARRHKRETL LUGVEVWNDM IMSMCTADQS NASTGYPFPM GEFEECMNRC HCPANYLHD NCGKVSKSF YLGDDMPDFG HWAPPFCDKF NKKTIEKLR SRPLNGLNVP DPLARTTRLT  UENCE  #: NM_003 .1043 21  GCAAAAAGGA GGCAGCGGG GCCGCGGGGGCCGGGGGGCCGGGGGGCCGGGGGG	31   VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVII DKCSVSQDPF GGIVMDHSDN VPSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPFRG QPQSTQRVLP HALARTPGQW  714 31   AGAGTGGGAG ACAAAGGATC TGGGGCAGTT ACGCCACCAA GCGTGTTTGA	41   EVVSASVRSG QDGTDVSLAR TMRYKLFPAK VADNREFORQ DAVCAHGLICC CYMGICQTHE GKIQCQGGAS GKICLNRQCQ IRQADNQGLT FQPCQAHLGH PLHRAPRAPS ETGLRLAPLR  41   GAGGAGGGGA CAGGTCTCCC CATGACCCTG CCCACCCGAG ATGTTTCGAG GCACAACGCT	51   DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVILWGFG RPVIGTNAVS NISVFGVHEC LGKGLMRKPP VPARPLPAKP PAPQYPHQVP  51   AGCGGCGAAG GACCGGAGGT GCTTTGGTGT GGTTTGGTGT AACAACTCTT GGAAAATTTG	60 120 180 240 300 360 420 480 540 720 780 900
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	AGATGCCCAA ACCAAAAAA ACCAAAAAAA Seq ID NO: Protein Acc      AARPLPVSP SKNHPEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGGGKCGNR ACRDSNSCD AKPAPGICFE IETNIPLQG AMQCHGRGVC LAAGFVVYLK DSYPPKDNPR ALRQAQGTCK RSTHTAYIK Seq ID NO: Nucleic Ac Coding seq      GAGGAGGAGG GAGGAAGAGG GAGGAAGAGG GAGGAAGAGG GAGGAG	ATCCTTAGAT ARAAAAAAA  78 Protein cession #: 1 11   ARAILLALAG RLQRESKELI SAVELSTCSG KNVFPPPSQT FYRPLNIRIV FQGTIGMAP MAVEKGGCIM FVEEGEECDC LPEFCTGASP RVNSAGDPYG GRILCRGTHV NNRNCHCEA ARKTLIRLLFT RLLQCQNVDI PNPPQKPLPA  79 DNA seq id Accessio uence: 135. 11   GAAAAAGGCGAA AGGAGGAGGAA CGCTGCGGCGAA CGCTGGCGAA CGCTGGCGCAT CGAGTCATTC	CTGGCATGTT AA  sequence IP_003465 21       ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGVEVWNDN NASTGYPFPM GEFEECMARC HCPANVYLHD NCGKVSKSSF YLGDDMPDPG HWAPPFCDK SRPLNGLNVP DPLARTTRLT  uence       GCAAAAAAGGA AGAGGGAGG GCCGACGGGG GGGCGCTGT GGGGGTGTG GGGGGTTGCA ATCAAAAACC	31   VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDF GGIVMDHSDN VFSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPFRG QPQSTQRVLP HALARTPGQW  714 31   AGAGTGGGAG ACAAAGGATC TGGGCCAGTT TGAGCCACCAA CCCTGCAGAA TGACTTTCT CCTTGAAATG	41   EVVSASVRSG QDGTDVSLAR TMRYKLFPAK VADNREFQRQ TSLHEFLDW FLGAAVTLAH ETSLEKGMGV DAVCAHGLCC CYNGICQTHE GKIQCQGAS GKICLNRQCQ IRQADNQGLT FQPCQAHLGH PLHRAPRAPS ETGLRLAPLR  41   GAGGAGGGGA CAGGTTTCCAG CCCACCCGAG ATGTTTCCAG GCACAACGCT TAAGGCCCAC	GAGGATATGA  51    DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGNNH CLFNLPEVRE EDCQLKPAGT QQCVTLWGFG RPVIGTNAVS NISVFGVEEC IGILVTILCL LGKGLMRKPP VPARPLPAKP PAPQYPHQVP  51    AGCGGCGAAG GACGGCGAAG GACCGCAAG ACCACTCTT GGTTTCGCTGT GGAAAAATTTG GGTTCTGCGGC	60 120 180 240 300 420 480 540 660 720 840 900
50 55 60 65 70 75	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc	ATCCTTAGAT ARAAAAAAA  78 Protein cession #: 1 11   ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV FQGTTIGMAP MAVEKGGCIM FVEEGEECDC LPEFCTGASP GRILCRGTHV NNRNCHCEA RKTLIRLLFT RLLQCQNVDI PNPPQKPLPA  79 DNA seq id Accessio cence: 135. 11   GAAAAGCGAA AGGAGGAGGA AGGAGGAGGA CGCTGGCGAT CCGCCGCC CCAGCAGAAA CGCTGGCGAT CCGCCGAT CCTGCATAAGC	SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  ALLAPCEARG INLERNEGLI LIGLIVFENE WARRHKRETL LUGVEVWNDM GEDEECMNCT HOMMOTADQS NASTGYPFPM GEDEECMNCT HCANVYHD NCGKVSKSSF YLGDDMPDPG HWAPPFCDKF NKKTTIEKLR SRELNGLNVP DPLARTTRLT  UERICE  SECUENCE GCAAAAAGGA AGAGGGGAGC GCGGGGACCGG GCGGGGACCGG GGCGGCCTGTG GGGGGTTGCG ATCAAAGACG CCGGAAGTGCC	31   VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VPSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQRVLP HALARTPGQW  714  31   AGAGTGGGAG ACAAAGGATC TGGGCCACTA CCCTGCAGAA GCGTGTTTGA TGGCTTTGAAATG CCTGCAGAA CCCTTGCAGAA CCCTGCAGGA CCCTTGCAGAA CCCTGCAGGA CCCTTGCAGAA CCCTGCAGGA CCCTTGCAGAA CCCTGCAGGA CCCTTCGCAGAA CCCTGCAGGA CCCTTCGCAGAA CCCTGCAGGA CCCTGCAGGA CCCTCCCCCC CCCCCCCCCC	41	51   DLWIPVKSPD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILLL LGKGLMRKPP VPARPLPAKP PAPQYPHQVP  51   GCTTGGGGC GAAG GACGGGAGGT GCTCCCAAG ATCAGCACT AACAACTCTT GGGAAAATTTG GGTCCGGGG GCTCCCGGGG TCCCCAGTTGC TCCCAGTTGC	60 120 180 240 300 420 480 540 660 720 780 900
50 55 60 65 70 75	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc       MAARPLPVSP SKNHPEVINI   HIGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGQQKCGNR ACRDSSNSCD AKPAPGICFE LIETNIFLQQG AMQCHGRGVC LAAGFVVVLK DSYPPKDNPR ALRQAQGTCK RSTHTAYIK Seq ID NO: Nucleic Ac Coding seq       GAGGAGGAGG GAGGAGGAGG GAGGAGGAGG TAATACCAAG TGGCCACCTT ACCAGGAGTTCC GTTTGGTCAA GTGAGATTCC ATGCCCAGGG ACCAGGTTCCG AGCGGGAATTCCG AGCGGGGAATTCCG AGCGGGGAATTCCG AGCGGGGAATTCCG AGCGGGGAATTCCG AGCGGGGAATTCCG AGCGGGGAATTCCG AGCGGGGAATTCCG AGCGGGGAATTCCGGGGGAATCCCGGGGGGAGGGGA	ATCCTTAGAT ANAAAAAAA  78 Protein Cession #: 1 11   ARALLALAG RLQRESKELI SAVSLSTCSG KNVFPPSQT FYRPLNIRIV FQGTTIGMAP MAVEKGGCIM FVEEGEECDC LPEECTGASP GRILCRGTHV NNRNCHCEA RKTLIRLLFT TRLLQCQNVDI PNPPQKPLPA  79 DNA seq id Accessio uence: 135. 11   GAAAAGGCGAA AGCATTGTG TGACCGGGGG CCCAGCAGAAA GGGGGTTACAT GGGGCTTACAT GGGGCTTACAT GCTGCATAAGG CTACCTCAAAG	SEQUENCE UP 003465 21   003465 21   ALLAPCEARG INLERNEGLI LUCYEVWNDM IMSMCTADQS WASTGYPFPM GEPECMNRC HCPANYYLHD NCGKVSKSF YLEDDMPDFG HWAPPFCDKF NKKTTIEKL USELE  ##: NM_003 .1043 21   GCAAAAAGGA AGAGGGGAGC GCCGAGCGGC GCCGAGCGGC GGCGCTGTI GGGGATTTGCA CGGGAGTGCC CGGGAGTGCC CGGGAGTGCC CGGGAGTGCC CGGGGAGTGCC CGGGGAGTGCC CGCGAAGTGCC CCGGAAGTGCC	31   VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSODPF GGIVMDHSDN VPSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPFRG QPOSTQRVLP HALARTPGQW  714  31   AGAGTGGGAG ACAAAGGATC TGGGCCAGTA ACGCCACCAA CCCTGCAGAA GGGTGTTGAATG CGGGCATCAG GGGCGCTGC	41	GAGGATATGA  51	60 120 180 240 300 360 420 480 540 720 780 900 60 120 180 240 300 420 480 540 900
50 55 60 65 70 75	AGATGCCCAA ACCAAAAAAA ACCAAAAAAA Seq ID NO: Protein Acc	ATCCTTAGAT ARAAAAAAA 78 Protein cession #: 1 11   ARAILLALAG RILQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRI FQGTTIGMAP MAVEKGGCIM FVEEGEECDC LPEFCTGASP RVMSAGDPYG GRILCRGTHV NNRKNCHCEA RKTLIRLLFT RLLQCQNVDI PNPPQKPLPA 79 DNA seq cid Accessio vence: 135. 11   GAAAAGGCGA AACCATGTGT TGACCCGGCG CCAGCAGAAA CGGTGGCGTTACAT GGGGTTACAT GGGCTTACAT GGGTTACAT GGGTTACAT GGGTTACAT GGGTCATACG CTACCTCAAC GGATCCATTY	SEQUENCE  P_003465  INLERNEGLI LIAPCEARG INLERNEGLI LIGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADQS NASTGYPFPM GEFEECMARC HCPANYLHD NCGKVSKSSF YLGDDMPDPG HWAPPFCDKF NKKTIEKLR SRPLNGLNVP DFLARTTRLT  UENCE  #: NM_003  1043  21    GCAAAAAAGGA AGAGGGGAGC GCCGACCGGG GGGGACCG GGGGGTGTG GGGGGTTGC ATCAAAGACC CGGGAGTGCC CACGACCTGT AAGGACTTGC CACACCCTGT AAGGACTTGC CACGACCTGT CACGACCTCT CACGACCTCT CACGACCTCT CACGACCTCT	31   VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDP GGIVMDHSDN VPSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPFRG QPQSTQRVLP HALARTPGQW  714 31   AGAGTGGGAG ACAAAGGATC TGGGCAGTTTGA CCCTGCAGAA CCCTGCAGAA CCCTGCAGAA CCCTGCAGCA TGACTTTCT CCTTGAAATG CCGTGCACCAC TGGCCGCTGC TGGGCGGCTGC TGGCGCGCTGC TGCTGCACCAC	41   EVVSASVRSG QDGTDVSLAR TMRYKLFPAK VADNREFQRQ TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV DAVCAHGLCC CYNGICQTHE GKIQCQGAS GKICLNRQCQ IRQADNQGLT FQPCQAHLGH PLERAPRAPS ETGLRLAPLR  41   GAGGAGGGGA CAGGTCTCCC CATGACCCTG CATGACCCTG GCACAACGCT TAAGGCCAAC TAAGGCCAAC TAAGCCCAAC TAAGGCCAAC CAGGAAATGGTC CCCAGGAAAC AACCCTACCTAC	GAGGATATGA  51    DLWIPVKSFD	60 120 180 240 300 360 420 480 540 660 720 780 840 900
50 55 60 65 70 75 80	AGATGCCCAA ACCAAAAAAA ACCAAAAAAA Seq ID NO: Protein Acc        AARPLPVSP SKNHPEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGGOKCGNR ACRDSSNSCI LAAGFVYVLK DSYPPKDNPR ALRQAQGTCK RSTHTAYIK Seq ID NO: Nucleic Ac Coding seq       GAGGAGGAGG GAGGAAGGG TAATACCAAG TAGCCACCT ACGGGGATTCG ATGCCAGGG ACAGGTTCGC AGGGGAAGT AGGGGGAAT TAGTGGAGATT TAGTGGAGAT TAGTGGAGATT TAGTGGAGAT TAGTGGAGATT TAGTGGAGAT TAGTGCTGCT	ATCCTTAGAT ARAAAAAAA  78 Protein Cession #: 1 11   ARALLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV FQGTIIGMAP MAVEKGGCIM FVEEGEECDC LPEFCTGASP RVNSAGDPYG GRILCRGTHV NNRNCHCEA ARKTLIRLFT RLLQCQNVDI PNPPQKPLPA  79 DNA seq cidence: 135. 11   GAAAAAGGCGA AGGAGGAGGA AGGAGGAGGAGAA CGCTGGCGATACCT CTGCATAAGG CTACCTCAAAG GGTTCATTC CTGCATTAGG CGACTGTGGC CGACCTGTGGC CGACCTGTGCC CGCCCC CGACCTGTGCC CGCCCCTGTGCC CGCCCCC CGCCCCC CGCCCCC CGCCCC CGCCCC CGCCCCC CGCCCC CGCCCC CGCCCC CGCCCC CGCCCC CGCCCC CGCCCC CGCCCC CCCCCC	SEQUENCE  SEQUEN	31   VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPY GGIVMDHSDN VPSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQRVLP HALARTPGQW  714  31   AGAGTGGGAG ACAAAGGATC TGGGCCAGTA ACGCCACCAA CCCTGCAGAA CCCTGCAGCCCCTGCCGCGCTGCCCCTGCAGAA CCCTGCAGCACA CCGCCCTCCCCCCTTCCTCCCTCGAGAA CCCTGCAGCACACACACACACACACACACACACACACACA	41	51    DLWIPVKSFD DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSE ELGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC LGKGLMRKPP VPARPLPAKP PAPQYPHQVP  51    AGCGGCGAAG GACGGCGAAG GACGGCGAAG GACCACC AACAACTCTT GGAAAATTTG GGTCTGCGGC TCCCAGTTGC CACCCGGTGA GGTCCAGGTTC	60 120 180 240 300 420 480 540 660 720 900 60 120 180 240 360 420 480 540 600 600 720
50 55 60 65 70 75	AGATGCCCAA ACCAAAAAAA ACCAAAAAAA Seq ID NO: Protein Acc        AARPLPVSP SKNHPEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGGOKCGNR ACRDSSNSCI LAAGFVYVLK DSYPPKDNPR ALRQAQGTCK RSTHTAYIK Seq ID NO: Nucleic Ac Coding seq       GAGGAGGAGG GAGGAAGGG TAATACCAAG TAGCCACCT ACGGGGATTCG ATGCCAGGG ACAGGTTCGC AGGGGAAGT AGGGGGAAT TAGTGGAGATT TAGTGGAGAT TAGTGGAGATT TAGTGGAGAT TAGTGGAGATT TAGTGGAGAT TAGTGCTGCT	ATCCTTAGAT ARAAAAAAA  78 Protein Cession #: 1 11   ARALLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV FQGTIIGMAP MAVEKGGCIM FVEEGEECDC LPEFCTGASP RVNSAGDPYG GRILCRGTHV NNRNCHCEA ARKTLIRLFT RLLQCQNVDI PNPPQKPLPA  79 DNA seq cidence: 135. 11   GAAAAAGGCGA AGGAGGAGGA AGGAGGAGGAGAA CGCTGGCGATACCT CTGCATAAGG CTACCTCAAAG GGTTCATTC CTGCATTAGG CGACTGTGGC CGACCTGTGGC CGACCTGTGCC CGCCCC CGACCTGTGCC CGCCCCTGTGCC CGCCCCC CGCCCCC CGCCCCC CGCCCC CGCCCC CGCCCCC CGCCCC CGCCCC CGCCCC CGCCCC CGCCCC CGCCCC CGCCCC CGCCCC CCCCCC	SEQUENCE  SEQUEN	31   VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPY GGIVMDHSDN VPSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQRVLP HALARTPGQW  714  31   AGAGTGGGAG ACAAAGGATC TGGGCCAGTA ACGCCACCAA CCCTGCAGAA CCCTGCAGCCCCTGCCGCGCTGCCCCTGCAGAA CCCTGCAGCACA CCGCCCTCCCCCCTTCCTCCCTCGAGAA CCCTGCAGCACACACACACACACACACACACACACACACA	41	GAGGATATGA  51    DLWIPVKSFD DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVTLWGFG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAKP PAPQYPHQVP  51    AGCGGCGAAG GCTTTGGTGT GGTAAAATTG GGTCCCAAG ATCCAGCACT AACAACTCTT GGAAAATTG GCTCTGCGGC TCCCAGTGA GCTCTGCGGC ACCCGGTGA GGCCCTGTGA GGTCCAGGTGA GGTCCAGGTTC TCGGCCATCC	60 120 180 240 300 360 420 480 540 660 720 780 840 900

	AGAAGCCTCC	CACGGGGGCCC	CCCGAGCGCC	AGCCCCAGGT	GGACAGAACC	AAGCTCTCCA	840
	GGGCCCACCA	CGGGGAAGCA	GGACATCACC	TCCCAGAGCC	CAGCAGTAGG	GAGACTGGCC	900
	GAGGTGCCAA	GGGTGAGCGA	GGTAGCAAGA	GCCACCCAAA	CGCCCATGCC	CGAGGCAGAG	960
				GAAGCAGCGA			1020
5				GGCCTGGCCA			1080
•	GTCCATTTTC	TTATCTATGG	ACATTCCAAA	ACATTTACCA	TTAGAGAGGG	GGGATGTCAC	1140
	ACCCACCATT	CTGTGGGGAC	TGTGGACTTC	ATCGAGGTGT	GTGTTCGCGG	AACGGACAGG	1200
	TGAGATGGAG	ACCCCTGGGG	COTTGGGGTC	TCAGGGGTGC	CTGGTGAATT	CTGCACTTAC	1260
	ACCTACTOAA	GGGAGCGCGC	CCGCGTTATC	CTCGTACCTT	TGTCTTCTTT	CCATCTGTGG	1320
10	ACTIVACTOR	TOTOGOGG	TOTATTATA	GGGAGGTGAA	CCAGGGAGGG	GCAGGGCAAG	1380
10	CCFCCCCCCC	CAGAGCTGGG	CCACACAGTG	GGTGCTGGGC	CTCGCCCCGA	AGCTTCTGGT	1440
	CCACCACCCC	CTCCTCCTCT	CTCCGCGAA	GTCAGGGCGG	CTGGATTCCA	GGACAGGAGT	1500
	GCAGCAGCCI	CIGGIGCIGI	CTTAGAATGC	AGGAGAAGGG	TGGAGAGGAG	GCAGGGGGCCG	1560
	PECCECACEA.	TOTAL	CTGABATTCA	GTTTCTTGTG	TGGGGCCTTG	CGGTTCAGAG	1620
15	WOOOGGIGGI	CCCTCCACCC	ACCACTCTCA	TTTCTATGTG	TAATTTCTGA	GCCATTGTAC	1680
10	TOTAL	CCCCCCCCACA	CTCTCCAAGG	GAGTGGCCCC	TATGAGTTTA	TATTTTAACC	1740
	POTCHOOCE I	ATCTCGATCT	CIGICORIOC	ATTTATCCAG	TTATATCTAC	ATATCTCTCA	1800
	MCIGCIICAA	WICIOGWIII	ACADAGCAAC	TGGGTCATTA	AAACCAGCTC	AAAGGGGGTT	1860
	ICIMMAIAM	NANACCACCC	CATCCTTTCA	GGCTGATTTT	The second secon	AAGTTCTATT	1920
20	IMMAMMA	MANACCAGCC	ACATACCCAT	ACATCTGACT	CCCTCACATC	CACTCCTCCC	1980
40				AATACACACC			2040
	CACTTGGGGG	AAACCTTATA	CCCAGAGGAA	ACCCTCAGCC	100000ACIAC	ALLIGACAAA	2100
	TTTCCCTTAG	GATTTCGTTA	TCTCACCTIG	ACCC TCAGCC	ANGAI IGGIA	CATCCCAAAC	2160
	CIGGOGATIC	CAGGAGACCC	AGCIGGAAAC	CTGGCTTCTC	CAIGIGAGGG	CATOGGAMAG	2220
25	GAAAGAAGAG	AATGAAGACT	ACTTAGTAAT	TCCCATCAGG	MAAIGCIGAC	CITITACATA	
25	AAATCAAGGA	GACTGCTGAA	AATCTCTAAG	GGACAGGATT	TICCAGATCC	TAATTGGAAA	2280
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	GGGAGAGGAA	GAAAAGAGAG	AGAGAAAAGA	GCCTCGTGCC			
20	Seq ID NO:						
30	Protein Acc						
	1 .	11	21	31	41	51	
			1		1	1	
	MCAERLGQFM	TLALVLATFD	PARGTDATNP	PEGPQDRSSQ	QKGRLSLQNT	AEIQHCLVNA	60
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35	ISRKCPAIRE	MVSQLQRECY	LKHDLCAAAQ	ENTRVIVEMI	HFKDLLLHEP	YVDLVNLLLT	180
	CGEEVKEAIT	HSVQVQCEQN	WGSLCSILSP	CTSAIQKPPT	APPERQPQVD	RTKLSRAHHG	240
	EAGHHLPEPS	SRETGRGAKG	ERGSKSHPNA	HARGRVGGLG	AQGPSGSSEW	EDEQSEYSDI	300
	RR						
40							
40		81 DNA sequ					
	Nucleic Aci	ld Accession	#: CAT clu				
	1	11	21	31	41	51	
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4.5	AATCATGTTT	TTGGAATAAA	AATGGTAAAT	GTTTTTTTT	TTTTTTTTT	GTTAGTAATG	60
45	GAAGTATTCT	ATTATTTTA	ATTTTATGTA	TGTACAGACA	AGAGCTATAT	GGGAAAGTAG	120
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				CATCTCTTTC			240
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	GAGTGTTGGG	TCAACTGATA	AGCAGTGCAG	ACTOTTCATT	TTGCTTTGTT	GGTGCCTTGG	360
50	AGGCATGTGA	GGGCACAGCC	TCAAATTCCA	GAGACCTTGC	CTTCAGGATT	TGAGGTGGGC	420
	AAAGATGTGA	AAGAAGACCT	TTAGCCACTC	AGTGTTATCA	AAAGCAATCA	CCAAAGAAGT	480
	TTTTGCATCT	GGCATTGTGT	TGGGACGTCC	ATCAGCAGTA	CCGTACGGTC	TCTTTACTGG	540
	ACAAGTATTT	ACACCTTGTT	AACAGCAGTG	TACACCCGGT	GGAAAACTCC	TATCTAATGG	600
	CATGGCAGAA	TTGTAAACAT	TTCCTCCTTC	ACCAAATTTG	TGGATGGAAT	AAACATGTAG	660
55	CCTTAAACTT	TATTGGCTTC	TCCGGTCTTG	CCACTGCGGG	GCCCAAAAAC	TTTCAGAAGT	720
	AGGAATCCTG	TGGCATCTGC	TAATGGTGAT	TGGAAGAAAG	AGTAGAGGTG	ACAGTATCTA	780
	TGGGTGCAGT	ACCAGAACTA	TTACGAAATG	TTCCAGCTGC	GATTTCAGAG	GAATCCCCCC	840
	TGACCCCTGG	ACGTGGTTCT	CCTATTTCAG	TCACCCTGTG	CCC		
<b>CO</b>							
60 ·		82 DNA seq					
			n #: XM_061	091.1		•	
	Coding seq	uence: 12	481				
	1	11	21	31	41	51	
65		1	1	l	<u> </u>	1	
65	ATGCCAAATA	CTTCAGGAAC	AACCAGGATT	GAAATTTGGC	TTCTCCAAGA	GCCGCCCGGG	60
						GGCTCTGGCG	120
						GATTGGAGGT	180
	CAGATGCATG	GTGAGAAGGT	AGATCTCTGG	AGCCTTGGTG	TTCTTTGCTA	TGAATTTTTA	240
70	GTTGGGAAGC	CTCCTTTTGA	. GGCAAACGAA	GTCCATGTAA	GCAAAGAAAC	CATCGGGAAG	300
70	ATTTCAGCTG	CCAGCAAAAT	GATGTGGTGC	TOGGCTGCAG	TGGACATCAT	GTTTCTGTTA	360
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	GTCTGTGACG	GTCTGGACAT	CAGCCCCGAG	AGGGTCAGAG	TGGGAGCATT	CCAGTTCAGT	480
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7.5	AGAATCAAGA	GGATGGTTTT	CAAAGGAGGG	CGCACGGAGA	CGGAACTTGC	TCTGAAATAC	600
75	CTTCTGCACA	GAGGGTTGCC	TGGAGGCAGA	AATGCTTCTG	TGCCCCAGAT	CCTCATCATC	660
	GTCACTGATG	GGAAGTCCCA	GGGGGATGTG	GCACTGCCAT	CCAAGCAGCI	GAAGGAAAGG	720
	GGTGTCACTG	TGTTTGCTGT	GGGGGTCAGG	TTTCCCAGGT	GGGAGGAGCT	GCATGCACTG	780
	GCCAGCGAGC	CTAGAGGGCA	GCACGTGCTC	TTGGCTGAGC	AGGTGGAGG	TGCCACCAAC	840
00	GGCCTCTTCA	GCACCCTCAG	CAGCTCGGCC	ATCTGCTCCA	. GOGCCACGCC	: AGCTGGGAGC	900
80	CCCGAGCTTG	TCTTCATGG	GCGGTTAATC	GGCATCTCTC	TGATAGGCCC	CTGTGACTCG	960
	CAGCCCTGCC	AGAATGGAGG	CACATGTGTT	CCAGAAGGAC	TGGACGGCT	CCAGTGCCTC	1020
	TGCCCGCTGG	CCTTTGGAGG	GGAGGCTAAC	: TGTGCCCTGA	AGCTGAGCCT	GGAATGCAGG	1080
	GTCGACCTCC	TCTTCCTGCT	GGACAGCTC	GCGGGCACCA	CTCTGGACGC	CITCCIGCGG	1140
	GCCAAAGTCT	TOGTGAAGCC	GTTTGTGCGC	GCCGTGCTGA	GOGAGGACTO	TCGGGCCCGA	1200
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	GATGTGCCTG .	ACCTGGTCTG	GAGCCTCGAT	GGCATTCCCT	TCCGTGGTGG	CCCCACCCTG	1320
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	700000000	CCTTGCGGCA	GGCGGCGGGGG	CTCACTCACT	CACACTOCCA	CONTORCOTT	1440
	CAGGACUGGC	CACGTAGAGT	GGTGGTTTTG	CTCACTGAGT	CACACICCGA	GGWIGWGGII	
_	GCGGGCCCAG	CGCGTCACGC	AAGGGCGCGA	GAGCTGCTCC	TGCTGGGTGT	AGGCAGTGAG	1500
5	GCCGTGCGGG	CAGAGCTGGA	GGAGATCACA	GGCAGCCCAA	AGCATGTGAT	GGTCTACTCG	1560
•	CATCCTCACC	P declaration P	CONNECT	GAGCTGCAGG	GGAAGCTYCTG	CAGCCCCAG	1620
	GATCCICAGG .	AICIGIICAA	CCAMICCCI	OTTOTOTO TO	TOTAL CLOSE	CHOCOCOCOCO	1680
	CGGCCAGGGT	GCCGGACACA	AGCCCTGGAC	CTOGTCTTCA	IGITGGACAC	CICIGCCICA	
	GTAGGGCCCG	AGAATTTTGC	TCAGATGCAG	AGCTTTGTGA	GAAGCTGTGC	CCTCCAGTTT	1740
	CACCACAACC	CALCULATION C.	A CACCOTOCCO	CTGGTGGTGT	ATGGCAGCCA	CGTGCAGACT	1800
10	GNGGIGNACC	CIGACGIGAC	ACADO10000	CONCOCARCO	TCCCCCC.	m) COC) CCCC	1860
10	GCCTTCGGGC	TGGACACCAA	ACCCACCOGG	GCTGCGATGC	16CGGCCA1	TAUCCAGGCC	
	CCCTACCTAG	GTGGGGTGGG	CTCAGCCGGC	ACCGCCCTGC	TGCACATCTA	TGACAAAGTG	1920
	ATCACCCTCC	AGAGGGGTGC	CCCCCCTCGT	GTCCCCAAAG	CTGTGGTGGT	GCTCACAGGC	1980
	AIGACCOICC	7070000100		CCCCACAACC	TCACCAACAA	TO CONTON	2040
	GGGAGAGGCG	CAGAGGATGC	AGCCGTTCCT	GCCCAGAAGC	IGAGGAACAA	IGGCVICICI	
	GTCTTGGTCG	TGGGCGTGGG	GCCTGTCCTA	AGTGAGGGTC	TGCGGAGGCT	TGCAGGTCCC	2100
15	CCCCATTOCC	TEATOCACET	CCCACCTTAC	GCCGACCTGC	GGTACCACCA	GGACGTGCTC	2160
13	COGGATICCC	10/1001001	100011001	CCAGTCAACC	TOTOCOANACO	CVGCCCCGAAGC	2220
	ATTGAGTGGC	TGTGTGGAGA	AGCCAAGCAG	CCAGTCAACC	TCTGCAAACC	CHOCCOTOC	
	ATGAATGAGG	GCAGCTGCGT	CCTGCAGAAT	GGGAGCTACC	GCTGCAAGTG	TCGGGATGGC	2280
	TRECARRECT	TOTAL CONTRACTOR	GAACCGTGAG	TGGAGCTCTT	GCTCTGTATG	TGTGAGCCAG	2340
	100000000		CONCACCAC	ATGGCTCCCG	TOCACCACCG	CAGCAGCCCC	2400
20							
20	ACCCCTCCCA	GCAACTACAG	AGAAGGCCTG	GGCACTGAAA	TGGTGCCTAC	CITCIGGAAT	2460
	GTCTGTGCCC	CAGGTCCTTA	G				
	Seq ID NO:	83 Protein	sequence				
	Protein Acc	ession #: )	CP 061091.1	•			
25	1	11	21	31	41	51	
23	÷	••	7-		i -	ĭ	
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	MPNTSGTTRI	EIWLLQEPPG	HRALVAALLP	VSPSPELALA	PGYPPVPAAD	DRFTLPMIGG	60
	OWICEWIDLW	CT CUT CVERT.	VCKDDEENNE	VHVSKETIGK	ISAASKMMWC	SAAVDIMPLL	120
	Gungeranna	SPGADCIPER	VGICEFERING			ODOROOTH TAX	
20	DGSNSVGKGS	FERSKHFAIT	VCDGLDISPE	RVRVGAFQFS	STPHDEFPLD	PERIOGRAKY	180
30	RIKRMVFKGG	RTETELALKY	LLHRGLPGGR	NASVPQILII	VTDGKSQGDV	ALPSKQLKER	240
50	CHILD THE COLOR	DODLING III	* CEDBCOUUT	T. A EXCUSED A TRI	CT.POTT.CCCA	TOSSATPAGS	300
	GVTVFAVGVR	FPRWEELHAL	ASEPROQUVL	LAEQVEDATN	GDESINSSON	ICOUNTERGO	
	PELVFMERLM	GISLIGPCDS	QPCQNGGTCV	PEGLDGYQCL	CPLAFGGEAN	CALKLSLECK	360
	VDI.I.FI.LDSS	ACTTI-DGET.R	AKVFVKRFVR	avlsedsrar	VGVATYSREL	LVAVPVGEYO	420
	**************************************			DODGC S MDMC	ODDDDDDDDD	t meeticenest	480
0.5	DABOPAM2PD	GIPFRGGPTL	TGSALRQAAE	RGFGSATRTG	QDRPRRVVVI	BIESHSEDEV	
35 ·	AGPARHARAR	ELLLLGVGSE	AVRAELEEIT	GSPKHVMVYS	DPQDLFNQIP	ELQGKLCSRQ	540
	DOCCOROALD	T TOME DECAR	ACCREMENONO.	SFVRSCALQF	EUNDDVTOVG	LVVYGSOVOT	600
	REGCETORID	DVFFIDDISAS	VGFEMFAQMQ	or moomer.	74445 PAG	THE STREET WAS	660
				TALLHIYDKV			
	GRGAEDAAVP	AOKLRNNGIS	VLVVGVGPVL	SEGLRRLAGP	RDSLIHVAAY	ADLRYHQDVL	720
	TENT OCENIO	DIMIT CANDEDC	MATERICATION	GSYRCKCRDG	WEGDHCENER	WSSCSVCVSO	780
40							
40	GWILETPLRH	MAPVQEGSSR	TPPSNYREGL	GTEMVPTFWN	VCAPGP		
	COG ID NO.	04 5173	10000				
		84 DNA seq					
			n #: Eos se	quence			
	Nucleic Aci	ld Accession	n#: Eos se	quence			
45	Nucleic Aci Coding sequ	id Accession	n #: Eos se 424		41	51	
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45	Nucleic Aci Coding sequ 1 ATGCCCCCTT	id Accession lence: 12- 11   TCCTGTTGCT	n #: Eos se 424 21     GGAGGCCGTC	31   TGTGTTTTCC	TGTTTTCCAG	AGTGCCCCCA	
45	Nucleic Aci Coding sequence  ATGCCCCCTT TCTCTCCCTC	id Accession lence: 12- 11   TCCTGTTGCT TCCAGGAAGT	n #: Eos sei 424 21   GGAGGCCGTC CCATGTAAGC	31   TGTGTTTTCC AAAGAAACCA	TGTTTTCCAG TCGGGAAGAT	AGTGCCCCCA TTCAGCTGCC	120
	Nucleic Aci Coding sequ 1   ATGCCCCCTT TCTCTCCCTC AGCAAAATGA	id Accession sence: 12  11  TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC	n #: Eos sei 424 21   GGAGGCCGTC CCATGTAAGC GGCTGCAGTG	31     TGTGTTTTCC AAAGAAACCA GACATCATGT	TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC	120 180
	Nucleic Aci Coding sequ 1   ATGCCCCCTT TCTCTCCCTC AGCAAAATGA	id Accession sence: 12  11  TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC	n #: Eos sei 424 21   GGAGGCCGTC CCATGTAAGC GGCTGCAGTG	31     TGTGTTTTCC AAAGAAACCA GACATCATGT	TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC	120
45	Nucleic Aci Coding sequ 1 ATGCCCCCTT TCTCTCCCTC AGCAMATGA AGCGTCGGGA	id Accession sence: 12  11  TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGGAGCTT	n #: Eos sei 424 21   GGAGGCCGTC CCATGTAAGC GGCTGCAGTG TGAAAGGTCC	31   TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG	TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT	120 180 240
	Nucleic Aci Coding sequ 1   ATGCCCCCTT TCTCCCCTC AGCARAATGA AGCGTCGGGA CTGGACATCA	id Accession sence: 12  11    TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGGAGCTT AGGGAGCTT GCCCCGAGAG	m #: Eos sei 424 21   GGAGGCCGTC CCATGTAAGC GGCTGCAGTG TGAAAGGTCC GGTCAGAGTG	31   TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC	TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT	120 180 240 300
	Nucleic Aci Coding sequ  ATGCCCCCTT TCTCTCCCTC AGCANATGA AGCGTCGGGA CTGGACATCA CTGGACATCA CTGGACATCA	id Accession lence: 12  11  TCCTGTTGCT TCCAGGAAGT TCTGGTGCTC AAGGAAGCTT GCCCCGAGAG CCTTGGATTC	n #: Eos sei 424 21   GGAGGCCGTC CCATGTAAGC GGCTGCAGTG TGAAAGGTCC GGTCAGAGTG ATTTCAACC	31   TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG	TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG	120 180 240
	Nucleic Aci Coding sequ  ATGCCCCCTT TCTCTCCCTC AGCANATGA AGCGTCGGGA CTGGACATCA CTGGACATCA CTGGACATCA	id Accession lence: 12  11  TCCTGTTGCT TCCAGGAAGT TCTGGTGCTC AAGGAAGCTT GCCCCGAGAG CCTTGGATTC	n #: Eos sei 424 21   GGAGGCCGTC CCATGTAAGC GGCTGCAGTG TGAAAGGTCC GGTCAGAGTG ATTTCAACC	31   TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG	TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG	120 180 240 300 360
	Nucleic Aci Coding sequi 1   ATGCCCCCTT TCTCCCTC AGCANATGA AGCGTCGGGA CTGGACATCA CTGGAATTCC ATGGTTTTCA	id Accession lence: 12  11    TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGGAGCTT GCCCCGAAGG CCTTGGATTC AAGGGGGCG	m #: Eos sei 424 21	31     TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC	TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA	120 180 240 300 360 420
50	Nucleic Aci Coding sequi 1   ATGCCCCCTT TCTCCCTC AGCANANTGA AGCGTCGGGA CTGGACATCA CTGGATTCC ATGGTTTCCA GGGTTGCCTG	id Accession ence: 12  11    TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGCTT GCCCGAGAG CCTTGGATTC AAGGAGGCAGAAAA	m #: Eos sei 424 21   GGAGGCCGTC CCATGTAAGC GGCTGCAGTG TGAAAGGTCC GGTCAGAGTG ATTTTCAACC TGCTTCTGTG	31     TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCCAGATCC	TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG	120 180 240 300 360 420 480
	Nucleic Aci Coding sequi 1 ATGCCCCCTT TCTCTCCCTC AGCANANTGA AGCGTGGGGA CTGGACATCA CTGGACATCA CTGGACATCA GGGTTGCTG AAGTCCCAGG	id Accession sence: 12  11    TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC GCCCGAGAG CCTTGGATTC AAGGAGGGCT AAGGAGGGGAGG	n #: Eos ser 424 21   GGAGGCCGTC CCATGTAAGC GGCTGCAGTG TGAAAGGTCC ATTTTCAACC CACGGAGACG TGCTTCTTCTACC ACTTCTTCTACC ACTTCTTCTACC	31   TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCCAGATCC AAGCAGCTGA	TGTTTTCAG TCGGGAAGAT TCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA AGTGCCCCC TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGT	120 180 240 300 360 420 480 540
50	Nucleic Aci Coding sequi 1 ATGCCCCCTT TCTCTCCCTC AGCANANTGA AGCGTGGGGA CTGGACATCA CTGGACATCA CTGGACATCA GGGTTGCTG AAGTCCCAGG	id Accession sence: 12  11    TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC GCCCGAGAG CCTTGGATTC AAGGAGGGCT AAGGAGGGGAGG	n #: Eos ser 424 21   GGAGGCCGTC CCATGTAAGC GGCTGCAGTG TGAAAGGTCC ATTTTCAACC CACGGAGACG TGCTTCTTCTACC ACTTCTTCTACC ACTTCTTCTACC	31   TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCCAGATCC AAGCAGCTGA	TGTTTTCAG TCGGGAAGAT TCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA AGTGCCCCC TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGT	120 180 240 300 360 420 480
50	Nucleic Aci Coding sequi I ATGCCCCTT TCTCTCCTC AGCANANTGA AGCGTCGGGA CTGGACATCA CTGGAATTCC ATGGTTTTCA GGGTTGCCTG AAGTCCCAGG TTTGCTGTGGG TTTGCTGTGGG	id Accession Lence: 12.  11    TCCAGGAAGT TCCAGGAAGT TCCAGGAGCT AAGGAGCT ACCCGACAGA CCTTGGATTC AAGGAGCCG AGGCAGAAA GGGATGTGGC GGGTCAGGTT	m #: Eos ser 424 21   GGAGGCCGTC CCATGTAAGC GGCTCAGAGTG TGAAAGGTCC GGTCAGAGTG ATTTCAACC CACGGAGACG TGCTTCTGTG ACTGCCATCC	31    TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTGT GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCCAGATCC AAGCAGCTGA GAGGAGCTGC	TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACCGT CACTCCTCAT AATCAACAGG TCTGCACAGA CACTGATTGGG CACTGATTGGG CAGCAGACCT	120 180 240 300 360 420 480 540 600
50	Nucleic Aci Coding sequ  I I ATGCCCCTT TCTCTCCTC AGCANATGA AGCGTGGGA CTGGACTTCA CTGGACTTCA GGGTTGCCTG AAGTCCCAGG TTTGCTGTGG AGAGGGCAGC	id Accession Lence: 12.  11    TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGCTT GCCCGAGAG CCTTGGATTC AAGGAGGCG GAGCAGAAA GGGATGTGGC GGGTCAGGTT ACGTGCTGTT	m #: Eos ser 424 21 	31   TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCCAGATCC AAGCAGCTGA GAGGAGCTGC GTGGAGGATG	TGTTTTCCAG TCGGAAGAT TCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGTG CAGCGAGCCT CCTCTTCAGC	120 180 240 300 360 420 480 540 600 660
50	Nucleic Aci Coding sequ 1	id Accession sence: 12  11    TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGCTT GCCCCAGAG CCTTGGATTC AAGGAGGCGG GAGCCAGAAA GGGATGTGGC GGGTCAGGTT ACTGCGTTGCTGTT GCTCGGCCTT	m #: Eos ser 424 21   GGAGGCCGTC CCATGTAAGC GGCTGCAGTG TGAAAGGTCC GGTCAGAGTG ATTTCAACC TGCTTCTGTG ACTGCCATCC TCCCAGGTGG GGCTGAGCG CTGCTCAGCG CTGCTCAGCG	31   TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCCAGATCC AAGCAGCTGA GAGGAGCTGC GTGGAGGATG GCCACGCCAG	TGTTTTCCAG TCGGAAGAT TCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGTG CAGCGAGCCT CCTCTTCAGC CGAGGGTCAC	120 180 240 300 360 420 480 540 600 660 720
50	Nucleic Aci Coding sequ 1	id Accession sence: 12  11    TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGCTT GCCCCAGAG CCTTGGATTC AAGGAGGCGG GAGCCAGAAA GGGATGTGGC GGGTCAGGTT ACTGCGTTGCTGTT GCTCGGCCTT	m #: Eos ser 424 21   GGAGGCCGTC CCATGTAAGC GGCTGCAGTG TGAAAGGTCC GGTCAGAGTG ATTTCAACC TGCTTCTGTG ACTGCCATCC TCCCAGGTGG GGCTGAGCG CTGCTCAGCG CTGCTCAGCG	31   TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCCAGATCC AAGCAGCTGA GAGGAGCTGC GTGGAGGATG GCCACGCCAG	TGTTTTCCAG TCGGAAGAT TCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGTG CAGCGAGCCT CCTCTTCAGC CGAGGGTCAC	120 180 240 300 360 420 480 540 600 660
50	Nucleic Aci Coding sequi I ATGCCCCTT TCTCTCCTC AGCARANTGA AGCGTCGGA CTGGACATCA ATGGTTTTCA GGGTTGCCTG AAGTCCCAGG TTTGCTGTGA AGAGGCCAGC ACCCTCAGCA CCCTGTGAGC	id Accession Lence: 12.  11  11  TCCTGTTGCT TCCAGGAAGT TGTGGTCC AAGGAGCT GCCCGAGAGG CCTTGGATTC AAGGAGGCG AGGCAGAAA GGGATGTGGC GGGTCAGGTT ACGTGCTGTT ACGTGCTGTT ACTGGCCAG ACAGGACAGCAA ACAGGACGCT ACGTGCTGTT ACGTGCTGTT ACAGGACGCT ACAGGACGCT	m #: Eos ser 424 21   GGAGGCCGTC CCATGTAAGC CGCTGCAGTG TGAAAGGTCC GGTCAGAGT GATTTCAACC CACGGAGACG TGCTTCTGTG ACTGCCATCC TCCCAGTGG GGCTGAGCAG GGTGAGCAG GGGAGATGGTC	31    TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCCAGATCC AAGCAGCTGA GAGGAGCTGC GTGGAGGATGC GCGAGGATGC CGGAGGATCC	TGTTTTCAG TGGGAAGAT TTCTGTTAGA CCATCAGT AGTTCAGTTC	AGTGCCCCA TCAGCTGCC TGGGTCTAAC TGTGACCGT CACTCCTCAT AATCAACAGG TCTGCACAGA CACTGATGGG TGTCACTGTG CAGCGAGCCT CCTCTTCAGC CCCATGCTGG CCCATGCTGG	120 180 240 300 360 420 480 540 600 660 720 780
50	Nucleic Aci Coding sequi I ATGCCCCTT TCTCTCCT AGCANANTGA AGCGTCGGA CTGGACATCA CTGGACTTCC ATGGTTTTCA GGGTTGCCTG AAGTCCCAGG ATTTCCTGTGG AGAGGCAGC ACCTCAGCA ACCTCAGCA AGAGGATCGC	id Accession ience: 12.  11    TCCTGTTGCT TCCAGGAAGT TCCAGGAAGT CCTTGGATGC AAGGAGGCT AAGGAGGCG GAGCAGAAA GGGATGTGGC GGGTCAGGTT ACGTGCTGTT GCTCGGCCAT ACGGCCCATGT GCTCGGCCATGT GCTCGGCCATGT GCTCGGCCATGT GCTGGCCACGT GCGGGACCCT	m #: Eos sei 424 21	31   TGTGTTTTCC AAAGAAACCA AACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCCAGATCC AAGCAGCTGA AGCAGCTGC GTGGAGGATG GCCACGCCAG CCGGAGTTCG GCGCACTCACCACC	TGTTTTCCAG TCGGGAGAT TTCTGTTAGA CCATCAGTT GGAGGCAAG TGAAGTACATT TCATCATTC TCATCATCAT AGGAAAGGGG ATGCACTGGC CCACCAACGG ACTGCACGGT CTGGCAATGC GTCCCTTCTA	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACCGT CACTCCTCAT AATCAACAGG TCTGCACAGA CACTGATGGG CAGCGAGCCT CCTCTTCAGG CCAGGGTCCAC CCCATGGTGG CAGCTGGAGCT CCCATGGTGGAGCT CCCATGGTGGAGCT	120 180 240 300 360 420 480 540 600 720 780 840
50	Nucleic Aci Coding sequ  I I ATGCCCCTT TCTCTCCTC AGCANATGA AGCGTCGGGA CTGGACATCA CTGGACTTC GGGTTGCCTG AAGTCCCAGG TTGCTGTGG AGAGGCAGC ACCCTCAGCA CCCTGTGAGC AGAGGATGCC AGAGGTTCCC AGGGTTCCCAGGA ACCCTCAGCA ACCCTCAGCA ACAGGATCGC AGAGGTCTCC AGAGTGTTCC AGAGGTCTCC	id Accession ience: 12.  11    TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGCT GCCCGAGAG GCTTGGATTC GAGGAGGT GAGGAGGAGAAA GGGATGTGGC GGGTCAGGTT GCTCGGCCAT ACAGGACGCT TAACCACCC	m #: Eos ser 424 21	31   TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCCAGATCC AAGCAGCTGA GAGGAGCTGC GTGGAGGATGC GTGGAGGATTCG GCCACGCCAG GCTGCACACT TACAGGACCA	TGTTTTCCAG TGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGTG CAGCGAGCT CCTCTTCAGC CAGCGAGCT CCATGCTGG CAGCGAGGG CAGCTGAGAG CACCTGGAAG	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50	Nucleic Aci Coding sequ  I I ATGCCCCTT TCTCTCCTC AGCANATGA AGCGTCGGGA CTGGACATCA CTGGACTTC GGGTTGCCTG AAGTCCCAGG TTGCTGTGG AGAGGCAGC ACCCTCAGCA CCCTGTGAGC AGAGGATGCC AGAGGTTCCC AGGGTTCCCAGGA ACCCTCAGCA ACCCTCAGCA ACAGGATCGC AGAGGTCTCC AGAGTGTTCC AGAGGTCTCC	id Accession ience: 12.  11    TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGCT GCCCGAGAG GCTTGGATTC GAGGAGGT GAGGAGGAGAAA GGGATGTGGC GGGTCAGGTT GCTCGGCCAT ACAGGACGCT TAACCACCC	m #: Eos ser 424 21	31   TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCCAGATCC AAGCAGCTGA GAGGAGCTGC GTGGAGGATGC GTGGAGGATTCG GCCACGCCAG GCTGCACACT TACAGGACCA	TGTTTTCCAG TGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGTG CAGCGAGCT CCTCTTCAGC CAGCGAGCT CCATGCTGG CAGCGAGGG CAGCTGAGAG CACCTGGAAG	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50	Nucleic Aci Coding sequi I ATGCCCCTT TCTCTCCTC AGCANANTGA AGCGTCGGA ATGCTCCTC ATGGTTTTCA GGGTTGCCTG AGGTCCAGG TTTGCTGTG AGAGGCAGC ACCTCAGCA ACCTCAGCA ACCTCAGCA ACCTCAGCA ACCTCAGCA ACCTCAGCA TCTGTGTGG AGAGGATCGC AGAGGATCGC AGAGGATCTC TCGCAGCCCTT	id Accession Lence: 12.  11  1 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGCTT GCCCCGAGAG GCCCCGAGAG GGCAGCAGAA GGATGTGGCC GGGCAGAGT ACGGCAGAA ACGGCGCAG ACGCAGAA ACGGCCCT TAACCCACCC GCCGGACCCT TAACCCACCC	n #: Eos sei 424 21   GGAGGCCGTC CCATGTAAGC CGCTGCAGTG ATTTCAACC CACGGAGACG TGCTTCTAGC ACTTCCAGCG ACTGCCATCC TCCCAGGTGG GGTGAGCAG CTGCTCCAGC GGAGATGGTC TGCGGTGTC TGCGGTGCT TGCGGTGCT	31   TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCCAGATCC AAGCAGCTGA GGAGGATGG GGCACGCCAG CCGCGAGTTCG GCTGCACACC GTTGCACACC GTTGCACACC GTTGCACACC GTTGCACACC GTTCCAGAACC GTTCCAGAACC GTTCCAGAAG	TGTTTTCAG TGGGAAGAT TTCTGTTAGA CCATTACAGT TGAAGGCAG TGAAATACCT TCATCATCT TCATCATCT TCATCATCT TCATCATCGC CCACCAACAG ACGAAAGAGG CCACCAACAG GTCCCTCTA CTGCAATGC GTCCCTTCTA CCTGCCAAGG GACTGGAACG GACTGGACG GACTGGACG GACTGGACG	AGTGCCCCA TTCAGCTGCC TTGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGTG CAGCGAGCCT CCCTTCAGC CGAGGCTCAC CCCATGCTGG CAGCTGGAAC CCCCTGTGAC CCCCTGTGAC	120 180 240 300 360 420 480 540 600 660 720 780 840 900 960
50	Nucleic Aci Coding sequi I ATGCCCCTT TCTCCCTC AGCARANTGA AGCGTCGGA AGCGTCGGA ATGGTTTTCA GGGTTGCTG AAGTCCAGG ATTCCTGGAGCAGCA ACCTCAGCA ACCTCAGCA AGAGGATCGC AGAGGTTCC TCGCAGCCT TCGCAGCCCT CTCTGCCCCGC	id Accession ience: 12.  11                TCCAGGAAGT TCCAGGAAGT TGGGGTGCT AAGGAGGCT AAGGAGGCT AAGGAGGCT AAGGAGGCT AAGGAGGCT AAGGAGGCGGAAAA GGGATGTGGC GGGTCAGGTT ACGGCCAT ACGGCCTGT GCCCGACAGG GGCGAACCCT TAACCACCCC TGACCAGATTG	m #: Eos ser 424 21   GGAGGCCGTC CCATGTAAGC GGTTCAAGTG TGAAAGGTCC GGTCAGAGTG ACTTCTATC ACTGCATCC TCCCAGGTGG GGCTGAGCAG CTGCTCCAGC GGAGATGGTC TGCGCTCCAGC TGCTCCAGC TGCTCCAGC TGCTCCAGC TGCTCCAGC TGCAGCAG TGCACCT TGCGGTGCT	31   TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CCACAGAGG GAACTTGCTC CCCCAGATCC CGCAGGCTGA GAGGAGGTGG GTGGAGGATG GCCACGCAG GCGCAGTTCG GCTGCACACT TACAGGACCA ATTCCAGAAG AACTGTGCCC	TGTTTTCCAG TCGGAAGAT TCTCTTAGA CCATCAGTT TGAAGGCAG TGAATACCT TCATCATCT TCATCATCT TCATCATCT TCATCATCAT TCATCAT TC	AGTGCCCCA TTCAGCTGCC TTGGTCTAAC CTGTGACCGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG CAGCGAGCCT CCTTCAGC CCCATGCTGG CAGCTGGAAG CCCCTGTGAAG CCCCTGTGAAG CCCCTGTGAAG CCCCTGTGAAG CCCCTGTGAAG	120 180 240 300 420 480 540 600 660 720 780 840 900 960 1020
50 55 60	Nucleic Aci Coding sequi I I ATGCCCCTT TCTCTCCTC AGCANAATGA AGCGTCGGA CTGGACTTCA CTGGACTTCA GGGTTGCCTG AAGTCCCAGG TTTGCTGTGG AGAGGCCAGC ACCCTCAGCA CCCTGTGAGC AGAGGATTCC TCGCAGCCCT CTCTGCCGCA CCCTTGCCGCA	id Accession ience: 12.  11    TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGCTT GCCCGAGAG GCAGAGAGGAGGAGAAA GGGATGTGGC GGGTCAGGTT ACGGGCCTTTG GCCAGAAAA CGGACCTT GCCCACCCC GCCAGAATGG TGCCCTTCCT	m #: Eos ser 424 21	31   TGTGTTTTCC AAAGAAACCA AAGAAACCA AAGACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGGTC CCCCAGATCC AAGCAGCTGA GAGGAGCTGC GTGGAGGATG GCCACGCCAG GCTGCACACT TACAGGACCA GTTCCAGAAG AACTGTGCC TTCTGGGGGCA TCTGGGGGGCA TCTGCGGGGCA TCTGCGGGGCA	TGTTTTCCAG TGGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGTG CCAGCGGAGCCT CCCTCTCAGC CCAGCTGG CAGCTGGAAG CCCTGTGAC CTACCAGTGC CCTGGAATGC CCTGGAATGC CCTGGAATGC CCTGGAATGC CCTGGAATGC CCTGCATGCTG	120 180 240 300 360 420 480 540 600 660 720 780 840 900 960
50 55 60	Nucleic Aci Coding sequi I I ATGCCCCTT TCTCTCCTC AGCANAATGA AGCGTCGGA CTGGACTTCA CTGGACTTCA GGGTTGCCTG AAGTCCCAGG TTTGCTGTGG AGAGGCCAGC ACCCTCAGCA CCCTGTGAGC AGAGGATTCC TCGCAGCCCT CTCTGCCGCA CCCTTGCCGCA	id Accession ience: 12.  11    TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGCTT GCCCGAGAG GCAGAGAGGAGGAGAAA GGGATGTGGC GGGTCAGGTT ACGGGCCTTTG GCCAGAAAA CGGACCTT GCCCACCCC GCCAGAATGG TGCCCTTCCT	m #: Eos ser 424 21	31   TGTGTTTTCC AAAGAAACCA AAGAAACCA AAGACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGGTC CCCCAGATCC AAGCAGCTGA GAGGAGCTGC GTGGAGGATG GCCACGCCAG GCTGCACACT TACAGGACCA GTTCCAGAAG AACTGTGCC TTCTGGGGGCA TCTGGGGGGCA TCTGCGGGGCA TCTGCGGGGCA	TGTTTTCCAG TGGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGTG CCAGCGGAGCCT CCCTCTCAGC CCAGCTGG CAGCTGGAAG CCCTGTGAC CTACCAGTGC CCTGGAATGC CCTGGAATGC CCTGGAATGC CCTGGAATGC CCTGGAATGC CCTGCATGCTG	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020
50	Nucleic Aci Coding sequil I ATGCCCCTT TCTCTCCTC AGCANATGA AGCGTCGGGA CTGGACATCA CTGGATTTCA GGGTTGCCTG AAGTCCCAGG TTTGCTGTGG AGAGGCCAGC ACCCTCAGCA CCCTGTGAGC AGAGGATCCC TCGCAGCCCT CTCGCAGCCCCCCCCCC	id Accession ience: 12.  11    TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGCT GCCCGAGAG GCAGGAGGCT AAGGAGGCT AAGGAGGCT AAGGAGGCT GCCCGAGAAA GGGATGTGGC GGGTCAGGTT ACTGGCCGTTGG TAACCAGCC GCCAGAAT TGGCCTTTCG TCCTCTTCCT TCTTCGTGAA	#: Eos ser 424 21	31   TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCCAGATCC AAGCAGCTGA GAGGAGGTGA GCGACGCCAG GCGCACGCCAG GCTGCACACT TACAGGACCA GTTCCAGAAG AACTGTGCC CTCTGCGGGCA CCGCCCGCCCC CTCTGCGGGCA CCGCCCTGCCCCGCCCC	TGTTTTCCAG TCGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTTGT CAGCGAGCCT CCTCTTCAGC CGAGGCTCAC CCCATGCTGG CAGCTGGAAG CCCCTGTGAC CTACCAGTGC CGGGTTCCTGG CGGGTTCCTGGATGC CGGGTTCCTGGATGC CGGGTTCCTGGATGC CGGGTTCCTGGATGC CGGGTTCCTGG	120 180 240 300 360 420 480 540 600 720 780 840 900 960 1020 1080
50 55 60	Nucleic Aci Coding sequi I ATGCCCCTT TCTCTCCTC AGCARANTGA AGCGTCGGA AGCGTCGGA ATGCTTTCA GGGTTGCTG AAGTCCAGG ATTTGCTGTGG AGAGGCAGC ACCTCAGCA ACCCTCAGCA ACCCTCAGCC AGAGGTTGTC TCTCGCCCGC AGGGTCGACC CGGGCCARA CGAGTTGGAC CGGGCCARG AGAGTTGGC AGGGTCGACC CGGGCCARG CGAGTGGTGG AGAGTGGTGG	id Accession Lence: 12.  11  11  TCCAGGAAGT TGCAGGAAGT TGTGGTTGCT TAGGGAGGT CCTTGGATTC AAGGAGGCT AAGGAGGCG AGGCAGAAA AGGAGGCG AGGCAGAAA ACGAGCAGT ACGTGCTGTT ACTGGCCAT CCTCGGCAT TACCCACCC GCCAGAATGG TCCTCTTCCT TCTCTTCAT	m #: Eos ser 424 21   GGAGGCCGTC CCATGTAAGC CCATGTAAGC GGTCAGATG TGAAAGGTCC GTTCAGAGC ATTTTCAACC CACGGAGACG TGCTTCTGTG ACTGCCAGC GGCTGAGCAG GCTGCAGC GGAGATGGTC TGCCACGG GGAGATGGTC TGCGCATGC TGCCACTGC TGCCACTGC TGCCACTGC TGCGCATGT TGCGCATGT AGGGGAGGCT GCTGGACAGC GCGGTTTGTC CGCGGTTGTGC	31   TGTGTTTCC AAAGAAACCA GACATCATGT AAGCACTTGG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCCAGATCC AAGCAGCTGA GGAGCAGCTGA GGCACCCAGATCG GTGGAGCATC GCCACACCT TACAGGACCT TACAGGACCT TCCAGAAG AACTGTGCC TCTGCGGGCC TCTGCGGGCC CTGCTCGTGGCC CTGCTGGTGC	TGTTTTCCAG TCGGAAGAT TCTCTTAGA CCATCAGTT GAAGGCAAG TGAATACCT TCATCATCT TCATCATCT TCATCATCT TCATCATCT TCATCATCT TCATCATCAT TCATCAT TC	AGTGCCCCA TCAGCTGCC TGGGTCTAAC TGGGTCTAAC TGTGACCGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG CAGCGAGCCT CCTCTTCAGC CCAGTGCTAGC CCAGTGCTGG CAGCTGGAAG CCCCTGTGAC CTACCAGTGC CTGCAGTGC CGGGGATAC CGGGGGCTCCTG GGGGGCTCCTG	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1080 1140 1200
50 55 60	Nucleic Aci Coding sequi I ATGCCCCTT TCTCTCCTC AGCARANTGA AGCGTCGGA AGCGTCGGA ATGCTTTCA GGGTTGCTG AAGTCCAGG ATTTGCTGTGG AGAGGCAGC ACCTCAGCA ACCCTCAGCA ACCCTCAGCC AGAGGTTGTC TCTCGCCCGC AGGGTCGACC CGGGCCARA CGAGTTGGAC CGGGCCARG AGAGTTGGC AGGGTCGACC CGGGCCARG CGAGTGGTGG AGAGTGGTGG	id Accession Lence: 12.  11  11  TCCAGGAAGT TGCAGGAAGT TGTGGTTGCT TAGGGAGGT CCTTGGATTC AAGGAGGCT AAGGAGGCG AGGCAGAAA AGGAGGCG AGGCAGAAA ACGAGCAGT ACGTGCTGTT ACTGGCCAT CCTCGGCAT TACCCACCC GCCAGAATGG TCCTCTTCCT TCTCTTCAT	m #: Eos ser 424 21   GGAGGCCGTC CCATGTAAGC CCATGTAAGC GGTCAGATG TGAAAGGTCC GTTCAGAGC ATTTTCAACC CACGGAGACG TGCTTCTGTG ACTGCCAGC GGCTGAGCAG GCTGCAGC GGAGATGGTC TGCCACGG GGAGATGGTC TGCGCATGC TGCCACTGC TGCCACTGC TGCCACTGC TGCGCATGT TGCGCATGT AGGGGAGGCT GCTGGACAGC GCGGTTTGTC CGCGGTTGTGC	31   TGTGTTTCC AAAGAAACCA GACATCATGT AAGCACTTGG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCCAGATCC AAGCAGCTGA GGAGCAGCTGA GGCACCCAGATCG GTGGAGCATC GCCACACCT TACAGGACCT TACAGGACCT TCCAGAAG AACTGTGCC TCTGCGGGCC TCTGCGGGCC CTGCTCGTGGCC CTGCTGGTGC	TGTTTTCCAG TCGGAAGAT TCTCTTAGA CCATCAGTT GAAGGCAAG TGAATACCT TCATCATCT TCATCATCT TCATCATCT TCATCATCT TCATCATCT TCATCATCAT TCATCAT TC	AGTGCCCCA TCAGCTGCC TGGGTCTAAC TGGGTCTAAC TGTGACCGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG CAGCGAGCCT CCTCTTCAGC CCAGTGCTAGC CCAGTGCTGG CAGCTGGAAG CCCCTGTGAC CTACCAGTGC CTGCAGTGC CGGGGATAC CGGGGGCTCCTG GGGGGCTCCTG	120 180 240 300 360 420 480 540 600 720 780 840 900 960 1020 1080
50 55 60	Nucleic Aci Coding sequi I ATGCCCCTT TCTCTCCTC AGCANANTGA AGCGTCGGGA CTGGACATCA CTGGACTTCC AAGTTCCAGG ATTTCCAGGA ACCCTCAGGA ACCCTCAGGA CCCTGTGAGC AGAGGATCGC AGAGGTTCC TCGCAGCCC CTCTGCCCGC CAGGGTCGACC CCGGGCCAAGG CCAGGGTCGACC CGGGCCAAGG CCAGGGTTGCC CAGGATGGTGC CAGGATTGCC CAGGATTGTC CAGGATTTC CAGGATTTTC CAGGA	id Accession ience: 12.  11    TCCTGTTGCT TCCAGGAAGT TCCAGGAAGT GCCCGAGAGG CCTTGGATTC AAGGAGCT AAGGAGCT AAGGAGCT AAGGAGCT ACGGCAGAAA GGGATGTGGC GCCAGAGT GCCCTTTGG GCCAGATC TCCTCTTCCT TCTTCGTGAA TCGCCACAT TCGTCAGAT TCGCCACAT TCGTCAGAT TCGCCACAT TCGTCAGAT TCGCCACAT TCGTCAGAT TCGCCACAT TCGTCAGAT TCGTCCTTCCT TCTTCGTGAA TCGCCCACAT TCGCCACAT TCGCCACAT TCGCCACAT TCGCCACAT TCGCCACAT TCGCCCACAT TCGCCACAT TCGCCACAT TCGCCACAT TCGCCACAT TCGCCACAT TCGCCACAT TCGCCCACAT TCGCCCACAT TCGCCCACAT TCGCCCACAT TCGCCCACAT TCGCCCCC	m #: Eos sei 424 21	31   TGTGTTTTCC AAAGAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTGGCTGA AGCAGCTGA GGGGAGTTCC GGTGCACACT TACAGGACCA GTTCCAGAAG GACTGACCAC TTCCAGAAG TTCCAGAAG TTCCAGAAG CACGGCCTGC TCTGCGGGCACCC TCTGCGGGCACC TCTGCGGGCACCC TCTGCGGCACCC TCTGCGGGCACCC TCTGCGGGCACCC TCTGCGGCACCC TCTGCGCACCC TCTGCCACCC TCTGCCACC TCTGCCACCC TCTCCCCC TCTCCCCCC TCTCCCCCCC TCTCCCCCC	TGTTTTCCAG TCGGAAGAT TCTCTTTAGA CCATCAGTT GAAGGCAAG TGAATACCT TCATCATCT TCATCATCT TCATCATCAT TCATCATCAT TCATCATCAT TCATCATCAT CATCATCAT TCATCATCAT CATCACCAG ACTGCACGAG ACTGCACGAG GACTGCACGAG GACTGACGAG GACTGACGAG CCACTCTGAA TGAAGCTGAG CCACTCTGGA CGGCAGGA CGGCGCAGC CCTTCCGTGC CCTTCCGTGG CCTTCCGTGG CCTCCGTGG CCCTCCGTGG CCCTCCGTGG CCCTTCCGTGG CCCTCCGTGG CCCTCCCGTGG CCCCTCCCGTGG CCCTCCCGTGG CCCTCCCT	AGTGCCCCA TTCAGCTGCC TTGGTCTAAC CTGTGACCGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG CAGCGAGCCT CCCATGCTGG CAGCTGGAGCCT CCCATGCTGG CAGCTGGAAG CCCCTGTACA CCCTGTACA CCCTGTGCACGGC CAGCTGGAAG CCCTGTGACAGTGC CCTGGAATGC GGGGGAGTAC TGGCCCCCCC TGGGCCC TCCTGGGCCC TGGGGCCT	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1080 1140 1200
50 55 60	Nucleic Aci Coding sequi I ATGCCCCTT TCTCTCCTC AGCANAATGA AGCGTCGGA AGCGTTGCATC ATGGTTTCA AGGTTGCCTG AAGTCCCAGG TTTGCTGTGA AGAGGCAGC ACCCTCAGCA CCCTGTGAGC CCCTGTGAGC CCCTGTGAGC CCCTGTGAGC CCCTGTGAGC CCCTGTGAGC CCCTGTGAGC CCCTGTGAGC CCGGCCAAAG CGAGTGTTCC CTGCAGGCCT CTGCCGGCCAAAG CGAGTGGTTG CAGGATGTTGC CTGACGGCCA	id Accession ience: 12.  11    TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGCTT ACCGGATGT AAGGAGGCT AAGGAGGCT AAGGAGGCT AAGGAGGCT AAGGAGGCT TACCAGATAT ACAGGACGCT TGCCCTTGTTCCT TCTTCGTGAA TGGCCACATA TG	#: Eos sei 424 21	31   TGTGTTTTCC AAAGAAACCA AAGAAACCA AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCAGATCC AAGCAGCTGA GGGAGCTGC GTGGAGGATG GCCACGCCAG GTTCCAGAAG ACTTCCAGAAG AACTGTGCC TCCGCGGCCAC CTCTGCGGGCAC CTCTGCGGGCAC CTGCTGTGG CGGCACTGC CTGCTGTGG	TGTTTTCCAG TCGGGAGAGAT TCTGTTAGA CCATCAGTT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TTGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG CAGCGAGCCT CCCTTCAGG CAGCTGGAAGG CCCATGCTGG CAGCTGGAAGG CCCTGTGAC CTACCAGTGC CCTGGAATGC CCGGGAGCCT CCTTCAGG CCTGGAATGC CCTGGAATGC CCTGGAATGC CGGCTTCCTG CTCTCGGACC CTCCAGCACC CACCAGGACAC	120 180 240 300 360 420 480 660 720 840 900 960 1020 1140 1200 1260 1320
50 55 60 65	Nucleic Aci Coding sequi I ATGCCCCTT TCTCTCCTC AGCANANTGA AGCGTCGGA AGCGTCGGA ATGCTTTCA GGGTTGCCTG AGGGTGCCTG AGGGGCAGC ACCTCAGCA CCCTGTGAGC AGAGGTTGCCTG AGAGGTTGCCTG AGAGGTTGCC CTGCAGCA CCTCAGCA CCCTCAGCA CCCTCAGCA CCCTCAGCA CCCTCAGCAC CCGGGCCAAAG CGAGTTGGTCG CGGCCAAAG CGAGTTGGTG CAGGATTGC CGGCAAAG CGAGTTGGTG CAGGATTGC CGGCAAAG CGAGTTGGTG CAGGATTGC CTGCAGGGC CTGCAGGGC CTGCAGGGC CTGCAGGGC CTGCAGGGC CTGCAGGGC CTGCAGGGC CTGCAGGGC CTGCAGGGC CTGCAGGAC CGCCAGGACC CCCCTCCCCC CGCAGGAC CGCCAGGAC CCCCTCCCCC CGCAGCAC CCCCCC CTCCCCCC CGCCCAGAC CGCCAGGAC CCCCC CCCCCC CCCCCC CCCCCCC CCCCCC CCCC	id Accession Lence: 12.  11  11  TCCTGTTGCT TCCAGGAAGT TGTGGTCC AAGGAGCTT GCCCCGAGAG GCCCCGAGAG GGGCCAGAAG AGGAGCGTA ACGTGTTGGT ACGTGTTGGT ACGTGCTGTT ACGTGCTGTT ACTGCAGCAGT ACAGGACGCT TAACCACCC GCCAGAATGG TCCTCTTCCT TCTTCTTGTGAA TTGGCCAGTT CTGACCTGTG GTGCCTTTCGT GTGCCTTTCGT GTGCCTTGGT GTGCTTGGT GTGCT GTGT	#: Eos sei 424 21   GGAGGCCGTC CCATGTAAGC CCATGTAAGC GGTTCAGATG TGAAAGGTCC GGTTCAGACG ATTTTCAACC CACGGAGACG TGCTTCTGTG GCTTCCAGGTGG GGTTGTCCAGC GGAGATGGTC TGCCAGCTGG GGAGATGGTC TGCGGTGCTC CGGGGAGATGGTC GGGGACAGC GGGGTTGTG GCGGTTGTG GCGGTTGTG GCGGTTGTG GCGGGCGCAGC GGGGAGACGGT GCGGGAGACGG GCGGTTGTG GCAGGCGGGGGGGGGG	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTGGTC CCCCAGATCC AAGCAGCTGA GAGCAGCTGA GCGAGCTGC GTGGAGGATC GCTGCACACT GTTCCAGAAG CTTCCAGAAG CTTCCAGAAG AACTGTGCC CTCTGCGGGCA CCGGCCGTGC CTGCTGGTGG CTGCTGGTGG CTGCTGGTGG CTGCTGCTGCTGCTGGTGG CTGCTGCTGCT	TGTTTTCAG TGGGAAGAT TTCTGTTAGA CCATCAGT TGAAGGCAG TGAAATACCT TCATCATCT TCATCATCGC ACTCAACGG ACTCACAGGAT CCACCAACGG TCACCATCGGA TGAAGCTGAA CCACTCTGGA TGAGCTGAG CCACTCTGGA TGAGCTGAG CCACTCTGGA TGAGCAGGAC CCACTCTGGA TGAGCAGGAC CCACTCTGGA TGAGCAGGAC CCACTCTGGA TGAGCAGGAC CCACTCTGGA TGGGGAGC CCACTCACACC AGTCACACC AGTCACACC AGTCACACC AGTCACACC AGTCACACC AGTCACACC AGTCACACC AGTCACACC TCAGAGGAC AGTCACACC AGTCAC	AGTGCCCCA TTCAGCTGCC TTGGGTCTAAC TTGGGTCTAAC TTGTGACCGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG CAGCGAGCCT CCTCTTCAGC CCATGCTGG CAGCTGAGAG CCCTGTGAC CCCTGTGAC CCTGCAGC CCTGCAGC CCTGCAGC CCTGCAGTGC CCTGCAGCC CCTGCACC CCCGTGCACC CCCGTGCACC CCCGTGCACC CCCCGTGCACC CCCGCCCCCCCCCC	120 180 240 300 360 420 540 600 720 780 840 900 960 1020 1140 1200 1220 1380
50 55 60 65	Nucleic Aci Coding sequi I ATGCCCCTT TCTCTCCTC AGCANANTGA AGCGTCGGA AGCGTCGGA ATGCTTTCA GGGTTGCCTG AGGGTGCCTG AGGGGCAGC ACCTCAGCA CCCTGTGAGC AGAGGTTGCCTG AGAGGTTGCCTG AGAGGTTGCC CTGCAGCA CCTCAGCA CCCTCAGCA CCCTCAGCA CCCTCAGCA CCCTCAGCAC CCGGGCCAAAG CGAGTTGGTCG CGGCCAAAG CGAGTTGGTG CAGGATTGC CGGCAAAG CGAGTTGGTG CAGGATTGC CGGCAAAG CGAGTTGGTG CAGGATTGC CTGCAGGGC CTGCAGGGC CTGCAGGGC CTGCAGGGC CTGCAGGGC CTGCAGGGC CTGCAGGGC CTGCAGGGC CTGCAGGGC CTGCAGGAC CGCCAGGACC CCCCTCCCCC CGCAGGAC CGCCAGGAC CCCCTCCCCC CGCAGCAC CCCCCC CTCCCCCC CGCCCAGAC CGCCAGGAC CCCCC CCCCCC CCCCCC CCCCCCC CCCCCC CCCC	id Accession Lence: 12.  11  11  TCCTGTTGCT TCCAGGAAGT TGTGGTCC AAGGAGCTT GCCCCGAGAG GCCCCGAGAG GGGCCAGAAG AGGAGCGTA ACGTGTTGGT ACGTGTTGGT ACGTGCTGTT ACGTGCTGTT ACTGCAGCAGT ACAGGACGCT TAACCACCC GCCAGAATGG TCCTCTTCCT TCTTCTTGTGAA TTGGCCAGTT CTGACCTGTG GTGCCTTTCGT GTGCCTTTCGT GTGCCTTGGT GTGCTTGGT GTGCT GTGT	#: Eos sei 424 21   GGAGGCCGTC CCATGTAAGC CCATGTAAGC GGTTCAGATG TGAAAGGTCC GGTTCAGACG ATTTTCAACC CACGGAGACG TGCTTCTGTG GCTTCCAGGTGG GGTTGTCCAGC GGAGATGGTC TGCCAGCTGG GGAGATGGTC TGCGGTGCTC CGGGGAGATGGTC GGGGACAGC GGGGTTGTG GCGGTTGTG GCGGTTGTG GCGGTTGTG GCGGGCGCAGC GGGGAGACGGT GCGGGAGACGG GCGGTTGTG GCAGGCGGGGGGGGGG	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTGGTC CCCCAGATCC AAGCAGCTGA GAGCAGCTGA GCGAGCTGC GTGGAGGATC GCTGCACACT GTTCCAGAAG CTTCCAGAAG CTTCCAGAAG AACTGTGCC CTCTGCGGGCA CCGGCCGTGC CTGCTGGTGG CTGCTGGTGG CTGCTGGTGG CTGCTGCTGCTGCTGGTGG CTGCTGCTGCT	TGTTTTCAG TGGGAAGAT TTCTGTTAGA CCATCAGT TGAAGGCAG TGAAATACCT TCATCATCT TCATCATCGC ACTCAACGG ACTCACAGGAT CCACCAACGG TCACCATCGGA TGAAGCTGAA CCACTCTGGA TGAGCTGAG CCACTCTGGA TGAGCTGAG CCACTCTGGA TGAGCAGGAC CCACTCTGGA TGAGCAGGAC CCACTCTGGA TGAGCAGGAC CCACTCTGGA TGAGCAGGAC CCACTCTGGA TGGGGAGC CCACTCACACC AGTCACACC AGTCACACC AGTCACACC AGTCACACC AGTCACACC AGTCACACC AGTCACACC AGTCACACC TCAGAGGAC AGTCACACC AGTCAC	AGTGCCCCA TTCAGCTGCC TTGGGTCTAAC TTGGGTCTAAC TTGTGACCGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG CAGCGAGCCT CCTCTTCAGC CCATGCTGG CAGCTGAGAG CCCTGTGAC CCCTGTGAC CCTGCAGC CCTGCAGC CCTGCAGC CCTGCAGTGC CCTGCAGCC CCTGCACC CCCGTGCACC CCCGTGCACC CCCGTGCACC CCCCGTGCACC CCCGCCCCCCCCCC	120 180 240 300 360 420 480 660 720 840 900 960 1020 1140 1200 1260 1320
50 55 60	Nucleic Aci Coding sequi I ATGCCCCTT TCTCCCTC AGCANANTGA AGCGTCGGA AGCGTCGGA ATGGTTTTCA GGGTTGCTG AAGTCCAGG ATTGCTGTGG AGAGGCAGC ACCTCAGCA CCTGAGCA CCTGAGC AGAGGTTCC TCGCAGCCT TCTCCCCGC AGGGTCGACC CGGGCCAAAG CGAGTGGTC CGGGCCAAGG CGAGTGGTC CAGGATTGC CGGGCCAAGG CGAGTGGTC CAGGCTAAGG CGAGTGGTC CAGGCTAAGC CGGCCAAGAC CGGGCCAAGAC CGGGCCAAGAC CGGCCAAGAC CGGCCAGGAC CGGCCAGGAC CGGCCAGGAC CGGCCAGGAC CGTTGCCGGC CGTTGCCGGCC CGTTGCCGGCC CGTTGCCGGCC CGTTGCCGCC CTTGCCGGCCC CTTGCCGCCC CTTGCCGGCCC CTTGCCGCCC CTTGCCGCCC CTTGCCGCCC CTTGCCGCCC CTTGCCGCCC CTTGCCCCC CTTCCCCC CTTGCCCCC CTTGCCCCC CTTGCCCCC CTTGCCCCC CTTCCCCCC CTTCCCCCC CTTCCCCC CTTCCCCCC	id Accession ience: 12.  11  1    TCCAGGAAGT TCCAGGAAGT TGGGTCC AAGGAGGT CCTTGGATTC AAGGAGGCT AAGGAGGCT AAGGAGGCT AAGGAGGCT AAGGAGGCC AAGGAGAC GGGACAGAAA ACGAGAC GCAGAAT ACGCACCC GCCAGATCG TCCTCTTCCT TCTTCGTGAA TCGCCCTTCCT TCTTCGTGCAC TCGCCCACT CCTCCTCCC CCAGACCC CCAGACCC CCAGACCC TCCTCCTCCC TCTTCCTGCACC CCAGACCC CCAGACCC CCACCCC CCACCC CCCC CCACCC CCACC CCACCC CCACC CCACCC CCACC CCACCC CCACCC CCAC	#: Eos sei 424 21   GGAGGCCGTC CCATGTAAGC GGTCAGAGG GGTCAGAGG GTCAGAGGG ATTTCAACC CACGGAGACG TGCTTCTGTG ACTGCCATC GGTGAGCAG GGCTGAGCAG GGAGATGGT GGAGATGGT GGAGATGGT GGAGAGCGT GCTGGACAGC CTGCACCGG CGAGATGGT CGCAGCGGAGAGC CTGCACCGG AGGCACAGC AGGCACAGC CGCGGTGGACAGC CGCGGTGGACAGC CGCGGTGGACAGC CAGCAGGGGG CTGGAGCCT CGGAGGCGCGCAGC AGTCGTGAGCCT AGGCGGGGGGGGGG	31   TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCAGATCC AAGCAGCTGA GAGCAGCTGA GGCGACGTGA GCTGCACACCA GTTCCAGAAG ACTGTTCCAGAAG ACTGTTCCAGAAG TCTCAGGAGCA CTGCGGGCACCTGC CTGCTGGTGG GATGGCTTCG GAGGCTTCC CTGCTGGTGG CTGCTGTGGTGG CTGCTGCTGTGG GATGGCATTCC GAGGCGTGCC TTGCTCACTG	TGTTTTCCAG TCGGGAGAT TCTCGTTAGA CCATCAGTT TGAGGCAG TGAATACCT TCATCATCT TCATCATCT TCATCATCT TCATCATCT TCATCATCAT TCATCAT TCATCATCAT TCATCAT	AGTGCCCCA TTCAGCTGCC TTGGTCTAAC TTGAGCTGCC TTGGTCTAAC CTGTGACCGT AATCAAGAGG TCTGCACAGA CACTGATGGG CAGCGAGCCT CCCATGCTGG CCAGTGCTGG CCCATGCTGG CAGCTGGAAG CCCCTGTCAG CTACCAGAC CTACCAGAC CTCTCCGG CGGGGAGTAC TGGCCCACC CGCGGACAC TGGCCCACC CGCGGACAC TGGCCCACC CGCGGACAC TGGCCCACC CCCCAGGACA TGGCCCCACC CCCCAGGACA TGGCCCCACC CCCCAGGACA TGTAGGCACT	120 180 240 300 360 420 600 660 720 780 840 900 1020 1140 1200 1260 1380 1440
50 55 60 65	Nucleic Aci Coding sequil ATGCCCCTT TCTCTCCTT AGCANANTGA AGCGTCGGGA CTGGACATCA CTGGACTTCC ATGGTTTTCA GGGTTGCCTG AAGTCCCAGG ACCCTCAGCA ACCCTCAGCA ACCCTCAGCA CCCTGTGAGC AGAGGATCGC AGAGGTCGCCC CTGCCAGCCCT CTCTGCCCGC CAGGGTCGACC CGGGCCAAAG CGAGTGGTGC CAGGGTTGCCGGC GGCCAGGACC GGCCAGGACC GGCCAGGACC GGCCAGGACC GGCCAGGACC GAGGCCTTGC	id Accession ience: 12.  11    TCCTGTTGCT TCCAGGAAGT TCCAGGAAGT CCTTGGATAC AAGGAGGCT AAGGAGGCT AAGGAGGCT AAGGAGGCT AAGGAGGCT AAGGAGGCT TACCAGATAG GGATATGGC TCCTCTTT TCTTCGTGAT TGGCCACATA TGGCCACTT TCTTCTTGAT TGGCCACTT TCTTCTTGAT TGGCCACTT TGGCCACT TGGCCACT TGGCCACT TGCCCTT TGGCACACT TGGCCACT TGCCCT TGCCCT TGCCCT TGCCCACT TGCCCACC TGCCCACT TGCCCACC TCCCCACC TCCCCCACC TCCCCCACC TCCCCCACC TCCCCCACC TCCCCCACC TCCCCCCACC TCCCCCCCC	#: Eos sei 424 21 21 GGAGGCCGTC CCATGTAAGC GGTTCAGGTG TGAAAGGTCC GGTCAGAGTG ATTTCAACC CACCGAGACG TGCTTCTGTG ACTCCCAGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGGTC CCCCAGATCC AAGCAGCTGA GAGCAGCTGA GGCGCACAC GTTCAGAAG AACTGTGCC TCCAGAAG CGGCCGTGC CTGCTGGGGCA CGGCCGTGC CTGCTGGTGG GATCGCATCT TTCCTCACTG GAGCGTTGC CGAGCATTCC AAAGGCAGCC ACAGGCAGCC ACAGGCAGCC ACAGGCAGCC ACAGGCAGCC ACAGGCAGCC ACAGGCAGCC ACAGGCAGCC ACAGGCAGCC ACAGGCAGCC	TGTTTTCCAG TGGGAGAGAT TCGGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	AGTGCCCCA TTCAGCTGCC TTGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGT CCAGCGAGCCT CCCCATGCTGG CAGCTGGAAGG CCCTGGAAGG CCTGGAATGC CCTGGGATGC CGGGGGAGCT CCTCTCGGCC CCTGGAATGC CGGCTTCCTG CTCTCGGGCC CGGGGATAC TGGGGCAC CGGGGATAC TGGGGACA TGGGGACAC TGGGGACAC TGGGGACAC TGGGGACAC TGGGGCCCCACC CACCAGGACAC TGGGGACTAC TGGGCCCCACC CACCAGGACAC TGGGGACTAC TGGGCCCCACC CACCAGGACAC TGTAGGCAGT TGTAGGCAGT TGTAGGCAGT	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1140 1260 1320 1380 1440 1500
50 55 60 65	Nucleic Aci Coding sequit I ATGCCCCTT TCTCTCCTC AGCANANTGA AGCGTCGGGA AGCGTCGGGA AGGGTTGCCTG AGGTTGCCTG AGGTTGCCTG AGGGTGCAGCA ACCTCAGCA CCCTCAGCA CCCTGTGAGC AGAGGTTGCCTG AGAGGTTGCCCG AGGGTCGACC CTGCAGCAC CTGCAGCAC CTGCAGCAC CTGCAGCAC CTGCAGCAC CTGCAGGCAAAG CGAGTTGGTG CAGGATTGCCGG CAGGATTGCCGG CAGGATTGCCTC CTGCAGGCC CTGCAGGCC CTTGCAGGCC CTTGCAGGCC CTTGCAGGCC CTTGCAGGCC CTTGCAGGCC CTTGCGGCCC CGAGGCCCTC CTTGCGGCC CTTGCGGCCC CTTGCGGCC CTTGCCGC CTTGCCGC CTTGCCGC CTTGCCGC CTTGCCTC CTTGCCCC CTTGCCC CTTGCC CTTGC CTTGCC CTTGC CTTTGC CTTGC CTTGC CTTGC CTTGC CTTTC CTTT	id Accession Lence: 12.  11  11  TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGTT GCCCCGAGAG GGCCCCGAGAG GGGCCAGAAG GGGACCAGAAA ACGTGCTGTT ACTGCTGTT GCTCGGCAT CCTGGCAT CTGCGACAG GCCAGAAT GCCAGAAC TGCCTTTCCT TCTTCTTCT TCTTCTTCTTCTTCTTCTTCT	m #: Eos sei 424 21	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTGCTGC GGAGGATGC GTGAGGATGC GCTGCAGATGC GTTCCAGATGC GCTGCAGATGC GTTCCAGATGC GTTCCAGATGC GTTCCAGAAG AACTGTGCC TCTGCGGGCA CGGCCGTGC TCTGCTGGTGG GATGCCATTCC CGAGGTGGCT TTGCTGGTGGC CGAGAGCTGC CAAGGCAGCC CCCGAGGCTGC	TGTTTTCAG TGGGAAGAT TTCTGTTAGA CCATCAGT TGAAGGCAG TGAAATACCT TCATCATCT TCATCATCT TCATCAGTC TCATCAGTC TCATCAGTC TCATCAGTC TCATCAGTC TCATCAGTC TCATCAGGA AGGAAAGGGG ATGCACTGGC ACTGCAAGGG TCACCAGGGT CCACCAGGGT CCACCTGGA CGACCTCTGAA CCACTCTGGA CGGTCCTGT TCCGTGG AGGCAGCAC TCCGGCAGCC AGTCACCC TCCTGCTGGG CCAAGCACT AGGGGAAGCT AGGGGAAGCAT AGGGGAAAGCATGT AGGGGAAGCAT AGGGAAAGCAT AGGGGAAGCAT AGGGGAAAGCAT AGGGGAAAGCAT AGGGGAAGCAT AGGGGAAGCAT AGGGGAAGCAT AGGGGAAAGCAT AGGGGAAAGCAT AGGGGAAGCT AGGGGAAGCAT AGGGGAAGCT AGGGAAGCT AGGGAAGCT AGGGGAAGCT AGGGGAAGCT AGGGGAAGCT AGGGGAAGCT AGGGGAAGCT AGGGGAAGCT AGGGGAAGCT AGGGAAGCT AGGGGAAGCT AGGGGAAGCT AGGGGAAGCT AGGGGAAGCT AGGGGAAGCT AGGGGAAGCT AGGGGAAGCT AGGGGAAGCT AGGGAAGCT AGGGGAAGCT AGGGAAGCT AGGGGAAGCT AGGGGAAGCT AGGGAAGCT AGGGAAGCT AGGGAAGCT AGGGAAGCT AGGGAAGCT AGGGAAGCT AGGGAAGCT AGGGAAGCT AGGGA	AGTGCCCCA TTCAGCTGCC TTGGGTCTAAC TTGGGTCTAAC TTGTGACCGT TATCAACAGG TCTGCACAGA CACTGATGGG TGTCACTGTG CAGCGAGCCT CCTCTTCAGC CCATGCTGG CAGCTGATGG CACTGATGG CCCTGTGAC CCCTGTGAC CCTGCAGATGC CCTGCAGTGCC CCTGGAATGC CTCTCGGGCC GGGGGAGTAC TGGCCCACC CACAGGACA CGAGGATGAC TGTAGCAGTGC CGAGGATGAC TGTAGCAGTC CGAGGATGAC TGTAGCAGTC CGAGGATGAC TGTAGCAGTC CGAGGATGAC TGTAGGCAGT TGAGGCAGC TGTAGGCAGC	120 180 240 300 360 420 540 600 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1560
50 55 60 65	Nucleic Aci Coding sequit I ATGCCCCTT TCTCTCCTC AGCANANTGA AGCGTCGGGA AGCGTCGGGA AGGGTTGCCTG AGGTTGCCTG AGGTTGCCTG AGGGTGCAGCA ACCTCAGCA CCCTCAGCA CCCTGTGAGC AGAGGTTGCCTG AGAGGTTGCCCG AGGGTCGACC CTGCAGCAC CTGCAGCAC CTGCAGCAC CTGCAGCAC CTGCAGCAC CTGCAGGCAAAG CGAGTTGGTG CAGGATTGCCGG CAGGATTGCCGG CAGGATTGCCTC CTGCAGGCC CTGCAGGCC CTTGCAGGCC CTTGCAGGCC CTTGCAGGCC CTTGCAGGCC CTTGCAGGCC CTTGCGGCCC CGAGGCCCTC CTTGCGGCC CTTGCGGCCC CTTGCGGCC CTTGCCGC CTTGCCGC CTTGCCGC CTTGCCGC CTTGCCTC CTTGCCCC CTTGCCC CTTGCC CTTGC CTTGCC CTTGC CTTTGC CTTGC CTTGC CTTGC CTTGC CTTTC CTTT	id Accession Lence: 12.  11  11  TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGTT GCCCCGAGAG GGCCCCGAGAG GGGCCAGAAG GGGACCAGAAA ACGTGCTGTT ACTGCTGTT GCTCGGCAT CCTGGCAT CTGCGACAG GCCAGAAT GCCAGAAC TGCCTTTCCT TCTTCTTCT TCTTCTTCTTCTTCTTCTTCT	m #: Eos sei 424 21	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTGCTGC GGAGGATGC GTGAGGATGC GCTGCAGATCG GTTCCAGATCG GTTCCAGATCG GTTCCAGATCG GTTCCAGATCG GTTCCAGATCG GTTCCAGATCG TACAGGACCA TCTGCGGGCA CGGCCGTGC TCTGCTGGTGG GATGCCATTC GAGGATGGCT TTGCTCACTGC GAGAGCTGCC CACAGGCAGCC CCTGAGGTGCC CCTGAGGTGCC CCTGAGGTGCC CCTGAGCTGCC	TGTTTTCAG TGGGAAGAT TTCTGTTAGA CCATCAGT TGAAGGCAG TGAAATACCT TCATCATCT TCATCATCT TCATCAGTC TCATCAGTC TCATCAGTC TCATCAGTC TCATCAGTC TCATCAGTC TCATCAGGA AGGAAAGGGG ATGCACTGGC ACTGCAAGGG TCACCAGGGT CCACCAGGGT CCACCTGGA CGACCTCTGAA CCACTCTGGA CGGTCCTGT TCCGTGG AGGCAGCAC TCCGGCAGCC AGTCACCC TCCTGCTGGG CCAAGCACT AGGGGAAGCT AGGGGAAGCAT AGGGGAAAGCATGT AGGGGAAGCAT AGGGAAAGCAT AGGGGAAGCAT AGGGGAAAGCAT AGGGGAAAGCAT AGGGGAAGCAT AGGGGAAGCAT AGGGGAAGCAT AGGGGAAAGCAT AGGGGAAAGCAT AGGGGAAGCT AGGGGAAGCAT AGGGGAAGCT AGGGAAGCT AGGGAAGCT AGGGGAAGCT AGGGGAAGCT AGGGGAAGCT AGGGGAAGCT AGGGGAAGCT AGGGGAAGCT AGGGGAAGCT AGGGAAGCT AGGGGAAGCT AGGGGAAGCT AGGGGAAGCT AGGGGAAGCT AGGGGAAGCT AGGGGAAGCT AGGGGAAGCT AGGGGAAGCT AGGGAAGCT AGGGGAAGCT AGGGAAGCT AGGGGAAGCT AGGGGAAGCT AGGGAAGCT AGGGAAGCT AGGGAAGCT AGGGAAGCT AGGGAAGCT AGGGAAGCT AGGGAAGCT AGGGAAGCT AGGGA	AGTGCCCCA TTCAGCTGCC TTGGGTCTAAC TTGGGTCTAAC TTGTGACCGT TATCAACAGG TCTGCACAGA CACTGATGGG TGTCACTGTG CAGCGAGCCT CCTCTTCAGC CCATGCTGG CAGCTGATGG CACTGATGG CCCTGTGAC CCCTGTGAC CCTGCAGATGC CCTGCAGTGCC CCTGGAATGC CTCTCGGGCC GGGGGAGTAC TGGCCCACC CACAGGACA CGAGGATGAC TGTAGCAGTGC CGAGGATGAC TGTAGCAGTC CGAGGATGAC TGTAGCAGTC CGAGGATGAC TGTAGCAGTC CGAGGATGAC TGTAGGCAGT TGAGGCAGC TGTAGGCAGC	120 180 240 300 360 420 540 600 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1560
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	Nucleic Aci Coding sequil I ATGCCCCTT TCTCCCTC AGCARANTGA AGCGTCGGA AGCGTCGGA ATGGTTTTCA ATGGTTTTCA AGGTTGCTGG AGAGTCCAGG ATTCCTCCAGC AGAGGTCGCAGC AGAGGTTCC AGAGGTTCC AGAGGTTCC CTCTCGCCGC AGGGTCGACC CGGGCCAAAG CCAGGGTCGACC CGGGCCAAGG CAGTTGGTGGTC CAGCCCAGGCC CGGGCCAGGC CAGGGCCAGGC CTGACGGCCAGGC CTGCGGCCCAGGCCAGG	id Accession lence: 12.  11  12  13  15  16  TCCAGGAAGT TCCAGGAAGT TGAGGAGCT AAGGAGGCT AAGGAGGCT AAGGAGCT AAGGAGCT AAGGAGCC AAGGAGCAAAA AGGACAGAAA AGGACAGAAA ACGACAGAAT ACGCACCC GCCAGAAT ACGCACCC GCCAGATCG TCCTCTTCCT TCTTCGTGAA TCGCCTTCCT TCTTCGTGAA TCGCCTTCCT TCTTCGTGAA TCGCCACATA CCGCCACATA CCGCCACATA CCGCCACATA CCGCCACATA CCGCCACATA CCGCCCCCC AGGACCGTCC CGCCACAGACC CAGCCCGTCAC CAGCCCGTCC CGCCACAGACC CAGCCCGTCAC CAGCCCGTCC CGCCACACACACACACACACACACACACACACACACA	m #: Eos sei 424 21	31   TGTGTTTTCC AAAGAACCA GACATCATGT AAGCACTTTG GGAGCATCC CAACAGGAAG GAACTTGCTC CCCAGATCC AAGCAGCTGA GAGCATCC GTGGAGGATG GCCACGCAG GTTCAGAAG GTTCAGAAG AACTGTTCAGAAG ACTGTTCAGAAG TTCAGGACA TTCTGCGGGCA TCTGCGGGCA CTGCTGGTGG CTGCTGGTGG CTGCTGGTGG CTGCTGTGG CTGCTGGTGG CTGCTGGTGG CTGCTGGTGG CTGCTGGTGG CTGCTGGTGG CTGCTGGTGG CTGCTGGTGG CTGCTGGTGG CTGCTGGTGG CTGGTGGTG CTGCTGGTGG CTGGTGGTG CTGGTGGTGG CTGGTGGTG CTGGTGGTG CTGGTGGTGG CTGGTGGTG CTGGTGGTGG CTGGTGGTG CTGGTGGT CTGGTGGTG CTGGTGGTG CTGGTGGTG CTGGTGGTG CTGGTGGT CTGGTGGT CTGGTGGTG CTGGTGGT CTGGT CTGGTGGT CTGGTGGT CTGGT CTGGT CTGGTGGT CTGGT	TGTTTTCCAG TGGGAGAGAT TTCTGTTAGA CCATCAGTT TGAGGCAG TGAATACCT TCATCATCT TCATCAGTC TCATCAGTC TCATCAGTC TCATCAGTC TCATCAGTC TCATCAGTC TCATCAGTC TCATCAGCAG ACTGCAGAGGG ACTGCAGAGGG GACTGCAGAGG GACTGCAGGG TGAGCTGAC TGAGCAGGG TGAGCAGGAGCA TGAGCAGGAGCA TCATCTGGA TCAGGAGCAG TCATGTTGGA	AGTGCCCCA TTCAGCTGCC TTGGTCTAAC TTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG CACTGATGGG CAGCGAGCCT CCCATTCAGC CCCATGCTGG CAGCTGGAAG CCCCTGTGAA CCCTGTGAGG CCCTGTGAGG CCCTGTGAGG CCCTGTGAGG CCCTGTGAGG CCCTGTGAGG CCCTGGAATGC CGGGGGGCC CGGGGAGTAC TGCCCGGACA TGGCCCCACC CACCAGGACA TGTAGGCAGT TGTAGGCAGT CGATGGTCTAG CGGGGAGTAC CGAGGATGAG CGAGGATGAG CGAGGATGAG CGAGGATGAG CGAGGATGAG CGAGGACT CGAGGACT CGAGGACT CGAGGCCG CGGGGCC CGGGGCC CGCGGCC CGCGGACC CGGGGCC CGGGCC CGCC CGCC CGCC CGCC CGCC CGCC CGCC CCCC CCCC CCCC CCCC CCCC CCCC CCCC CCCC	120 180 240 300 360 420 540 600 660 720 780 840 906 1020 1140 1260 1320 1440 1500 1500
50 55 60 65 70	Nucleic Aci Coding sequil ATGCCCCTT TCTCTCCTT AGCANANTGA AGCGTCGGA AGCGTTGGAATTCA ATGGTTTTCA GGGTTGCTG AAGTCCAGG ATTGCTGTGG AGAGTCCAGG ACCTCAGCA ACCTCAGCA ACCTCAGCA CCTGTGAGC AGAGGTTCC TGCAGCCT CTGTCGCCCC CGGGCCAAGG CGAGTCGTC CTGCAGCCC CGGGCCAAGG CGAGTGGTC CAGGGTTGC CAGGGTCGACC CTGACGGCC CTGACGGCC CTGACGGCC CTGACGGCC CTGGGGCCC CGGGCCAGACC CTTCGGCGCC CAGGGCCCTCC CTGGACCCC CAGGGCCTGC CAGGCCCTCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCC CAGGCCCCCCC CAGGCCCCCC CAGGCCCCCCC CAGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCC CAGGCCCCCCC CAGGCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCC CAGGCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCC CAGGCCCCCC CAGGCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCC CAGGCCCCC CAGGCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCC CAGGCCCCC CAGGCCCCC CAGGCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCC CAGGCCCCC CAGCCCCC CAGGCCCCCC CAGGCCCCCC C	id Accession ience: 12.  11    TCTGTTGCT TCCAGGAAGT TCCAGGAAGT GCCCGAGAG GGGAGCCT AAGGAGCT AAGGAGCT AAGGAGCT AAGGAGCT ACGCAGAAA ACGGCAGAAA ACGGCAGAAA ACGGACCT TAACCACCC GCAGAATCG TCCTCTTCCT TCTTCGTGAA TCGCCACTAG TCGCCACTAG CGGCCACTAG CGGCCACTAG CGGCCACTAG CAGCCGTCC CAGCAGCTC CAGCAGTCG CAGGAACCC CAGCAGTCG CAGCAGTCC CAGCAGTCG CAGCAGTCG CAGCAGTCG CAGCAGTCG CAGCAGTCG CAGCAGTCAC CAGCAGCAC CAGCAGTCAC CAGCAGTCAC CAGCAGTCAC CAGCAGTCAC CAGCAGTCAC CAGCAGTCAC CAGCAGTCAC CAGCAGTCAC CAGCAGTCAC CAGCAGCAC CAGCAGTCAC CA	m #: Eos sei 424 21    GAGGCCGTC CCATGTAAGC CCATGTAAGC GGTCAGAGTG TGAAAGGTCC GGTCAGAGTG ACTTCAACC CACGAGACG TGCTTCTGTG ACTGCATCC TGCCAGCTG GGAGATGGTC TGCAGCTG GGAGATGGTC TGCGGTGCTG CGGAGCAGGT CGCAGCTGC CGGAGCAGCT CGCAGCAGGT CGCAGCAGGT CGCAGCAGGT CGCAGCAGCT CGCAGCAGGT CGCAGCAGAGT CGCAGGGGG CGGAGGGGGC CGGAGGGGGC CGGAGGGGGCCT CGCACCAAATC CACAAACCCT CACAAACCCT CTGCTCAGATC TTGCTCAGATC TTGCTCA	31 TGTGTTTTCC AAAGAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGGTC CCCAGATCC AAGCAGCTGA GAGCAGCTGA GGCGAGCTGC GGTGCACACT TACAGGACCA GTTCCAGAAG AACTGTGCC CTGTGTGGCC GGTGCACACT TACAGACCA TTCCAGAGG AACTGTGCC CTGTGTGGCC CTGTGTGGCC CTGTGTGGCC CTGTGTGGCC CTGTGTGGCC CTGTGTGGCC CTGTGTGGCC CTGTGTGGCC CTGTGTGGCC CTGAGGCTGC CGAGCTGCC CCTGAGGCTGC CGACCTCGTCT CGGGCCTGC CGACCTCGTCT CGGGCCTGC CCTGAGGCTGC CGACCTCGTCT CGGGCCTCT CAGAGCTTTC	TGTTTTCCAG TCGGAAGAT TCTCTTTAGA CCATCAGTT GAAGGCAAG TGAATACCT TCATCATCT TCATCATCT TCATCATCT TCATCATCAT TCATCATCAT TCATCATCAT CATCACCAG ACTGCACAGG ACTGCACAGG GACTGCACAGG GACTGCACGG GACTGCACGG TGAAGCTGACGG TGAAGCTGACGG TGAAGCTGACGG TGAAGCTGAG CCATCTCGGA TGAGCAGGAGCC TCATCACACT TCCTCCTGGG CCAAGCATGT AGGGAAGCT TCCTGCTGGG TCCTCTTGGA TCCTTCTGGA TCCTTCTGGA TCCTTCTTGGA TCCTTCTTGGA TCCTTTTGGA TCAGAAGCT TCAGAAAGCT TCAGAAAGCT TCAGAAAGCT TCAGAAAGCT TCAGAAAGCT TCAGAAAGCT TCAGAAAAGCT TCAGAAAAACAT TCAGAAAAACAT TCAGAAAAAAAAAA	AGTGCCCCA TTCAGCTGCC TTGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG CAGCTGTGCCCCAT CCCATGCTGG CAGCTGGAGCCT CCCATGCTGG CAGCTGGAAG CCCCTGTGAC CCTCTCCGG CAGCTTCCTG CTCTCCGGGCCC CACCAGGAGTAC TGGCCCCACC CACCAGGACAC TGGCCCCACC CACCAGGACAC TGGCCCCACC CACCAGGACAC TGGCCCCACC CACCAGGACA TGTAGGCAGT GATGGTCTAC TGTCAGGCCGG ACCCCTCCCC CACCAGGACA TGTAGGCAGT CGAGGCCGG CACCTCTGCC CACCTCCCCC	120 180 240 300 360 420 480 540 660 720 780 900 960 1080 1140 1260 1320 1320 1350 1560 1680
50 55 60 65 70	Nucleic Aci Coding sequil ATGCCCCTT TCTCTCCTT AGCANANTGA AGCGTCGGA AGCGTTGGAATTCA ATGGTTTTCA GGGTTGCTG AAGTCCAGG ATTGCTGTGG AGAGTCCAGG ACCTCAGCA ACCTCAGCA ACCTCAGCA CCTGTGAGC AGAGGTTCC TGCAGCCT CTGTCGCCCC CGGGCCAAGG CGAGTCGTC CTGCAGCCC CGGGCCAAGG CGAGTGGTC CAGGGTTGC CAGGGTCGACC CTGACGGCC CTGACGGCC CTGACGGCC CTGACGGCC CTGGGGCCC CGGGCCAGACC CTTCGGCGCC CAGGGCCCTCC CTGGACCCC CAGGGCCTGC CAGGCCCTCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCC CAGGCCCCCCC CAGGCCCCCC CAGGCCCCCCC CAGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCC CAGGCCCCCCC CAGGCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCC CAGGCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCC CAGGCCCCCC CAGGCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCC CAGGCCCCC CAGGCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCC CAGGCCCCC CAGGCCCCC CAGGCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCC CAGGCCCCC CAGCCCCC CAGGCCCCCC CAGGCCCCCC C	id Accession ience: 12.  11    TCTGTTGCT TCCAGGAAGT TCCAGGAAGT GCCCGAGAG GGGAGCCT AAGGAGCT AAGGAGCT AAGGAGCT AAGGAGCT ACGCAGAAA ACGGCAGAAA ACGGCAGAAA ACGGACCT TAACCACCC GCAGAATCG TCCTCTTCCT TCTTCGTGAA TCGCCACTAG TCGCCACTAG CGGCCACTAG CGGCCACTAG CGGCCACTAG CAGCCGTCC CAGCAGCTC CAGCAGTCG CAGGAACCC CAGCAGTCG CAGCAGTCC CAGCAGTCG CAGCAGTCG CAGCAGTCG CAGCAGTCG CAGCAGTCG CAGCAGTCAC CAGCAGCAC CAGCAGTCAC CAGCAGTCAC CAGCAGTCAC CAGCAGTCAC CAGCAGTCAC CAGCAGTCAC CAGCAGTCAC CAGCAGTCAC CAGCAGTCAC CAGCAGCAC CAGCAGTCAC CA	m #: Eos sei 424 21    GAGGCCGTC CCATGTAAGC CCATGTAAGC GGTCAGAGTG TGAAAGGTCC GGTCAGAGTG ACTTCAACC CACGAGACG TGCTTCTGTG ACTGCATCC TGCCAGCTG GGAGATGGTC TGCAGCTG GGAGATGGTC TGCGGTGCTG CGGAGCAGGT CGCAGCTGC CGGAGCAGCT CGCAGCAGGT CGCAGCAGGT CGCAGCAGGT CGCAGCAGCT CGCAGCAGGT CGCAGCAGAGT CGCAGGGGG CGGAGGGGGC CGGAGGGGGC CGGAGGGGGCCT CGCACCAAATC CACAAACCCT CACAAACCCT CTGCTCAGATC TTGCTCAGATC TTGCTCA	31 TGTGTTTTCC AAAGAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGGTC CCCAGATCC AAGCAGCTGA GAGCAGCTGA GGCGAGCTGC GGTGCACACT TACAGGACCA GTTCCAGAAG AACTGTGCC CTGTGTGGCC GGTGCACACT TACAGACCA TTCCAGAGG AACTGTGCC CTGTGTGGCC CTGTGTGGCC CTGTGTGGCC CTGTGTGGCC CTGTGTGGCC CTGTGTGGCC CTGTGTGGCC CTGTGTGGCC CTGTGTGGCC CTGAGGCTGC CGAGCTGCC CCTGAGGCTGC CGACCTCGTCT CGGGCCTGC CGACCTCGTCT CGGGCCTGC CCTGAGGCTGC CGACCTCGTCT CGGGCCTCT CAGAGCTTTC	TGTTTTCCAG TCGGAAGAT TCTCTTTAGA CCATCAGTT GAAGGCAAG TGAATACCT TCATCATCT TCATCATCT TCATCATCT TCATCATCAT TCATCATCAT TCATCATCAT CATCACCAG ACTGCACAGG ACTGCACAGG GACTGCACAGG GACTGCACGG GACTGCACGG TGAAGCTGACGG TGAAGCTGACGG TGAAGCTGACGG TGAAGCTGAG CCATCTCGGA TGAGCAGGAGCC TCATCACACT TCCTCCTGGG CCAAGCATGT AGGGAAGCT TCCTGCTGGG TCCTCTTGGA TCCTTCTGGA TCCTTCTGGA TCCTTCTTGGA TCCTTCTTGGA TCCTTTTGGA TCAGAAGCT TCAGAAAGCT TCAGAAAGCT TCAGAAAGCT TCAGAAAGCT TCAGAAAGCT TCAGAAAGCT TCAGAAAAGCT TCAGAAAAACAT TCAGAAAAACAT TCAGAAAAAAAAAA	AGTGCCCCA TTCAGCTGCC TTGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG CAGCTGTGCCCCAT CCCATGCTGG CAGCTGGAGCCT CCCATGCTGG CAGCTGGAAG CCCCTGTGAC CCTCTCCGG CAGCTTCCTG CTCTCCGGGCCC CACCAGGAGTAC TGGCCCCACC CACCAGGACAC TGGCCCCACC CACCAGGACAC TGGCCCCACC CACCAGGACAC TGGCCCCACC CACCAGGACA TGTAGGCAGT GATGGTCTAC TGTCAGGCCGG ACCCCTCCCC CACCAGGACA TGTAGGCAGT CGAGGCCGG CACCTCTGCC CACCTCCCCC	120 180 240 300 360 420 480 540 660 720 780 900 960 1080 1140 1260 1320 1320 1350 1560 1680
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	Nucleic Aci Coding sequit I ATGCCCCCTT TCTCTCCTC AGCANANTGA AGCGTCGGGA CTGGACATCA CTGGACATCA CTGGACATCA CTGGACATCA CTGGACATCA CTGGACATCA CTGGACATCA CTGGACATCA CTGGACATCA CCTCAGCA CCCTCAGCA CCCTCAGCAC CTGCCGGCCAAG CGAGTCGTC CTGCCGGCCAAG CGAGCCGTC CTGCGGGCC GTTGCGGGCC GAGGCCCTC CCAGCGCCAG TCAGTAGGCC TCAGTAGGCCT TTTGAGGTCA TCAGTAGGGCA TCAGTAGGGCA TCAGTAGGGCA TCAGTAGGGCA TCAGTAGGGCA TCAGTAGGGCA TCAGTAGGGCA TCTTTGAGGTCA	id Accession Lence: 12.  11  11  TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAAGT TGTGGTGCTC AAGGAGGTT AAGGAGGTT AAGGAGGTT AAGGAGGTA ACGTGTGTGCT AAGGAGGCAGAAA ACGTGCAGTA ACGTGCTGTT ACTGCCAGAGAGTT ACGTGCTGTT ACTGCCAGAATG GCCAGAATG TCTTCTTCTTGTGAA TGGCACATA CTGACCTGCT GGCGAGAGTC GGGCAGAGCT AGGACTGTG GGCCAGAGATTG GGCCAGAGATTA CAGGAGGGTCA GGCCAGAGATTG AGGACTGGT AAGGACTGGT AAGGACTGTG AAGGACTGTG AAGGACTGTT AACCAGAGAATTG AACCAGAGAATTA AACCAGAGAGAATTA AACCAGAGAATTA AACCAGAATTA AACCAGAGAATTA AACCAGAATTA AACCAGAGAATTA AACCAGAGAATTA AACCAGAGAATTA AACCAGAATTA AA	m#: Eos sei 424 21	31   TGTGTTTTCC AAAGAAACCA AACACATCATGT AACACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCCAGATCC AAGCAGCTGA GAGCATGC GTGCAGCAGT GCCACGCCAG GTTCCAGAAG GATTCGGCACACT TACAGGACCA GTTCCAGAAG AACTGTGCCC TCTGCTGGGGCA CGGGCCGTGC CTGTGTGGG GATGCATTC GAGAGCTGC CTGGCAGCTGC CTGGCAGCTGC CTGGCAGCTGC CTGGCAGCTGC CTGGAGACTTCC CAGAGCTTGCC CCTGAGCTGC CCTGAGCTGCC CCTGAGCTGCC CCTGAGCTGCC CCTGAGCTTGC GAGCTTTGC CAGAGCTTTGC CAGAGCTTGC CAGAGCTCC CAGAGCTTGC CAGAGCTTCC CAGAGCTTGC CAGAGCTTGC CAGAGCTTGC CAGAGCTTGC CAGAGCTCC CAGAGC CAGAGCTCC CAGAGCTCC CAGAGCTCC CAGAGCTCC CAGAGCTCC CAGAGCTCC CAG	TGTTTTCCAG TGGGAAGAT TTCTGTTAGA CCATCAGTT TGAGGCAAG TGAAAGGGA TGAAAGGGA AGGAAGGG CCACCAGG ACTGCACGGC CCACCAGG ACTGCACGGC TCAGCAGGGA TGAAGGGA TGAGCAGGG TCCGCCAGG GACTGACGG TCAGCAGGG TCAGCCAGG TCAGCAGGG TCAGCAGGG TCAGCAGGG TCAGCAGGA TCAGCAGGG TCGGAAGGC TCTTCGAGG TCGGAGGG TCGGAGGG TCGGAGGG TCAGCTGT AGGGAAGGC TCATGTTGGG TCGGAGGGC TCATGTTGGG TGAGGGAAGCT TCATGTGGG TGAGGGAAGCT TCATGTGGG TGAGGGAAGCT TCATGTGGG TGAGAGGATGT TGAGAAGGT TGAGAGGT TGAGAAGGT TGAGAGGT TGAGGGG TGAGGT TGAGAGGT TGAGAGGT TGAGGGG TGAGGT TGAGGGG TGAGGT TGAGGGG TGAGGT TGAGGGG TGAGGT TGAGGGG TGAGGT TGAGGGG TGAGGT TGAGGGG TGAGGG TGAGGG TGAGGT TGAGGGG TGAGGG TGAGG TGAGGAGG TGAGGAGG TGAGG TGAGGAGG TGAGGG TGAGG TGAGGG TGAGG TGAGGG TGAGGG TGAGGG TGAGGG TGAGGG TGAGGG TGAGGG	AGTGCCCCA TTCAGCTGCC TTGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAG TCTGCACAGA CACTGATGGG TGTCACTGT CCAGTGGAGCCT CCCCATGCTGG CAGCTGGAAG CCCTGTGAC CTACAGTGC CCTGGAATGC CCTGGAATGC CCTGGAATGC CTGCACTGGGACC CCGGAATGC CGGGAGCTAC CGGGGAGTAC CGCCCCCCC CACCAGGACA CCACCCCCCC CACCAGGACA CGACCCCCGG CGGGCACGC CGGGCACGC CGGCTCCAG CGGGCACGC CGGCTCCAG CGGGCACGC CGGGCACGC CGGCCCCCC CGGGCACGC CGGGCACGC CGCCCCCCC CGCCCCCCC CGCCCCCCC CGCCCCCC	120 180 240 300 360 420 540 660 720 780 960 1020 1140 1260 1320 1380 1440 1560 1560 1680 1740
50 55 60 65 70	Nucleic Aci Coding sequil Tottocott AGCANANTGA AGCGTCGGA AGCGTTTCA CTGGACATCA ATGGTTTTCA AGGTTGCTGG AGAGGGCAGC ACCTCAGCA ACCCTGGAGC AGAGGTTGCTGG AGAGGGCAGC ACCTCAGCA CCCTGTGAGC AGAGTGTCC TCGCAGGCCAAG CGAGGACCG CGAGGACCG CGAGGACCG CTGCAGGGCCAGG CTGGACGCCT CCAGGGCCAGACC CTGGACGCCT CCAGGGCCAGACC CTGGATGCGCC CTGGATGCGCCT CAGGGCCAGACC CTTGGACGGCCAG TCAGTAGGGCCAG TCAGTAGGCTCAC TCAGTAGCTCAC TCAGTAGCTCAC TCAGTAGCAC TCAGTAGCTCAC TCAGTAGCAC TCAGTAGCTCAC TCAGTAGCAC TCAGTA	id Accession Lence: 12.  11  11  TCCTGTTGCT TCCAGGAAGT TGTGGTCC AAGGAAGT TGTGGTGCTC AAGGAGGT CCTTGGATTC AAGGAGGCT AAGGAGGCG AGGCAGAAA ACGGACAGAAA ACGGACCCT GCCAGAGG GCCAGAATG TCTCCTTCCT TAACCACCC CCCAGAATG TGCCCTTCCT TCTCTCTCT TCTCTCTCT TCTCTCTC	#: Eos sei 424 21   GGAGGCCGTC CCATGTAAGC CCATGTAAGC GGTTCAGGTG TGAAAGGTCC GGTCAGGTG ACTTCTGTG ACTTCTGTG GGCTGCATCG TGCACTCG TGCCACTCG TGCCACTCG TGCCACTCG GGAGAATGGTC TGCGGTGTGT AGGGGACATGT CGGGTTGTG AGGCACTCG GCGGTTTGTG AGGGACATGT CGAGCAGGCCT AGGGAGAATGTC CGAGCAGGCCT AGGGAGAATGTC AGGGAGAGCT AGGGAGAGCT AGGGAGAGCT AGGAGAGCCT AGGAGGAGAT AGGAGAGGCCT AGGAGAGGCT AGGAGAGCCT AGGAGAGGCT CGAACAAATC AACAAGCCCT TGCACAATC CAAACAATC CAAACAATC CAAACAATC CAAACAATC CAAACAATC CAAACAATC CAAACAATC CAAACAATC CAAACAATC CAAACAACCCCC CAAACCCCACC CAAACCCCACC CAAACCCCACC CAAACCCACC CCAAACCCACC	31   TGTGTTTTCC AAAGAAACCA AAGAATCATTG GAGCATTTG GAGCATTGC CAACAGGAAG GAACTTGCTC CCCCAGATCC CAACAGGATGC GTGGAGGATG GTGCACCAG GTGCACCAC GTGCACCAC TACAGGACC TTCCAGAAG AACTGTGC CTGCTGGTGG CTGCTGCTGGTGG CTGCTCGTGG CTGCTGGTGG CTGCTGGTGG CTGCTGGTGG CTGCTGGTGG CAGAGCTTCC CAGAGCTTGC CAGAGCTGC CAGAGCTGC CAGAGCTGC CAGAGCTGC CAGAGCTGC CAGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCGGGCTGCC CCGGGCTGCC CCGGGCTGCC CCGGGCTGCC CGGGCTGCC CGGGCTGCGCAC CCGGGCTGCCC CGGGCTGCGCAC CCACACCATTCT CCACACCAT	TGTTTTCCAG TGGGAAGAT TTCTGTTAGA CCATCAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC TTGAGCTGCC TGGGTCTAAC TGTGACCGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG CAGCGAGCCT CCTCTTCAGC CCATGCTGG CAGCTGGAAG CCCCTGTGAC CTACCAGTGC CTGCAGCT CCTGCAGC CCGAGGTTCCT CCTCCAGC CCACAGCTACC CGGGGACTAC CGGGGACAC CGAGGACAC CGAGGACAC CGAGGACAC CGAGGACAC CGAGGACAC CGACGGCCGC CACCAGGCCG CCCCGTGCCCCCC CCCCGGACAC CGGGGACTCCTCCCGC CGCCGCCCCCCCCCC	120 180 240 300 360 420 540 600 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1500 1620 1680 1680 1740
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50 55 60 65 70 75	Nucleic Aci Coding sequil I ATGCCCCTT TCTCTCCTC AGCARANTGA AGCGTCGGA AGCGTCGGA AGCGTTGCTG ATGGTTTTCA AGGTTGCTG AGGAATTCC ATGGTTGCTGG AGAGGCAGC ACCTCAGCA CCTCAGCA CCTCAGCA CCTCAGCA CCTCAGCA CCTCAGCA CCTCAGCA CCTCAGCA CCTCAGCA CCTCAGCAC CTGCAGCCCT CTGCCGGC AGGGTCGACC CGGGCCAAG CGAGTCGGTC CAGCAGCAC GTTGCGGCC CAGGCCTACC CAGCGCCAG TCAGTAGGCC TTGACGGCC TTGACGCC TTGACGGCC TTGACGCC TTGACGGCC GCCCCTACC GCCCCGCGCAGAAC CGCCCCGCC CGGCCGGGAGAC CGCCCGCC	id Accession Lence: 12.  11  11  TCCTGTTGCT TCCAGGAAGT TGTGGTTCCT TCCAGGAAGT TGTGGTGCTC AAGGAGGTT ACCCAGAAG GGACCAGAAA ACGTCAGTTGCT GCCCGAGAAG GGATCTGTT ACTGTGTTGT ACTGTCTTTT ACTGCACT ACTGCTTTT ACTGCACT ACTGCTTTCT TAACCACCC GCCAGAATG TCCTCTTCCT TCTTCTTCT TCTTCTTCT TCTTCTTC	#: Eos sei 424 21	31   TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCAGATCC AAGCAGCTGA GAGCAGCTGA GGCACGCCAG GCTGCACACT TACAGGACCA GTTCCAGAAG GACTTCCCCAGATCC TACAGGACCA GTTCCAGAAG AACTGTGCC TTGCTGGGGCTGC CTGCTGGGGCTGC CTGCTGGGGCTGC CACAGGCAGCC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGCC CCTGAGCTGCC CCTGAGCTGCC CCTGAGCTGCC CGGGCTGCGGCC CGGGCTGCGGCCCCCCCCCC	TGTTTTCCAG TGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TCAGCTGCC TGGGTCTAAC TGGGTCTAAC TGGGTCTAAC TGTGACCGT TAACAGAG TCTGCACAGA CACTGATGGG TGTCACTGTG CAGCGAGCCT CCTCTTCAGC CAGCTGAGAG CCCTGTGAC CCATGCTGG CAGCTGAAC CCTAGCAGG CCCTGTGAC CCTGGAATGC CGGGGGATGAC CTTACGGGCC CGAGGCTACC CGAGGATGAC CTGCAGCACC CGACGGATGAC CGAGGATGAC CGAGGATGAC CGAGGATGAC CGAGGATGAC CGAGGATGAC CGACGACACC CGACAGGACAC CGAGGATGAC CGAGGATGAC CGACGACCACC CGCCACCC CCCACCACC CCACCAGGACAC CCACGGACAC CCACGGACAC CCACGGACAC CCACGGACAC CGAGGATGAC CCACGTGCAC CCACTGCCC CCACCACC CCACCACC CCACCACC CCACCACC CCACCA	120 180 240 300 360 420 540 600 720 780 900 960 1020 1140 1200 1320 1380 1440 1560 1620 1620 1740 1860 1980
50 55 60 65 70 75	Nucleic Aci Coding sequil I ATGCCCCTT TCTCTCCTC AGCARANTGA AGCGTCGGA AGCGTCGGA AGCGTTGCTG ATGGTTTTCA AGGTTGCTG AGGAATTCC ATGGTTGCTGG AGAGGCAGC ACCTCAGCA CCTCAGCA CCTCAGCA CCTCAGCA CCTCAGCA CCTCAGCA CCTCAGCA CCTCAGCA CCTCAGCA CCTCAGCAC CTGCAGCCCT CTGCCGGC AGGGTCGACC CGGGCCAAG CGAGTCGGTC CAGCAGCAC GTTGCGGCC CAGGCCTACC CAGCGCCAG TCAGTAGGCC TTGACGGCC TTGACGCC TTGACGGCC TTGACGCC TTGACGGCC GCCCCTACC GCCCCGCGCAGAAC CGCCCCGCC CGGCCGGGAGAC CGCCCGCC	id Accession Lence: 12.  11  11  TCCTGTTGCT TCCAGGAAGT TGTGGTTCCT TCCAGGAAGT TGTGGTGCTC AAGGAGGTT ACCCAGAAG GGACCAGAAA ACGTCAGTTGCT GCCCGAGAAG GGATCTGTT ACTGTGTTGT ACTGTCTTTT ACTGCACT ACTGCTTTT ACTGCACT ACTGCTTTCT TAACCACCC GCCAGAATG TCCTCTTCCT TCTTCTTCT TCTTCTTCT TCTTCTTC	#: Eos sei 424 21	31   TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCAGATCC AAGCAGCTGA GAGCAGCTGA GGCACGCCAG GCTGCACACT TACAGGACCA GTTCCAGAAG GACTTCCCCAGATCC TACAGGACCA GTTCCAGAAG AACTGTGCC TTGCTGGGGCTGC CTGCTGGGGCTGC CTGCTGGGGCTGC CACAGGCAGCC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGCC CCTGAGCTGCC CCTGAGCTGCC CCTGAGCTGCC CGGGCTGCGGCC CGGGCTGCGGCCCCCCCCCC	TGTTTTCCAG TGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TCAGCTGCC TGGGTCTAAC TGGGTCTAAC TGGGTCTAAC TGTGACCGT TAACAGAG TCTGCACAGA CACTGATGGG TGTCACTGTG CAGCGAGCCT CCTCTTCAGC CAGCTGAGAG CCCTGTGAC CCATGCTGG CAGCTGAAC CCTAGCAGG CCCTGTGAC CCTGGAATGC CGGGGGATGAC CTTACGGGCC CGAGGCTACC CGAGGATGAC CTGCAGCACC CGACGGATGAC CGAGGATGAC CGAGGATGAC CGAGGATGAC CGAGGATGAC CGAGGATGAC CGACGACACC CGACAGGACAC CGAGGATGAC CGAGGATGAC CGACGACCACC CGCCACCC CCCACCACC CCACCAGGACAC CCACGGACAC CCACGGACAC CCACGGACAC CCACGGACAC CGAGGATGAC CCACGTGCAC CCACTGCCC CCACCACC CCACCACC CCACCACC CCACCACC CCACCA	120 180 240 300 360 420 540 600 720 780 900 960 1020 1140 1200 1320 1380 1440 1560 1620 1620 1740 1860 1980
50 55 60 65 70	Nucleic Aci Coding sequi I ATGCCCCTT TCTCTCCTC AGCARANTGA AGCGTCGGA AGCGTCGGA AGGGTTGCTG AGGTTGCTG AGGTTGCTG AGGTCCAGG ATTTGCTGTGG AGAGGCAGC AGGGTGGTG AGAGGTTGCT CCTCTGCCCGC AGGGTGGTCCT CTCTGCCCGC AGGGTCGACC CGGCCAAGG CCAGGACC CGGCCAAGG CTGACGGCCAG CTGACGGCCAGG CTGACGGCCAGGC TCGGATCCT CAGCGGCCAG TCAGTAGGCC GGGCCAGGAC CGGGCCAGGAC GTGATGCCT CGGATCCTC CGGATCTCT CGGGCCTACC GCCCCTACC GCCCGGAGGC GCCGGAGGC CTGGCTTCC CGCCCTTCC CGCCCCTACC CGCGGAGGC CGGGAGGC CTTGCTCTTCC CGCCCCTACC CGCCCGGAGGC CTTGCTCTTCC CGCCCCTTCC CGCCCCTACC CGCGGAGGAC CTTGTCTTCC CTCTCTCTCTCTCTCTCTCTCTCTCTC	id Accession lence: 12.  11  11  TCCTGTTGCT TCCAGGAAGT TGTGGGTC AAGGAGGT GCCCGAGAGG GGGCAGAGT ACGGCAGAT CTGCCTTCCT TCTTCGTGAA TGGCCACAT CTGACCAGT CGGCAGAT CTGACCTGGC GGCAGAGC CGGCAGAGC CGGCAGAGC CGGCAGAGC CGGCCAGTAG CGGCCAGTAG CGGCCAGTAG CGGCCAGTAG CGGCCAGTAG CGGCCAGAGC CCGAGAAT CTGACCTGGC CGGCAGAGC CCGAGAAT CTGACCTGCG CGGCAGAGC CTGACGGGG CCGGAGAGC CTGAGGGGGG CTCGGGGAGAGG CTGAGGGGGGGGGG	m #: Eos sei 424 21	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTGGCTGC CAACAGGAAG GACATCACTC CCCAGATCC AAGCAGCTGA GGCACCACCAC GCTGCACACC TACAGGACAC TTCAGGACA AACTGTTCCAGAAG AACTGTTCCAGAAG AACTGTTCCAGAAG CTGCTGGTGGC CTGCTGGTGGC CTGCTGGTGGC CACGCCTGCC CACGCCTGCC CACGCCTGCC CACGCCTGCC CACGCCCCCC CGGTGCTCCC CCCCCAGGCCCCC CCTCCCCCAGGCCCCC CCTCCCCCAGGCCCCCC CCTCCCCCAGGCCCCCCCCCC	TGTTTTCCAG TGGGAGAGAT TTCTGTTAGA CCATCAGT AGTCAGTTCAGT	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC TTGAGCGGC TGGGTCTAAC CTGTGACCGT TGTGACCGA TCTGCACAGA CACTGATGGG CAGCGAGCCT CCTCTTCAGC CCAGTGCTGG CAGCTGGAAG CCCCTGTGAC CCTGCAGAG CCCTGTGAC CCTGCAGGC CCAGGAGCC CCAGGAATGC CCTGCAGATGC CCTGCAGATGC CCTGCAGATGC CCTGCAGTCCTG CTGCAGCCC CGGGGAGTAC CGGGGGAGTAC CGGGGGAGTAC CGGGGGAGTAC CGGGGGAGTAC CGGGGGAGTAC CGGGGGAGTAC CGGGGGAGTAC CGGGGGAGTAC CGGGGGAGTAC CGGGGCCCACC CGGGGAGTAC CGGGGGAGTAC CGGGGGCAC CCACTAGCCAG CCATTAGCCAG CCATTAGCCAG CCATTAGCCAG CCATTGCCAGGT CGAGCCACA CACTGCCAGG CCATTAGCCAG CGCTTCCAGG CCATTGCCAGG CCATTAGCCAGG CCATTGCCAGG CCTTGCCAGGT CGCTTCCAGG CCTTGCCAGG CCTTTCCAGG CCTTGCCAGG CCTTTCCAGG CCTTGCCAGG CCTTTCCAGG CCT	120 180 240 300 360 420 540 600 720 780 840 900 960 1080 1140 1200 1320 1380 1440 1500 1680 1740 1680 1740 1800 1800 1920 1920
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50 55 60 65 70 75	Nucleic Aci Coding sequil I ATGCCCCTT TCTCCCTC AGCANANTGA AGCGTCGGA AGCGTTGGACATCA AGGGTTGCTG AAGTCCAGG ATTGCTGTGG AGAGCAGCA CCCTGTGAGC AGAGGTTCC AGGAGTTCC AGGAGTTCC AGGAGTTCC AGGGCAGCC CCGGGCCAAGG CCAGGAC CCTGCGGGCCAGG CCAGGCCAGG	id Accession lence: 12.  11  11  TCCAGGAAGT TCCAGGAAGT TCCAGGAAGT GCCCGAGAG GGGAGCCCT AAGGAGGCG AGGCAGAAA ACGGACCCT TACCAGACGC TCCAGCAG TCCAGCAGACCCT TACCCACCC GCCAGATCG TCCTCTTCCT TCTTCGTGAACCC TCCACCCAGACCCC TCACCCAGATCGC TCCTCTCCT TCTTCGTGAACCC TCCTCTCCT TCTTCGTGAACCC TCGCCAGATCGC GGCCACGTAC GGCCACGTAC GGCCACGTAC GGCCTCCC TAGCCAGGGC TCAGCCGGC TCAGCCGGC TCAGCCGGC TCAGCCGGC TCAGCGGCGCC TCAGCGGCGCC TCAGCGGCGCC TCAGCGGCGCC TCAGCGGCGCC TCAGCGGCGCC TCAGCGGGCGCC TCCAGAGGGC TCCAGATCC	#: Eos sei 424 21 21 GAGGCCGTC CCATGTAAGC GGTTCAAGT GGATCAGTG TGAAAGGTCC CACGAGACG TGCTTCAGC ACTGCAGCG GGTGAGCAG GGCTGAGCAG GGTGAGCAG GGCTGAGCAG GGAGATGCT TGCCACCT GGAGATGCT TGCGGTGCTG GGAGAGCGCT GGTGACAGC GGAGAGCGCT GGTGAGCAGC GGAGAGCGCT GGAGCAGCT GGAGCAGCT GGAGCAGCT GGACAAACCCAC TGCCCAGCCG TGCCAGCCGC TGCCAGCCCT GGACAAACCCAC TGCCCAGCCC TGCCCAGCCC TGCCCAGCCC TGCCCAGCCC TGCCCAGCCC TGCCCAGCCC TGCCCAGCCC TGCCCGGCC TGCCCGGCC TGCCCGGCC TGCCCGGCCT TGCCGGCCT TGCCCGGCCT TGCCCGGCCT TGCCCGGCCT TGCCGGCCT TGCCGCGCCT TGCCGCCT TGCCGCGCCT TGCCGCGCCT TGCCGCGCCT TGCCGCCCT TGCCGCGCCT TGCCGCCT TGCCGCGCCT TGCCGCCCT TGCCGCCCT TGCCGCCCT TGCCCGCCC	31 TGTGTTTTCC AAAGAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GACATCATGT AAGCAGCTGA AGCAGCTGA GAGCAGCTGA GAGCAGCTGA GGCACGCAG GTTCCAGAAG GCTGCACACT TACAGGACCA TTCCAGAAG AACTGTGACC CTGTGTGGC GAGCTGGC GAGCTGGC CTGTGTGGG CTGTGTGGG CTGTGTGGG CTGTGTGGG CTGTGTGGG CTGTGTGG CGAGCTGC CTGTGTGG CGAGCTGC CTGTGTGG CGAGCTGC CTGTGTGG CGACCTCCT CTGCGGCTTGC CGGCTTGGC CGGCTTCGC CGGCTTCGC CGGCTTCGC CGGCTCGTGG CGGCTCCCC CTGCCCCAGG CTTACGCCCCC CTTACTGAGC CTTACTCCCAGC CTTACTCCCAGC CTTACTCCCAGC CTTACTCCCAGC CTTACGCCGACC CTACGCCGACC CTTACGCCGACC CTACGCCGACC CTTACGCCGACC CTACGCCGACC CTTACGCCGACC CTACGCCGACC CTACGCCACC CTACGCCGACC CTACGCCGACC CTACGCCGACC CTACGCCGACC CTACGCCACC CTACGCCGACC CTACGCCACC	TGTTTTCCAG TGGGAGAGAT TTCTGTTAGA CCATCAGTT TGAGGGCAGG TGAATACCT TCATCATCT TCATCATCT TCATCATCT TCATCATCAGT TCATCATCAGT TCATCATCAGT TCATCATCAGT TCATCATCAGT TCATCAGCAG ACTGCAGAGG ACTGCAGCAG GACTGAGGG GACTGAGCG GACTGAGCG GACTCTGGA TGAGGCAGGA TGAGCAGGAG CCATCTCGGA TGAGCAGGAG CCATCTCGGA TCATCTCGGGAGCG TGAGCAGT TCATGCTGG TCCTGCTGG TCATGCTGGG TCATGCTGGG TCATGCTGGG TCATGCTGGG TCATGTTGGG TTGAGGAGCT TGAGGAGGCT TGAGGAGGAGGCT TGAGGAGGCT TGAGGAGGCT TGAGGAGGCT TGCTGCGGGA AGCTGAGGAT AGCTGAGGAT AGCTGAGGAT TGCGGGAGCT TGCTGCGGGA AGCTGAGGAT TGCGGGAGCT TGCTGCGGGA AGCTGAGGAT TGCGGGAGCT TGCGGGAGCT TGCGGGAGCT TGCGGGAGCT TGCGGGAGCT TGCGGGAGCT TGCGGGAGCT TGCGGGAGCT TGCGGGAGCT TGCGGGACCT TGCGGACCT TGCGGGACCT TGCGGGACC TGCGGACCT TGCGGACCT TGCGGGACCT TGCGGGACCT TGCGGACCT TGCGGGACCT TGCGGACCT TGCGGACC TGCGCACAC TGCGCACAC TGCGCACAC TGCGCACAC TGCGCACAC TGCGCACAC TGCGCACAC TGCCACAC TGCGCACAC TGCCACAC TGCCACAC TGCCCACAC TGCCACAC TGCCCACAC TGCCCCACAC TGCCCCACAC TGCCCCACC TGCCCCACC TGCCCCACC TGCCCCACC TGCCCCACC TGCCCCACC TGCCCCACC TGCCCCCC TCCCCCCC TCCCCCCC TCCCCCCC TCCCCCC	AGTGCCCCA TTCAGCTGCC TTGGTCTAAC TTGAGCTGCC TGGGTCTAAC CTGTGACCGT AATCAAGAGG TCTGCACAGA CACTGATGGG CCACTGTTCAGG CCAGTGCTGG CCAGTGCTGG CCAGTGCTGG CCAGTGCTGG CTACCAGTGC CCTACTGGATGC CTTCTGGGCC CTCCTGGATGC CTCTCGGGC CTCCAGGATAC CGGGGAGTAC CGGGGAGTAC CGGGGAGTAC CGGGGAGTAC CGACCAGGACA CGACTGCGG CTCCTGGCC CACCAGGACA CCACTGCGC CTCCAGGCCA CCACTGCGC CTCCAGGCCA CCACTGCCC CACCAGGACA CCACTTGCC CTCCAGGCCA CCACTGCCC CCACTGCC CCACTGCCC CCACTGCC CCACTCC CCACTGCC	120 180 240 300 360 420 480 540 660 720 780 900 960 1080 1140 1260 1320 1320 1440 1560 1680 1740 1800 1920 1980 2010
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50 55 60 65 70 75	Nucleic Aci Coding sequil I ATGCCCCTT TCTCTCCTC AGCARANTGA AGCGTCGGA AGCGTCGGA AGGGTTGCTG AGGTTGCTG AGGTCCAGG TTTGCTGTGG AGAGGCAGC AGAGGTTGCTG AGAGGTTGCTG AGAGGTTGCTG AGAGGTTGCCT CTCTGCCCGC AGGGTCGACC CGGGCCARAG CCAGGTTGCGGC AGGGTCGACC CGGGCCARAG CTGCAGCCT CAGGGCCAG CTGCAGGCC GTGAGGGCCAG TCAGTAGGGCCAG TCAGTAGGGCCAG TCAGTAGGGCCAG TCAGTAGGGCCAG TCAGTAGCGCCAG TCAGTAGCGCCAG TCAGTAGCCTCCCGCCGGGATTCCTCTCCCCGCGGATTCCCTCCC	id Accession lence: 12.  11  11  TCCTGTTGCT TCCAGGAAGT TGTGGGTC AAGGAAGT TGTGGTGCTC AAGGAGCT AAGGAGGCG AGGCAGAAGT ACGTCAGTTGCT CCTCGGCATT ACGTCAGTTGCT GCCCAGAGG GGGACACC GGCAGACC TAACCACCC GCCAGATCG TCCTCTTCCT TCTTCGTGAA TGGCCACATA CTGACCTGCT CTGCCTTCCT TCTCGTGAA TGGCCACATA CTGACCTGCT GGCCAGATTGG GGCCAGAGT GGCCACATA CTGACCTGCT GGCCAGAGGC TCAGCCGGAC TCAGCCGGAC TCAGCCGGAC TCAGCCGGAC TCAGCCGGAC TCAGCCGGAC TCAGAGGGC TCCCTGACC TCCTCCTC TCCTCCTC TCCTCCTC TCCTCCTC TCCTCC	m #: Eos sei 424 21 21 GGAGGCCGTC CCATGTAAGC GGCTCAGGTG GGAGAGCC GGTCAGGTG ACTTCTATG ACTCCAGTGG GGTGAGCG GGTGAGCG GGTGAGCG GGTGAGCG GGAGATGGT TGCCACTGC TGCCAGTGG GGAGATGGT CGGGGGGGG AGGAGCGT CGGGGGGGGGG	31 TGTGTTTTCC AAAGAAACCA AAGAAACCA AACAGGAAG GACATTGTG GAGCATTGC CAACAGGAAG GAACTGGTC CACCAGATCC CACCAGATCC AAGCAGCTGC GTGGAGGATG GCTGCACACT TACAGGACA AACTGGACA AACTGGACA AACTGGACA CGGGCCGTGC CTGCTGGTGG GATGCTCACACT TTGCTCACTG CGAGAGCTGC CAGAGCTGC CAGAGCTGC CAGAGCTGC CTGCTCGTGG GACCTCCTCT CAGAGCTTCC CAGAGCTCC CAGAGCTCC CAGAGCTCC CAGAGCTCC CAGAGCTCC CAGAGCTCC CAGAGCACC CAGACC CAGAGCACC CAGAC	TGTTTTCCAG TGGGAGAGAT TTCTGTTAGA CCATCAGT AGTTCAGTTC	AGTGCCCCA TTGGCTGCC TGGGTCTAAC TTGGGCGCC TGGGTCTAAC CTGTGACCGT TGTCACCAGA CACTGATGGG CACTGATGGG CAGCGAGCCT CCTCTTCAGC CCAGTGCTGG CAGCTGGAAG CCCCTGTGAC CTACCAGTGC CTGCAGATGC CCTGCAGATGC CCTGCAGATGC CCTGCAGATGC CCTGCAGTCCTG CTGCAGCTCCTG CTGCAGCTCCTG CTGCAGCTCCTG CTGCAGCTCCTG CTGCAGCTCCTG CTGCAGCTCCTG CTGCAGCTCCTG CTGCACCAGGACA CTGCAGCAGCAC CGGGGGAGTAC CGGGGGAGTAC CGGGGGAGTAC CGGGGCCACC CGGGGAGTAC CGGGGGAGTAC CGGGGAGTAC CGGGGAGTAC CGGGGAGTAC CGGGCCACC CGGGGAGTAC CGGGGGAGTAC CGGGGGAGTAC CGGGGGAGTAC CGGGGGAGTAC CGGGGGCCAC CCACCAGGACGT CGGGGCCAC CCACTCCAG CCACTCCAG CCACTCCAG CCACTCCAG CCACTCCAG CCACCAGCAC CCACCAGCAC CACCACCAG ACCCACCC	120 180 240 360 420 540 600 780 900 900 1020 1140 1200 1320 1380 1440 1500 1620 1680 1620 1680 1920 2040 2100 2160 2220
50 55 60 65 70 75	Nucleic Aci Coding sequil I ATGCCCCTT TCTCTCCTC AGCARANTGA AGCGTCGGA AGCGTCGGA AGGGTTGCTG AGGTTGCTG AGGTCCAGG TTTGCTGTGG AGAGGCAGC AGAGGTTGCTG AGAGGTTGCTG AGAGGTTGCTG AGAGGTTGCCT CTCTGCCCGC AGGGTCGACC CGGGCCARAG CCAGGTTGCGGC AGGGTCGACC CGGGCCARAG CTGCAGCCT CAGGGCCAG CTGCAGGCC GTGAGGGCCAG TCAGTAGGGCCAG TCAGTAGGGCCAG TCAGTAGGGCCAG TCAGTAGGGCCAG TCAGTAGCGCCAG TCAGTAGCGCCAG TCAGTAGCCTCCCGCCGGGATTCCTCTCCCCGCGGATTCCCTCCC	id Accession lence: 12.  11  11  TCCTGTTGCT TCCAGGAAGT TGTGGGTC AAGGAAGT TGTGGTGCTC AAGGAGCT AAGGAGGCG AGGCAGAAGT ACGTCAGTTGCT CCTCGGCAT ACGTCCTGTTGCT CCTCGGCAT TACCCACCG GCCAGAAGT TGCCCTTCCT TCTCCTTACT TCTCTTCAT TCTCCTTCCT	m #: Eos sei 424 21 21 GGAGGCCGTC CCATGTAAGC GGCTCAGGTG GGAGAGCC GGTCAGGTG ACTTCTATG ACTCCAGTGG GGTGAGCG GGTGAGCG GGTGAGCG GGTGAGCG GGAGATGGT TGCCACTGC TGCCAGTGG GGAGATGGT CGGGGGGGG AGGAGCGT CGGGGGGGGGG	31 TGTGTTTTCC AAAGAAACCA AAGAAACCA AACAGGAAG GACATTGTG GAGCATTGC CAACAGGAAG GAACTGGTC CACCAGATCC CACCAGATCC AAGCAGCTGC GTGGAGGATG GCTGCACACT TACAGGACA AACTGGACA AACTGGACA AACTGGACA CGGGCCGTGC CTGCTGGTGG GATGCTCACACT TTGCTCACTG CGAGAGCTGC CAGAGCTGC CAGAGCTGC CAGAGCTGC CTGCTCGTGG GACCTCCTCT CAGAGCTTCC CAGAGCTCC CAGAGCTCC CAGAGCTCC CAGAGCTCC CAGAGCTCC CAGAGCTCC CAGAGCACC CAGACC CAGAGCACC CAGAC	TGTTTTCCAG TGGGAGAGAT TTCTGTTAGA CCATCAGT AGTTCAGTTC	AGTGCCCCA TTGGCTGCC TGGGTCTAAC TTGGGCGCC TGGGTCTAAC CTGTGACCGT TGTCACCAGA CACTGATGGG CACTGATGGG CAGCGAGCCT CCTCTTCAGC CCAGTGCTGG CAGCTGGAAG CCCCTGTGAC CTACCAGTGC CTGCAGATGC CCTGCAGATGC CCTGCAGATGC CCTGCAGATGC CCTGCAGTCCTG CTGCAGCTCCTG CTGCAGCTCCTG CTGCAGCTCCTG CTGCAGCTCCTG CTGCAGCTCCTG CTGCAGCTCCTG CTGCAGCTCCTG CTGCACCAGGACA CTGCAGCAGCAC CGGGGGAGTAC CGGGGGAGTAC CGGGGGAGTAC CGGGGCCACC CGGGGAGTAC CGGGGGAGTAC CGGGGAGTAC CGGGGAGTAC CGGGGAGTAC CGGGCCACC CGGGGAGTAC CGGGGGAGTAC CGGGGGAGTAC CGGGGGAGTAC CGGGGGAGTAC CGGGGGCCAC CCACCAGGACGT CGGGGCCAC CCACTCCAG CCACTCCAG CCACTCCAG CCACTCCAG CCACTCCAG CCACCAGCAC CCACCAGCAC CACCACCAG ACCCACCC	120 180 240 300 360 420 540 660 720 780 900 960 1020 1140 1200 1320 1380 1440 1500 1620 1620 1620 1620 1740 1800 1980 2040 2160
50 55 60 65 70 75	Nucleic Aci Coding sequil I ATGCCCCTT TCTCCCTC AGCANANTGA AGCGTCGGA AGGGTTGCGG ATGGATTCC ATGGTTTCA GGGTTGCTG AGGTCGCAG ACCTCAGCA ACCTCAGCA ACCTGAGAC CCTGTGAGC AGAGTGTCC AGAGTTCC AGGATTCC AGGATTCC CTCTGCCCGC AGGGTCGACC CGGGCCAAAG CCAGGAC CCTGACGGC AGGGTGAC CGGGCCAGAC CTGCGGGCCAGAC CTGACGGCC GTGACGGCCAGAC CTGACGGCCAG CTTGCCGGC CTGGGTCC CGGGCCAGAC CTGGGTCC CGGGCCAGAC CTGGCTCC CGGGCCAG CTTGCCGCC CGGGCCAG CTTGCCGCC CTGGATCTC CCCCGGGATTCC CCCCGGGATCC CCCCGGGATTCC CCCCGGGATTCCC CCCCGGGATTCCC CCCCGGGATTCCC CCCCGGGATTCCC CCCCGGGATTCCC CCCCGGGATTCCC CCCCGGGATTCCC CCCCGGGATTCCC CCCCGGGATTCCC CCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATTCCCCCCGGGATCCCCCCCGGGATTCCCCCCGGGATTCCCCCCCGGGATTCCCCCCCGGGATTCCCCCCCGGGATCCCCCCCC	id Accession lence: 12.  11  11  TCCAGGAAGT TCCAGGAAGT TGGGTGCT AAGGAGGCT AAGGAGGCT AAGGAGGCG AGGCAGAAA GGATGGGC GGCAGAAGG GGCAGAAA ACGACCC GCCAGAGG TCCACCC GCCAGATCG GCCACAGA GGGCTCGC GCCAGATCG GGCGCACC GGCCAGATCG GGCGCACC GGCCAGATCG GGCGCACC GGCCAGACC GGCCACAGAC GGCCACAGC GGCCACAGC GGCCACAGC GGCCACAGC GGCCACAGC GGCCCCCC GGCCACCACC GGCCACCACC GGCCACCACC GGCCACCACC GGCCCCCCC GGCCCCCCC GGCCCCCCC GGCCCCCC	#: Eos sei 424 21 21 GAGGCCGTC CCATGTAAGC GGTCAGATG TGAAAGGTCC GGTCAGAGTG ACTCTCAGC TGCTCAGGT GCTCCAGGTG GGCTGAGCAG GGCTGAGCAG GGCTGAGCAG GGCTGAGCAG TGCTCCAGC GGAGATGTC TGCGGTGCT GGAGATGTC TGCGGTGCT GGAGATGTC TGCGGTGCT GGAGAGCGCT GGAGAGCGCT GGAGAGCGCT GGAGAGGGCGC GGAGAGGGCGC GGAGAGGCGC GGAGAGGCGC GGAGAGGCGC GGAGAGGCGC GGAGAGCGCT CCAACCAAATC CCAAACCCAC GGGGCCTGTT ACAAGCCTT CACAAGCCGC GGGGCCTGTT ACAGGCGCT CGGGGCCTGTT ACAGGCGCT CGGGGCCTGTT ACAGGCGCCTGCC CGGCCTTCTGCAGCCCTC CGGCCCTGTT CCTCAGAGCCAC CCTCCTGCAGCCCCCC CGGCCCTGTT CCTCAGAGCCAC CCTCCTGCAGCCCCCCCCCC	31 TGTGTTTTCC AAAGAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GACATGGTGA GACATGGTGA GACATGGTGA GACAGGAGTGA GCCACGCAG GTGCACACT TACAGGACCA TTCCAGAAG GACTGGACCAC TTCCAGAAG GACTGGACCAC TTCCAGAGA GACTGGACCAC TTCTGCTGCTGG GAGGGTGGCT CGGGCTGGCG CGACCTCGTGG CGACACTCGTGG CGACACTCGTGGG CGACACTCGTGGG CGACACTCGTGGG CGACACTCGTGGG CGACACTCGTGGG CGACACCCCC CGGGCTTGGGG CGACACCCCC CGGGCTGGGG CGACACCCCCC CGGGCTGGGG CTACAGGACC CTACAGCAGCC CTACAGCAGCC CTACAGCAGCC CTACAGCAGCC CTACAGCAGCC CTACAGCAGCC CTACAGCAGCC CTACAGCAGCC CTACAGCAGCC CTACAGCAGACC CTACAGCAGACC CTACAGCAGACC CTACAGCAGACC CTACAGCAGACC CAAGGCAGTCC CAAGGCAGCC CAAGGCAGTCC CAAGGCAGCC CAAGGCAGTCC CAAGGCAGTCC CAAGGCAGCC CAAGGCAGTCC CAAGGCAGCC CAAGGCAGTCC CAAGGCAGCC CAAGGCAGTCC CAAGCAGTCC CAAGGCAGTCC CAAGCAGTCC CAAGCCAGTCC CAAGCCAGTCC CAAGCCAGTCC CAAGCAGTCC CAAGCCAGTCC CAAGCCAGTCC CAAGCCAGCC CAAGCCAGTCC CAAGCAGTCC CAAGCCAGCC CAAGCCAGCC CAAGCCAGCC CAAGCCAGCC	TGTTTTCCAG TGGGAGAGAT TTCGGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	AGTGCCCCA TTCAGCTGCC TTGGGTCTAAC TTGGGTCTAAC TTGTGACCGT TCACTCTCAT AATCAAGAG TCTGCACAGA CACTGATGGG CAGCGAGCCT CCTCTTCAGC CAGCTGAGAG CCCATGCTGG CAGCTGAAG CCCTGTAAC CCTGGAATGC CCTGGAATGC CTGCAGGCC CGGGGGATAC TGGCCCACC CGAGGATAC CTACCAGTCGG CTTCTGGGCC CGCCAGGACA CGAGGATAC CGAGGATAC CGAGGATAC CGAGGATAC CGAGGATAC CGAGGATAC CGAGGACA CGAGGACA CGAGGACA CGAGGACA CGAGGACA CCACGGACA CCACGGACAT CCACGGACCT CCACGACCT CCACGACCT CCACGACCT CCACGACCT CCACGACCT CCACGACCT CCACGACCCC CCCACGACCT CCACGACCCC CCCACGACCCC CCCACGACCCC CCACGACCCC CCACGACCCC CCACGACCCC CCACGACCCC CCACGACCCC CCACGACCCC CCACGACCCC CCCACGACCCC CCACGACCCC CCACGACCCC CCACGACCCC CCACGACCCC CCACGACCCC CCACGACCCC CCACGACCCC CCACGACCCC CCACGACCC CCACGACC CCACCACC CCACGACC CCACGACC CCACGAC C	120 180 240 360 420 480 540 660 720 780 960 1020 1140 1260 1320 1440 1500 1680 1740 1800 1920 1980 2010 2160 2220

		CCCCAGGTCC					
•		85 Protein					
5	_		os sequence		41	51	
	1	11 1	21 1	31 1	ī	1	
	MPPFLLLEAV	CVFLFSRVPP	SLPLOEVHVS	KETIGKISAA	SKMMWCSAAV	DIMFLLDGSN	60
	SVGKGSFERS	KHFAITVCDG	LDISPERVRV	GAFQFSSTPH	LEFPLDSPST	QQEVKARIKR	120
10	MVFKGGRTET	ELALKYLLHR	GLPGGRNASV	PQILIIVTDG	KSQGDVALPS	KQLKERGVTV	180
				VEDATNGLFS			240
	PCEHRTLEMV	REFAGNAPCW	RGSRRTLAVL	AAHCPFYSWK	RVFLTHPATC	YRTTCPGPCD	300
	SQPCQNGGTC	VPEGLDGYQC	LCPLAFGGEA	NCALKLSLEC	RVDLLFLLDS	SAGTTLDGFL	360 420
15				LLVAVPVGEY LLTESHSEDE			480
1.5				PELQGKLCSR			540
	SVGPENFAOM	OSFVRSCALO	FEVNPDVTQV	GLVVYGSQVQ	TAFGLDTKPT	RAAMLRAISQ	600
	APYLGGVGSA	GTALLHIYDK	VMTVQRGARP	GVPKAVVVLT	GGRGAEDAAV	PAQKLRNNGI	660
٠.	SVLVVGVGPV	LSEGLRRLAG	PRDSLIHVAA	YADLRYHQDV	LIEWLCGEAK	QPVNLCKPSP	720
20				EMSSCSVCVS	QGWILETPLR	HMAPVQEGSS	780
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	Seg ID NO:	86 DNA sequ	ience				
			#: Eos sec	quence			
25	Coding sequ	ence: 892	2356				
	1	ļ1	21	31	41	51	
					000000000	COCTACOCCTAC	60
				TGAGTAGAGC GCCCCTTTC			120
30	TETTTTCTC	TTTTCCAGAG	TGCCCCCATC	TCTCCCTCTC	CAGGAAGTCC	ATGTAAGCAA	180
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35 <sup>-</sup>				GGTTTTCAAA			480
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				CTGTGAGCAC			840
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				AGTGTTCCTA			960 1020
45				GCAGCCCTGC CTGCCCGCTG			1080
10	CTGTGCCCTG	AAGCTGAGCC	TGGAATGCAG	GGTCGACCTC	CTCTTCCTGC	TGGACAGCTC	1140
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<b>5</b> 0				GGATGTGCCT			1320
50	TGGCATTCCC	TTCCGTGGTG	GCCCCACCCT	GACGGGCAGT	GCCTTGCGGC	AGGCGGCAGA	1380 1440
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				GGATCCTCAG			1620
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60				GATGACCGTC		GCTCAGCCGG	1980
00				CGGGAGAGGC			2040
	TGCCCAGAAG	CTGAGGAACA	ATGGCATCTC	TGTCTTGGTC	GTGGGCGTGG	GGCCTGTCCT	2100
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						TGTCTGTGCC	2460
						ACTGAGGGAG	2520
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						AGAATGTTGT	2760
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	Seg ID NO-	87 Proteir	seguence				
			Eos segueno	e ·			
	1	11	21	31	41	51	
90	l	1	1	1	1		
80	MPPFLLLEAV	CVFLFSRVPI	SLPLQEVHVS	KETIGKISAA	SKMMWCSAAV	DIMPLLDGSN	60
	SVGKGSFERS	KHPAITVCD	LDISPERVRV	GAFUFSSTPE	RECUDINATION PROPERTY.	QQEVKARIKR KQLKERGVTV	120 180
	WALVOORIE	EELHALACE	RCOHVI.I.AFY	VEDATNGI PS	TLSSSAICS	ATPDCRVEAH	240
	PCEHRTLEM	REFAGNAPC	RGSRRTLAVI	AAHCPFYSW	RVFLTHPATO	YRTTCPGPCD	300
85	SQPCQNGGT	VPEGLDGYQ	LCPLAFGGE	NCALKLSLEC	RVDLLFLLDS	SAGTTLDGFL	360

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                                                                                          540
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                                                                                        1080
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                                  21
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        AYQGEVTEKM MCAGIPEGGV DTCQGDSGGP LMYQSDQWHV VGIVSWGYGC GGPSTPGVYT
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         CGCGGCTCGC AGCCCTGGCA GGTCTCGCTC TTCAACGGCC TCTCGTTCCA CTGCGCGGGT
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                                                                                          420
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                                                                                           780
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                                                                                           960
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                                                                                         1140
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         CAAAGGTTTA TTCCAGAGAA GCCAGGAAGC CGGTCATCAC CCAGCCTCTG AGAGCAGTTA
                                                                                         1200
 75
                                                                                         1260
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                                                                                         1440
         AAAAAAAAA AAAA
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                      11
                                   21
         MRAPHLHLSA ASGARALAKL LPLLMAQLWA AEAALLPQND TRLDPEAYGA PCARGSQPWQ
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5	YHQGSGPILP RVKYNKGLTC	RRTDEHDLML	LKLARPVVPG CEVFYPGVVT	PLWARVGDDH PRVRALQLPY NNMICAGLDR KVIRSN	RCAQPGDQCQ	VAGWGTTAAR	120 180 240
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10	GCCCTTAGAG AGAAGCGCTA	TCTTGGTTGC GTAAGGTCTC	CAAACAGATT TGAGATCCTT	GGACCACTGG TGCAGATCAA GCACTAGCTA ATTGCTGAGC	GGAGAACCCA CATCCTCAGG	GGAGTTTCAA GTAGGAGGAA	60 120 180 240
15	CCTGGGTGAT TTGCTATGGT TTACGGAAAC AGAGTACATA	ATCATCATGA TACTTCAGGA GGAGCCCACC AGTGGCTATC	GACCCAGCTG AGCTGAGGAA TGGCATCTAT AGAGAAGCCA	TGCTCCTGGA CTGGTCTGAT CCTGAGTTTA GCCGATATGG GGCCATGTAT	TGGTTTTACC GCCGAGCTCG AAGGAAGCCA ATTGGCCTGC	ACAAGTCCAA AGTGTCAGTC GCACCATAGC ACGACCCACA	300 360 420 480 540
20	CAAGTCCATG TTGGAGCAGC CAAGAATCAA GCTAAATCTG	GGTGGGAACA AACGAATGCA GATTCTGCTA CTCATTATTT	AGCACTGTGC ACAAGCGCCA ACTCCTGCAC CAGAGGGGAA	TGAGATGAGC ACACTTCCTG AGCCCCGTCC ACCTAGCAAA GAAACTTTAG	TCCAATAACA TGCAAGTACC TCTTCCTTTC CTAAGAGTGA	ACTITITAAC GACCATAGAG TGCTAGCCTG TAAGGGCCCT	600 660 720 780 840
25	CTAGCTCTAA GTCTCTGGCT CTTTGGCCAT AGACCCCTTC	ATGTTTGCCC GTCTCGAGCA AAGAAGTAAA AGCTTCTACA	CGCCATCCCT GTCTAGAAGA GATTTGAAGA CCCTTCTGCC	TTCCACAGTA GTGCATCTCC CAGAAGGAAG CTCTCTCCAT CATAGGAAGG	TCCTTCTTCC AGCCTATGAA AAACTCAGGA TGCCTGCACC	CTCCTCCCCT ACAGCTGGGT GTAAGCTTCT CCACCCCAGC	900 960 1020 1080 1140
30	TAGGTTGATG		ATTCCTTTAA	TAAACCATTG			
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55	YGNGAHLASI		EYISGYQRSQ	APGWFYHKSN PIWIGLHDPQ HFLCKYRP			60 120
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45	1	11	21 	1	1		60
45	1   GAGCTAGCGC CGGCGCGGG AGCTACCACT	11   TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC	21   CCCAGCGCGG GCTGAGCGCG ACGCCCCGGG	 TGCTATCGGA GCCAGGGTCT AGCTCGCGGC	 CAGAGCCTGG GAACCCAGAT GCCTGGCGGT	CGAGCGCAAG TTCCCAGACT CAGCGACCAG	60 120 180
	1   GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGGGG	11   TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CCGCTGCGCT	21   CCCAGCGCGG GCTGAGCGCG ACGCCCCGGG CCTGGCCCGC	 TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG	CGAGCGCAAG TTCCCAGACT CAGCGACCAG CTACAGACCC	120 180 240
45 50	1   GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGGGG AGAGGGAGCA	11   TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CCGCTGCGCT CACTGCCAGG	21   CCCAGCGCGG GCTGAGCGCG ACGCCCCGGG CCTGGCCCGC ATGGGAGCTG	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGGGAGGCA	 CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCTC	CGAGCGCAAG TTCCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCA	120 180 240 300
	1   GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGGGG AGAGGGAGCA TGCTGACCAT	11   TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CCGCTGCGCT CACTGCCAGG CAGCTGGCTC	21   CCCAGCGCGG GCTGAGCGCG ACGCCCCGGG CCTGGCCCGC ATGGGAGCTG ACTCTGACCT	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGGGAGGCA GCTTCCCTGG	 CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCTC GGCCACATCC	CGAGCGCAAG TTCCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCA ACAGTGGCTG	120 180 240 300 360
	1   GAGCTAGCGC CGGCGCGGGG AGCTACCACT ACGTCCGGGG AGAGGGAGCA TGCTGACCAT CTGGGTGCCC	11   TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CCGCTGCGCT CACTGCCAGG CACGCTGGCTC TGACCAGAGC	21   CCCAGCGCGG GCTGAGCGCG ACGCCCCGGG CCTGGCCCGC ACTCTGACCT CCTGAGTTGC	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGGGAGGCA GCTTCCCTGG AACCCTGGAA	 CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCTC GGCCACATCC CCCTGGCCAT	CGAGCGCAAG TTCCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCA ACAGTGGCTG GACCAAGACC	120 180 240 300 360 420
50	1 GAGCTAGCGC CGGCGCGGGG AGCTACCACT ACGTCCGGGG AGAGGGAGCA TGCTGACCAT CTGGGTGCCC ACCATGTGCA	11   TCAAGCAGAG AGCCAGCGGG CCGCTGCGCT CACTGCCAGG CACTGGCTC TGACCAGAGC TATCGGCCAG	21   CCCAGCGCGG GCTGAGCGCG ACGCCCCGGG CCTGGCCCGC ACTCTGACCT CCTGAGTTGC GCCAAGACAC	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGGC CTGGGAGGCA ACCCTGGA ACCCTGGAA TGCTGCTCAC	CAGAGCCTGG CAGAGCCTGGCGGT ACTGTCTCGG GGACTTCCTC GGCCACATCC CCCTGGCCAT CTCTTCTGCC	CGAGCGCAAG TTCCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCA ACAGTGGCTG GACCAAGACC ACGGTCTATT	120 180 240 300 360
	1 GAGCTAGCGC CGGCGGGGGG AGCTACCACT ACGTCCGGGG AGAGGGAGCA TGCTGACCAT TGCTGGCCC ACCATGTGCAC CCATCCACAT	11   TCAAGCAGAG AGCCAGCGGG CCGCTGCGCT CACTGCCAGG CAGCTGGCTC TGACCAGAGC TATCGGCCAG CTCAGAGGGA	21   CCCAGCGCGG GCTGAGCCCGG ACGCCCCGGG CCTGGCCCGC ATGGGAGCTG ACTCTGACTG CCTGAGTTGC GGCAAGACAC GGCAAGCTGG	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGGGAGGCA GCTTCCCTGG AACCCTGGAA	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCTC GCCACATCC CCCTGGCCAT CTCTTCTGCC CCACGACGAG	CGAGCGCAAG TTCCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCA ACAGTGGCTG GACCAAGACC ACGGTCTATT CCGATTGTTT	120 180 240 300 360 420 480
50	1   GAGCTAGCGC CGGCGCGGGG AGCTACCACT ACGTCCGGGG AGAGGGAGCA TGCTGACCAT CTGGGTGCCC ACCATGTGCA CCATCCACAT TGCGAACCCG GCCCTTCCCA	11   TCAAGCAGAG AGCCAGCGGG CCGCTGGCCT CACTGCCAG CAGCTGGCTC TGACCAGAGC TATCGGCCAG GCACATCCTG GGGCAATTTC	21   CCCAGCGCGG GCTGAGCCCGG ACGCCCCGGG ACGCCCCGGG ACTGGAGCTG ACTCTGACCT CCTGAGTTGC GGCAAGACAC GGCAAGCAAC ACCATCATTT	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGGGAGGCA GCTTCCCTGGA ACCCTGGAA TGCTGCTCAC TCATTAAAGA GAGGAGAGCT TGTATGGAAG	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCTC CCCTGGCCAT CTCTTCTGCC CCACAGACGAG GCATGCTGGG GGCTGGTGGG GGCTGATGAA	CGAGCGCAAG TTCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCA ACAGTGGCTG GACCAAGACC ACGGTCTATT CCGATTGTTT AGTGCCCTCT GGTATTCAGC	120 180 240 300 360 420 480 540 600 660
50	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGGGG AGAGGGAGCA TGCTGACCAT CTGGTGCCA CCATCTACACT TGCGAACCCG GCCCTTTCCA CGGATCCTTA	11   TCAAGCAGAG AGCCAGCGG CCGCTGCGCT CACTGCCAGG CAGCTGGCT TGACCAGAGC TATCGGCCAG CTCAGAGGGA CTCAGAGGGA CTCAGAGGGA TTCCT CGCACATTCC CTATGGTCTG	21   CCCAGGGGG GCTGAGGGG GCTGAGCGG ACGCCGGG CCTGGCCGG ATGGGAGCTG ACTCTGAGTTG CGCAAGACAC GGCAAGACAC ATTGACAACG ACCATCATTT AAGTACATTG	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGGGAGGCA GCTTCCCTGGA ACCCTGGAA TGCTGCTCAC TCATTAAAGA GAGGAGAGC TGTATGGAAG GGGTTGGTAA	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCTC GGCCACATCC CCCTGGCCAT CTCTTCTGCC CCAGGACGAG GCATGCTGGG GGCTGATGAA AGGAGGCGCT	CGAGCGCAAG TTCCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCA ACAGTGCTG GACCAAGACC ACGGTCTATT CCGATTGTTT AGTGCCCTCT GGTATTCAGC CTTGAGTTGC	120 180 240 300 360 420 480 540 600 660 720
50	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGCGG AGAGGGAGCA TGCTGACCAT CTGGGTGCCA ACCATGTGCA CCATCCACAT TGCGAACCCG GCCCTTTCCA ATGGATCCTTA ATGGACAGAA	11   TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CCGCTGCGCT CACTGCCAGG CAGCTGGCTC TGACCAGAGGC TATCGGCCAG GCTCAGAGGGA GCACATCCTG GGGCAATTIC CATAGGCTGG AAAGCTCTCC	21   CCCAGCGCGG GCTGAGCGCG ACGCCCCGGG CCTGGCCCGG ACGCCCGCG ACGCAGACT ACTCTGACCT CCTGAGTTGC GGCAAGACAC GGCAAGACAC ACCATCATTT AAGTACATTG TGGACATTTC	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC AGGCGTGAC CTGGGAGGCA ACCCTGGAA TGCTGCTCAC TCATTAAAGA GAGGAGAGCT TGTATGGAAG TGGTTATGGAAG TGATCAACAAGAC	CAGAGCCTGG GACCCAGAT GCCTGGCGGT ACTGTCTCGG GGCACATCC CCCTGGCCAT CTCTTCTGCC CCACGACCAG GCATGCTGGGG GGCTGATGAA AGGAGGGGCT CCTTCACCCA	CGAGCGCAAG TTCCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCA ACAGTGGCTG GACCAAGACC ACGGTCTATT AGTGCCTCT GGTATTCAGC CTTGAGTTGGC CTTGAGTTGGC GGTGGCATGG	120 180 240 300 360 420 480 540 600 660 720 780
50	1 GAGCTAGCGC CGGCGCGGGG AGCTACCACT ACGTCCGGGG AGAGGGAGCA TGCTGACCAT CTGGGTGCCC ACCATGTGCA ACCATCCACAT TGCGAACCCG GCCCTTTCCA CGGATCCTTA ATGGACAGAA ATGGACAGAA	11   TCAAGCAGAG AGCCAGCGGG CCGCTGCCC CCGCTGCCCC CACTGCCAG CACCTGCCAG CACCTGGCCT TGACCAGAGC TATCGGCAG GCACATCCTG GGGCAATTTC CTATGGTCTG AAAGCTCTCC CTATTTTTTT	21   CCCAGGGGG GCTGAGCGG GCTGAGCCGG ACGCCCCGGG ACTGGCACCT CCTGAGTTG CGCAAGACAC GGCAAGCAC ATGACAAGCTG ATGACAACTGA ATGACAACTT AAGTACATTT GAAAGGAGCATTG GAAAGGAGCTG GAAAGGAGCTG AAGTACATTT GAAAGGAGCT	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGGGAGCA AGCTCCCTGG AACCCTGGAA TGCTGCTCAC TCATTAAGA GAGGAGAGCT TGTATGGAAG GGGTTGGTAA TGAACAAGAC GGGGCCACCG	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTGGG GGCCACATCC CCCTGGCCAT CCCTCGCCAT CCACGACGAG GCATGCTGGG GCTGATGAA AGGAGGCGCT CCTTCACCA TGGAGTTATT	CGAGCGCAAG TTCCAGACT CAGCGACCAG CTACAGGCCA TTCAAGGCCA ACAGTGGCTG GACCAAGACC ACGGTCTATT CCGATTGTT AGTGCCCTCT GGTATTCAGC CTTGAGTTGC GTTGGCATGG GTTCATGTCA	120 180 240 300 360 420 480 540 600 660 720
50 55	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGCGG AGAGGGAGCA TGCTGACCAT TGCGATCCACAT TGCGAACCGG GCCCTTTCA ATGGACAGAA CAGAAGGAGG TCGAACCCCAA AAGAAGAGGAGG	11   TCAAGCAGAG AGCCAGCGGG CCGCTGCGCT CACTGCCAG CAGCTGGCTC TGACCAGAGGC CTCAGAGGGA CTCAGAGGGA CTCAGAGGGA CTCATTCTTT ATCAGGCACA ACGTCTCGGTC	21   CCCAGCGCGG GCTGAGCGCG ACGCCCCGG ACGCCCCGG ACGCCCGC ACGCAGCTG ACTCTGACCT CCTGAGTTGC GGCAAGACAC GGCAAGACAC ACCATCATTT TAGTACATTG GAAAGGGGT GTCATCCATT CACTATTTGA	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC AGGCGAGGCA GCTTCCCTGG AACCCTGGAA TGCTGCTCAC TCATTAAAGA GAGGAGAGCT TGTATGGAAG TGGTATGGTA	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTTCTCGG GGCACATCC CCCTGGCCAT CCTCTTCTGCC CCAGGACGAG GCATGCTGGG GGCTGATGAA AGGAGGCGCT CCTTCACCCA TGGAGTTATT TGACACCTAT CGATGCCAGG	CGAGGGCAAG TTCCCAGACT CAGCGACCAG CTACAGGCCA ACAGTGGCTG GACCAAGACC ACGGTCTATT AGTGCCTCT GGTATTCAGC CTTGAGTTGGC CTTGAGTTGGC GTGGCATGG GTTCATTCAGC ACGATTGTCA AGATCCAAGA AGATCCAAGA ATCCTTTCTG	120 180 240 300 360 420 480 540 660 720 780 840 900 960
50 55	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGCGA TGCTGACCAT CTGGGTGCCA ACCATGTGCA ACCATCTCACAT TGCGAACCCG GCCCTTTCCA CGGATCCTTA ATGGACAGAA CAGAAGGAGG TCGACCCCAA AAGAAGTGA	11   TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CCGCTGCGCT CACTGCCTC TGACCAGAGC CTCAGAGGGA GCACATCCTG GGGCAATTCT AAAGCTCTCC CTATTTTTTT ATCAGGCACA ACGTCTGGTC TGATCAAGGGT	21   CCCAGGGGGG GCTGAGCGCG ACGCCCGGG CCTGGCCCGG ACGCCCGGG ACTCTGACCT CCTGAGTTGC GCCAAGACAC ACCATCATTT AAGTACATTC TGGACATTTC GAAAGGAGCT GTCATCCATTT CAGTATTTGA TCTCGAAATTC	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGGGAGGCA GCTTCCCTGG AACCCTGGAA TGCTGCTCAC TCATTAAGAA GAGGAGAGCT TGTATGGAAG GGGTTGGTAA TGAACAAGAC GGGGCCACCG CTGACCGGTT ACGCGGTGCC TGGAATGACAT	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTOTCTCG GGCCACATCC CCCTGGCCAT CCCTGGCCAT CCCACGACGAG GCATCCTGG GCTGATGAA AGGAGGGCGT TGACACCAT TGACACTAT TGACACTAT TGACACTAT CGATGGAGAGG GCCCAGGAGGAGG GCCCAGGAGGAGGGGGGGG	CGAGGGCAAG TTCCCAGACT CAGCACCAG CTACAAGACCA TTCAAGGCCA ACAGTGGCTG GACCAAGACC ACGGTCTATT AGTGCCTCT GGTATTCAGC CTTGAGTTCAG GTTCATGCATGC GTTCATGCAGAGA ACATTCAAGA ACATTCAAGA ACATTCATGC GCGATGACTCAGG GTTCATGTCA GGGATGACCAAGA	120 180 240 300 360 420 480 540 660 720 780 840 900 960
50 55	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCGGGG AGAGGGAGCA TGCTGACCAT CTGGATCCCA ACCATGTGCA CCATCCACAT TGCGAACCCG GCCCTTTCCA CGGATCCTTA ATGGACAGAA CAGAAGGAG TCGACCCCAA AAGAAGTGAA AATTGGGAAAG	11   TCAAGCAGAG AGCCAGCGG CCGCTGCGC CCCGCTGCCC CACTGCCAGG CACTGCCAG CACAGCAG CTACAGAGC TATCGGCCAG CTCAGAGGGA CTCAGAGGGA CTCAGAGGCAACTTC CTATGGTCTG AAAGCTCTCC CTATTTTTT ATCAGGCACA ACGTCTGGTC TGATGAAGGT CAAACACTTC	21   CCCAGGGGGG GCTGAGGGGG GCTGAGGCGG ACGCCCGGGG ATGGGAGCTG ACTCTGAGTTG CGCAAGACAC GGCAAGACAC GGCAAGATGG ACCATCATTT AAGTACATTG CGAAGATTG GAAAGACTG GTCATCATTT CAGTATTTGA TCTGAAATC CTGCAAATC	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGGGAGGCA ACCCTGGA ACCCTGGA TGCTGCTCAC TCATTAAAGA GAGGAGAGCT TGTATGGAAG TGAACAAGAC GGGGCCACCG CTGACCGGTT ACGCGGTGCC TGGATGACAT ACATTAAGAC ACGGGTGCC TGGATGACAT ACATTAAGAC	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGCCACATCC CCCTGGCCAT CCCTCGCCAT CCACGACGAG GCATGCTGGG GCATGCTGGG CCATCACCAG AGGAGGCGCT CCTTCACCCA TGGAGTTATT TGACACCTAT CGATGGCAGG GCCCAGGAGG CCCTTGGAGT CGCCAGGAGG CCCTTGGAGT	CGAGCGCAAG TTCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCA ACAGTGGTG GACCAAGACC ACGGTCTATT CCGATTGTT AGTGCCCTCT GGTATTCAGC CTTGAGTTGC GGTGGCATGG GTTCATGTCA AGATCCAAGA ATCCTTTCTG AGCATCCTTTCTG AGTCCTTCTCTCTTCTT	120 180 240 300 420 480 540 660 720 780 840 900 960 1020
<ul><li>50</li><li>55</li><li>60</li></ul>	1   GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCCGGG AGAGGGAGCA TGCTGACCAT TGCGATCCCA CCATCTCACAT TGCGAACCAG GCCTTTCCA CGGATCCTTA ATGGACAGAA AAGAGAGGAG TTGCAGTGAA AATTGCGAAAG ATTGCAGTAA	TCAAGCAGAG AGCCAGCGG CCGCTGCGCT CACTGCCAGG CACTGCCAGG CTACTGGCAG CTCAGAGGGA CTCAGAGGGA CTCAGAGGGA CTCAGAGGGA CTATTTTTT ATCAGGCACA ACGTCTGGT TGATGAAGGT TGATGAAGGT TGAAACACTTC TCCATCATCTT TCCATCATCTT TCCATCATCTT TCCATCATCTT TCAAACACTTC TCCATCATCTTCT TCCATCATCTTCT TCCATCATCTTCT TCAAACACTTC TCCATCATCTT	21   CCCAGGGGGG GCTGAGCGG GCTGAGCGG ACGCCCGGG CCTGGCCCGC ATGGGAGCTG ACTCTGACTTG CGCAAGCTGG ATTGACAACG GCAAGCTGG ACATCATTT AAGTACATTG CAAAGAGGTTG CTGCAAATTC CAGTATTTGA	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGGGAGGCA GCTTCCCTGGA ACCCTGGAA TGCTGCTCAC TCATTAAAGA GAGGAGAGCT TGTATGGAAG GGGTTGGTAA TGAACAAGAC GGGGCCACCG CTGACCGGTT ACCCGGTGC TGATTAAGAA ACCATATTGAACA ACCATATTGA	CAGAGCCTGG GACCCAGAT GCCTGGCGT ACTGTCTCGG GGACTTCCTC GGGCACATCC CCCTGGCCAT CTCTTCTGCC CCAGACCAG GGATGATGAA AGGAGGCGCT CCTTCACCCA TGTCACCCA TGACCACTAT CGACCCAT CACCCAT CGACCAGACAGA GGCCATTATT TGACACCTAT CGATGCCAGAAG GCCCAGGAAG ACCCTAT CGATGGAGT ATATCATGGA ATATCATGGA	CGAGCGCAAG TTCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCA ACAGTGCTAT CCGATTGTTT AGTGCCTCT GGTATTCAGC CTTGAGTTGC GTTGATTCAG GTTCATGCATGC TTCATGTCA ACACTCAAGA ATCCTTCTG GCATGCATGC ACACTCAAGA ATCCTTCTG CATCGAGAGCCT CATCGAGGCCT CATCGAGGCCT CATCGAGGCCT CATCGAGGCCT CATCGAGGCCT CATCGAGGCCT	120 180 240 360 420 480 540 660 720 780 840 900 960 1020 1080
50 55	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGCGG AGAGGGAGCA TGCTGACCAT TGCGATCCACAT TGCGAACCCG GCCCTTTCCA ATGGACCCTA ATGGACCGA AGGATGGA TCGACCCCAA AGGAGGAGG TTGCACCCAA ATTGCACTGA ATTGCAGTGAA ATTGCAGTGAA AATTGGGAAG TGAAGGAAA	11   TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CCGCTGCGCT CACTGCCAGG CAGCTGGCTC TGACCAGAGGC TATCGGCCAG GCAATTCC CTATTGTTT ATCAGGCAG ACGTCTGGTCAG ACGTCTGGTCAG TGATGAAGGT TGATGAAGGT CAAACACTTC CCAATCATCT CCGGGTATTC	21   CCCAGCGCGG GCTGAGCGCG ACGCCCCGG ACGCCCCGG ACGCCCGC ACGCACGATTGC CCTGAGTTGC GGCAAGACAC ACCATCATTT AAGTACATTC TGAACATTC GAAAGGGCT GTCATCATTTC GAAAGGAGCT GTCATCATTT CAGTATTTTGA TCTCGAAATC TCGCACCTTG TCAGTGGAAA	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGAGCA GCTTCCCTGG AACCCTGGAA TGCTGCTCAC TCATTAAAGA GAGGAGAGCT TGTATGGAAG TGATCAAAGA TGACAAGAC GGGGCCACCG CTGACCGGTT ACCGGGTGCC TGGATCACAGT ACGCAGTGCAA ACCATATTGAAA ACCATATTGA	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTOTCTCG GGCCACATCC CCCTGGCCAT CCCTGGCCAT CCACGACGAG GCATCCTGG GGCTGATGAA AGGAGGGCT CCTTCACCA TGGAGTTATT TGACACCTAT TGACACCTAT TGACACCTAT TGATGCAGG GCCTGGAGAG CCTTGGAGT TATATCATGGA TATATCATGGA TGGCAAATAT	CGAGGGCAAG TTCCCAGACT CAGCGACCAG CTACAGGCCA ACAGTGGCTG GACCAAGACC ACAGTGTTT AGTGCCTCT GGTATTCAG CTTCAGTTCAG	120 180 240 300 360 420 600 660 720 780 840 900 1020 1020 1140 1200
<ul><li>50</li><li>55</li><li>60</li></ul>	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGCGG AGAGGGAGCA TGCTGACCAT TGCGAACCCG ACCATTTCA TGCGAACCCG GCCCTTTCA ATGGACAGAA CAGAAGGAGG TCGACCCCAA AAGAAGTGA TTGCACTGAA AATTGGAAGAA CTGCACTGAA	11   TCAAGCAGAG AGCCAGCGGG CCGCTGCCC CCGCTGCCC TCACTGCCT TGACCAGAGC CTCAGAGGA GCACATCCTG GGGCAATTCT CTATGGTCTA ACAGCTCCC CTATTTTTT ATCAGGCACA ACGTCTGGTC TGATCAAGGT CCAACACTTC CCATCATTC TCCATCATCT TCCATCATCT TGAGTGATT TCCATCATCT TGAGTGAGTT TCCATCATCT TGAGTTGGTT TGAGTTGGTT TGAGTTGGTT	21   CCCAGGGGGG GCTGAGCGGG GCTGGGCCGG ACGCCCGGG CCTGGGCCGG ACGCCCGGG ACTCTGACCT CCTGAGTTGC GCCAAGACAC ACCATCATTT AAGTACATTG GAAAGGAGCT GTCATCCATT CAGTATTTGA TCTGCAAATC CTGCACCTTG TCACTGTGAAATC CTGCACCTTG TCAGTGGAAATC CTGCACCTTG CAAGACGTGG CAAGACGTGG CAAGACGTGG CCCAAGACGTGG CCCAAGACGTGG CCCACAGGGGGG CCCAAGACGTGG CCCAAGACGTGG CCCACAGGGGGGG CCCACAGGGGGGGG CCCAAGACGTGG CCCAAGACTGG CCCAAGACTGG CCCAAGACCTGG CCCAAGACGTGG CCCAAGACTCAAAACACTGC CCCAAGACGTGG CCCAAGACGTGG CCCAAGACTCAAAACTGCAACACTCAAAACTGCAACACTCAAAACTCAAAACTCAAAAACTCAAAAAAAA	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGGGAGGCA ACCCTGGAA TGCTGCTCAC TCATTAAGA GAGGAGAGCT TGTATGGAAG TGATCGTAA TGAACAAGAC CGGGCCACCG CTGACCGGTT ACGCGGTGC TGGATGACAT GATTTAGACA ACACATATTGA AGACAGAGCA AGCACAGGTGA	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGCCACATCC CCCTGGCCAT CCCTGGCCAT CCCTGGCCAT GCAGACGAG GCAGCAGG GCAGCTGGG GCTGATGAA AGGAGGCGCT TGGAGTTATT TGACACCTAT CGATGGCAGG GCCAGGAAG CCCTTGGAGT ATATCATGGA TGGCAGTATAT TGGCAGT TGGCAGT TGGCAGT TGGCAGT TGGCAGAAT TGGCAGAAT TGGCAGAT TGGCAGAT TGGCAGAT TGGCAGAT TGGCAGAT TGGCAGAT TGGCAGAT TGGCAGAT TGGCAGAT TGGCGAATAT TGGCAGAT TGGCGAATAT TGGCAGAT TGGCGAATAT TGGCTTCGAT	CGAGGGCAAG TTCCAGACT CAGCGACCAG CTACAGGCCC TTCAAGGCCC TTCAAGGCCC ACGGTCTATT CCGATTGTT AGTGCCTCT GGTATTCAGC CTTGAGTTGC GGTATTCAG GTTCATGTCA ACATCCAAGA ATCCTTCTG GGGATGACCA TTTCTAACTG CATCGAGGCT TTCAATGTTT CATGATTAACTG CATCGAGGCT TTCAATGTTT CATGATAAAG	120 180 240 300 360 420 540 660 720 780 840 900 1020 1080 1140 1200 1260
<ul><li>50</li><li>55</li><li>60</li></ul>	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGGGG AGAGGGAGCA TGCTGACCAT TGCGAACCAG CCATTCCACAT TGCGAACCAG GCCTTTCCA CGGATCCTTA ATGGACAGAA CAGAAGGAGG TCGACCCCAA AAGAGAGTGA TTGCAGTGAA CTGCTGCTGC CTTTCCAGC CTTTCTCAGC CTTTCTCAGC	TCAGGGGT TCAAGCAGAG AGCCAGGGGC CCGCTGCGCC CACTGCCCC CACTGCCCC CACTGCCCC CACTGCCCC CACTGCCCC CACTGCCCC CTACGAGGGA CTCAGAGGGA CTCAGAGGGA CTCAGAGGGA CTCAGAGGGA CTCAGAGGCACTCCC CTATTTTTT ATCAGGCACA ACGTCTCGCC TGATCAAGGTC CCATCATCT CCGGGTATTC CCGGGTATTC TGAGTGGGT TAAAGGTGGG TCCCATTGAT	21   CCCAGGGGGG GCTGAGCGG GCTGAGCGG ACGCCCGGG CCTGGCCCGG ACGCCCGG ACGCCAGACC CCTGAGTTGC GGCAAGACAC GGCAAGACAC GGCAAGACAC ATTGACACT AAGTACATTT AAGTACATTG ACAACTTG CTCACATTT CTCAAATC CTGCACTTG TCACTGGAAA AAATTGTTCC CAAGACTGG AAATTGTCACACTTG CAAGACACTGG AAATTGTTCC CAAGACATGG AAATTGTTCC CAAGACATGG AAAATTGTTCC CAAGACATGG GAGAAAATTT ATACAGGCCA	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGAGGC	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTTCTCGG GGCACATCC CCCTGGCCAT CCTCTTCTGCC CCAGGACGAG GCATGCTGGG GGCTGATGAA AGGAGGCGCT CCTTCACCCA TGGAGTTATT TGACACCTAT CGATGCAGG GCCTGGAGG GCCTTGGAGT TGACACCTAT TGACACCTAT CGATGCAGG GCCTTGGAGT TGACACTAT TGGCGAATAT TGGCGAATAT TGGCGAATAT TGGCGAATAT TGGCGAATAT TGGCGAATAT TGGCGAATAT TGGAGGTTAAC TGGAGTTAAC	CGAGGGCAAG TTCCCAGACT CAGCGACCAG CTACAGGCCA ACAGTGGCTG GACCAAGACC ACAGTGGCTG GACCAAGACC CTGAGTTGTT AGTGCCTCT GGTATTCAGC CTTGAGTTGC GTGGCATGG GTTCATGTCA AGATCCAAGA ATCCTTTCTG GCGATGACCA TTTCTAACTG CTTCAAGTCT TTCAATGTTT CATGAGAGCT TTCAATGTTT CATGAGAGCACCG CCAGGAAAAA CTCAGCACCG	120 180 240 300 360 420 540 660 660 720 780 840 900 960 1020 1140 1200 1250 1320
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTTCCGCGT ACGTCGCACAT TGCTGACCAT TGCGAACCCG ACCATGTGCA CCATCTCACAT TGCGAACCCG GCCCTTTCCA ATGGACCCCAA ATGGACGAGA TTGCACTCAA AAGAGGAGA AATTGGAAG TGAAGGAAA CTGCTGCTGC CTTTGTCCAG TATCTCAGAC TATCCAGAC TATCCAGAC	11   TCAAGCAGAG AGCCAGCGGC CCGCTGCGCT CACTGCCTC CACTGCCTC TGACCAGAGC CTATCGCCAG GCAATTCT GGGCAATTCT ATCAGGCAG AAGCTCTCC CTATTTTTT ATCAGGCACA ACGTCTGGTC TGATGAAGGT CAAACACTTC CCGCGTATTC TCAGCTGGT TGATGAGGT TGATGAGGT TGATGAGGT CAAAACACTC CCCCATTGAT CAAAAAAAGGC TCCCATTGAT CAAAAAAAGGC	21   CCCAGCGCGG GCTGAGCGCG ACGCCCCGGG ACGCCCCGG ACGCCCGGC ACGCAGACCC CCTGAGTTGC GCCAAGACAC GCCAAGACAC ACCATCATTT TAGACATTC GAAAGCGTACATTTC GAAAGCGCT TCCGAAATC TCTCGAAATC TCTCGAAATC TCTCGAAATC TCAGTGGAAG TCAGTGGAAG AAATTGTTCC CAAGACGTGG GAGAAAATTTATACAGGCCAC CAGGATTATA	TGCTATCGGA GCCAGGGTCT AGCTCGCGC GAGGCGTGAC CTGGGAGGCA GCTTCCCTGG AACCCTGGAA TGCTGCTCAC TCATTAAGAA GAGGAGAGCT TGTATGGAAG GGGTTGGTAA TGAACAAGAC GGGCCACCG CTGACCGGTT ACCCGGTGC TGGAATGACAT GATTTAGACA ACCATATTGA ACCATATTGA ACGATGACCGGT CGGATGGCA AGTCGACCGGA AGTCGACCGGA CCTACAATGGA GGTTTGCTTGG GGTTTGCTTGG	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTOTCTCG GGCCACATCC CCCTGGCCAT CCCTGGCCAT CCCACGACGAG GCATCCTGG GGCTGATGAA AGAGGGCCT TGACTATT TGACACTAT TGACACTAT TGACACTAT TGACACTAT TGACAGAGAG CCTTGAGAT TATATCATGAA TGGCAAATAT TGGCAAGAT TGGCAATAT TGGCAGAG TGGCAATAT TGACACTAT TGACACTACAC TACGACCGC TACGACCGG TACGACCAC TACGACCAG	CGAGGGGAAG TTCCCAGACT CAGCACCAG CTACAGACCC TTCAAGGCCCA ACAGTGGCTG GACCAAGACC ACAGTCTATT AGTGCCTCT GGTATTCAGC CTTGAGTTCCA GGTATTCAGC CTTGAGTTGC GTTCATGCATGC GTTCATGCATGC TTCATGTCA ACATCCAAGA ATCCTTTCTA CATCGAGTCC TTCTAACTG CATCGAGGCT TTCAATGTTT CATGAGTAAAG CCAAGGAAAAAA CCTCAGCACCG GGCAGAGCCT	120 180 240 300 360 420 600 660 720 780 840 900 1020 1140 1200 1260 1320 1380
<ul><li>50</li><li>55</li><li>60</li></ul>	1   GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCCGGG AGAGGGAGCA TGCTGACCAT CTGGGTGCC ACCATGTGCA CCATCCACAT TGCGAACCCG GCCTTTCCA CGGATCCTTA ATGGACAGAA AAGAAGGAG TTGCAGTGAA AAGAAGTGAA AATTGGAAAG TGAAAGGAAA CTGCTGCTGC CTTTGCTAGC TATCTACAGCA TATCTCAGAC TATCTCAGAC TATGCAATCA AGGATGTTAC AGGTTGTTCAGAC TATCTCAGAC TATCTCAGAC TATCTCAGAC TATCTCAGAC AGGTTGTTCTA AGCCGGAGCTA	TCAAGCAGAG AGCCAGCGG CCGCTGCGC CCGCTGCCC CCGCTGCCC CACTGCCAGG CACTGCCAG CACTGCCAG CTGACCAGG CTCAGAGGC TATCGGCCAG CTCAGAGGCAATTCC CTATGGTCTG AAAGCTCTCC TCAATCATCT CCATTATT TAAAGGTGGG TCCCATTGAT CAAAAAAAGC CCGTTTACCG	21   CCCAGGGGGG GCTGAGCGG GCTGAGCGG GCTGAGCGG ACGCCCGGG ATGGAGCTG ACTCTGAGTTG CGCAAGACAC GGCAAGACAC GGCAAGACAC GGCAAGATTG CAGAATTTC GAAAGGAGTTG GTCATCATT CAGTATTTGAACT TCAGAATTTC ATCACATT CAGTATTTGA TCTGAAATC TCAGAATTT CAGTATTTGA AAATTGTTCC CAAGACGTGG GAGAAAATTT ATACAGGCCA TCAGGATTAT ATACAGGCTA TCCTCTGTG TCACTTGTG TCAGTATTATA TTCCTCTGTG TTCAGTATT TTCAGTGTATAT TTCCTCTGTG TCAGTGTATA	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGGGAGCA ACCCTGGAA TGCTGCTCAC TCATTAAGA GAGGAGAGCT TGTATGGAAG TGATCGTAA TGAACAAGAC GGGTCCACCG TGAACAGAC CTGACCGGTT ACGCGGTGCA ACCCGTTGC ACCCGTTC TGAATGACA ACATATGA AGACAGAGC CTGACAGGAC CTGACAGGAC ACCTTTGCTTG CTACAATGGA CAGACCTCTG CTACAATGGA CAGACCTCTG CTACAATGGA CGGAACCTCTG CTACAATGGA CGGAACCTCTG CGAAGCCTTG CGAAGCCTTG CGAAGCCTGT	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTTCTCGG GGCCACATCC CCCTGGCCAT CCCTGGCCAT CCCTCGCCAT GCAGACAGG GCAGCAGG GCAGCAGG GCAGCAGG GCAGCAGG GCAGCAGG GCAGCAGG GCAGCAGG GCAGCAGG GCCTAGCAGA TGGAGTTAAT TGACCAGAGAG CCCTTGGAGT ATATCATGGA TGGGAGTAGA TGGGAGTAGA TGGGAGTAGA CCCTTGGAGT GAAGCTCAC TGGAGTTAAC CTACGACGG GAAGCCCCAA	CGAGGGCAAG TTCCAGACT CAGCGACCAG CTACAGGCCA CTACAGGCCA CTACAGGCCA CTACAGGCCA CTACAGGCCA ACAGTGGCTG GACCAAGACC ACGGTCTATT CGGATTGTT AGTGCCCTCT GGTATTCAGC CTTGAGTTGC GTTCATGTCA AGATCCAAGA ATCCTTTCTA ACTGCACTCT TTCAATGTCT TTCAATGTTT CATGATAAAG CCAGGAAAAA CTCAGGACCT CTCACAGCCC CGGCAGAGCCT CTCACAGTCA	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1140 1200 1320 1380 1380 1500
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	1   GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGCGG AGAGGGAGCA TGCTGACCAT TGCGAACCAT TGCGAACCAG TGCGAACCAG TGCGAACCAG TGCGAACCAG TGCGAACCAG ATGGAAGAGAA ATTGGAAGAA AATTGGAAGAA ATTGGAGAA CTGCTGCTGC CTTTTGTCCAG TTTGTCCAGA TATGCAGTAG TATCTCAGAC TATGCAGTAG AGGTTTTTCTCAG AGGTTTTTCTCAG AGGTTTTTTCTCAG AGGTTTTTTCTCAG AGGTTTTTTCTCAGAC TATGCAGTAG AGCTGAGCTA CCATTGACAC	TCAAGCAGAG AGCCAGCGG CCGCTGCGC CCGCTGCGCT CACTGCCAGG CAGCTGGCT CACTGCAGG CTATCGGCAG CTCAGAGGGA CTCAGAGGGA CTCAGAGGGA CTATTTTTT ATCAGGCAGT CAAACACTTC TCATCATCACAGGG TCAGAGGGA ACGTCTGGT TCAACACTTC TCCATCATCT CCGGGTATTC TGAATGTGGGT TCAAAAAAGGTCGGG CCATTGAT CAAAAAAAGGTCGGG CCGTGTACGG CCATTGTAGAGGT CCAATGTAGAGG CCATTGTAGAGCACACACTC	21   CCCAGGGGGG GCTGAGCGG GCTGAGCGG ACGCCCGGG CCTGGCCCGG ACGCCCGG ACGCAGCTG ACTCTGAGTTG ACTCTGAGTTG ACTACAACG GCAAGACAC ACCATCATTT CAGACATTC CAGACATCC CTGCACATT CTCGAAATC CTGCACATTG CTCACTTG CTCACTTG CAGACATGG AAATTGTCC CAGACATGT ATACAGGCCA CAGGATTATA ATACAGGCCA CAGGATTATA ATACAGGCCA CAGGATTATA TTCCTCTGTG AGCACCATTC CAGCACTTC CAGCATTCT ATACAGGCCA CAGGATTATA ATCCTCTGTG AGCACCATTC	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCAGGCA GCTTCCCTGG AACCCTGGAA TGCTGCTCAC TCATTAAAGA GAGGAGAGCT TGTATGGAAG CGGTGCACCGGT ACCGGTT ACGCGGTCACCGGT ACGCGGTGACACA GATTAGAAA GACAAGACA GATTAGAAGA GAGACCTCTG CTACAATGGA GGTTTGCTTG GGAAGCCTGT TGAACCTGT TGAACCTGT TGAACCTGT	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTTCTCGG GGCACATCC CCTGGCCAT CTCTTCTGCC CCAGGACGAG GCATGCTGGG GGCTGATGAA AGGAGGCGCT CCTTCACCCA TGGAGTTATT TGACACCTAT TGACACCTAT TGACACTAT TGACACTAT ATATCATGGA TGGGGAATAT TGGCGAATATGAG TGGGGATTAT TGGCGAGTTATAT TGGCTTCACCA TGGAGTTATAT TGGCTTCACCA TGGAGTTATAT TGGCTTCAGAT CTACGACCGG GAGAGTCAAA GGAGAATATTA	CGAGGGCAAG TTCCCAGACT CAGCGACCAG CTACAGGCCA ACAGTGGCTG GACCAAGACC TCCAAGACCC ACGGTCTATT AGTGCCTCT GGTATTCAGC CTTGAGTTGC GGTGGCATGG GTTCATGTCA AGATCCAAGA ATCCTTTCTG GCGATGACCA TTTCTAATGTC TTCAATGTTC TCAATGTTT CATGATAAAG CTCAGGAAAAA CTCAGCACCG GGCAGAGCCT CTCACAGTCA CATCATGGA	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1260 1320 1380 1440 1500 1500
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	1   GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGCGG AGAGGGAGCA TGCTGACCAT TGCGATCCACAT TGCGAACCCG GCCTTTCCA ATGGACAGAA CAGGATCCTTA ATGGACAGAA ATTGCAGAG TTGCAGTGAA CTGCTGCCCAA AAGAGAGGAG TGACCCCAA CTGCTGCTGC CTTTGTCAGA TATCTCAGAC TATCTCAGAC TATCTCAGAC TATCTCAGAC TATCTCAGAC AGCTTGTCTA AGCTTGTACA ACCTTGGAGAA ACCTTGGAGAA ACCTTGGAGAAA CCATTGAACAC AACCTTGGAGAA	TCAAGCAGAG AGCCAGGGGCCGCTGCGCCCGCTGCGCCCGCGGGTCCCCCTGGCTCGCTCGCCTGGCTGGCTCGAGAGGCCACATCCTGGCAGAGGCCACATCTCCCTATTTTTTTATCAGGCACAACACTTCCCGGGTATTCCGGGGTATTCCGGGGTATTCTGAGGGGGAGTTCCGGGGTATTCCACATCATCTGAGGTGGGGCAACACTTCCCCTCCATCATCTTGAGGTGGGTCCAAAAAAAGGCCCCGGTTACGGCCAATGAGAGGGCCAATGGAACACTTCCATCTTAAAGGTGGGTCCCAATGAGCGGGTATCCAAAAAAAGGCCCCGTGTACGGCCAATGAGACCATGAACACTTCCAAAAAAAGGCCCCGTGTACGGCCAATGAACACTCCAAAAAAAGGCCCAATGAACATCAAAAAAGGCCCAATGAACATCAAAAAAGGCCCAATGAACATGAACATGAACATGAACATGCAAAAAAAGGCCAATGAACATCCAAAAAAAGGCCAATGAACATACCCTGGTCACTGCAACAAAAAAAGGCCAATGTGAACATACCCTGGTCCAATGCAACATGCAACATGCAACATGCAACATGCAACATGCAACATGCAACATGCAACATGCAACATGCAACATGCAACATGCAACATGCAACATGCAACATGCAACATGCAACATGCAACATGCAACATGCAACATGCAACATGCAACATGCAACATGCAACATGCAACATGCAACATACCCTGGTCAACAACATGCAACATACACATGCAACATACAACATACAAAAAAAGACAAAAAAAA	21   CCCAGGGGGG GCTGAGCGG GCTGAGCGG ACGCCCGGG CCTGGCCCGG ACGCCCGG ACGCCCGG ACGCCGC ACGCAGACAC GGCAAGACAC GGCAAGACAC GGCAAGACAC GTATGACATT TAGTACATT GAAAGAGGTT TCCGAATT TCAGTATTTGA AATTATTGA TCTCGAATT TCAGTGGAAG AAATTGTTCC CAAGACGTGG GAGAAATTT TTCCTCTGTG AGGACTTGT ATTCCCATT	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC AGCGCAGGCA GCTTCCCTGG AACCCTGGAA TGCTGCTCAC TCATTAAGAA GAGGAGAGCT TGTATGGAAG GGGTTGGTAA TGAACAAGAC GGGGCCACCGT TGGATGACAT ACCCGGTGCA AGTGACAGT ACCCGGTT GATTAGACA GATTAGACA GATTAGACA GATTAGACA AGCACATCTGG CTACAATGGA GGTTTGCTTG GGAAGCCTCTG GGAAGCCTCTG GTACAATGGA GGTTTGCTTG GGAAGCTTTGCTTG GGAAGCTTTGGAC CTGATTACTC	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTOTTCTGG GGCACATCC CCCTGGCCAT CTCTTCTGCC CCAGGACGAG GCATGCTGGG GGATGATGAA AGGAGGGCT CCTTCACCA TGAGATTAT TGACACCTAT TGACACTAT TGACACTAC TGAGATTATCTGA TGGCGAATAT TGACACTCAC TGGAGTTAAC TGAGACTCAC TGGAGTTAAC CTACGACCGG GAGGCCCAAA	CGAGGGCAAG TTCCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCA ACAGTGGCTG GACCAAGACC ACAGTGGTTT AGTGCCTCT GGTATTCAGC CTTGAGTTCAG CTTCAGTTCAG	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1260 1320 1380 1440 1500 1500
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	1   GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCGCGGA AGAGGGAGCA TGCTGACCACT CTGGATCCCACAT TGCGAACCCG GCCCTTTCCA CGGATCCTTA ATGGACAGAA ACGAAGGAGG TCGACCCCAA AAGAGAGGAG TTGCAGTGAA AATTGGAAAG CTGTGCC CTTTTCTCCAG TATCTCAGAC TATCTCAGAC TATCTCAGAC AACTGTGCTA ACCTGGAGCTA ACCTGGAGCTA ACCTGGAGCTA ACCTGGAGCTA ACCTGGAGCTA ACCTGGAGCTA CCATTGACAGA ACCTGGAGA	11   TCAAGCAGAG AGCCAGCGG CCGCTGCCC CCGCTGCCC CACTGCCAG CACTGCCAG CACTGCCAG CACAGCAGC TATCGGCCAG CTACAGAGG CTAGAGGGA CTCAGAGGA CTATGTTTT ATCAGGCACA ACGTCTGGTC TGACTAGAGG TCAACACTTC TCCATCATCT CCAGTCATCT TCAACACTTC TCAACATTC TCAACATTC TCAATGTTGGT TAAAGGTGGG TCCCATTGAT CAAAAAAGGC CCGTGTACGG CAATGTAGAG CCGTGTACGG CAATGTAGAG TCCCATCAGAC TACCCTGGTC TACCCTGCAGA	21     CCCAGGGGGG GCTGAGGGGG GCTGAGGGGG GCTGAGCGG ACGCCCGGG ATGGAGCTG ACTCTGAGTTG CGCAAGACAC GGCAAGACAC GGCAAGACAC ACCATCATTT AAGTACATTG CAAGAGTTGC GAAAGAGGTGG GTCATCATTT CAGTATTTGA AATTGTACATC TCAGTGGAAT TCTGAAATTC TCAGTGGAAG AAATTGTTCA CAGTGGAAG AAATTGTTCA CAGGGACATTATA ATACAGGCCA CAGGATTATA TTCCTCTGTG AGCACCATTG ATTGCCAGTGA	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGGCA GCTTCCCTGG AACCCTGGAA TGCTGCTCAC TCATTAAAGA GGGTTGCTAC GGGCCACCG CTGAACGCA GGGCCACCG CTGACCGGTT ACGCGGTGC TGGATGACAT GATTAAGAA ACCATATTGA AGACAAGAC CTGAACTGG CTACATTGCT CTACATTGCT AGCCTCTT GATTACTCC CTACATTGCA ACCATATTGA ACCATATTGA ACCATATTGA ACTCATTGCT CTACAATGGA CGTTTGCTTG CTACATTGGA CGTTTGCTTG CGAACCTCTT CGAACTTGGA CTGATTACTC CCAACCAGGT	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTOTTCTGG GGCCACATCC CCCTGGCCAT CCCTGGCCAT CCCTGGCCAT CCCTGGCCAT CCTTCTGGC CCACGAGCAGG GCATGCTGGG GCTGATGAA AGGAGGCGCT TGGAGTTATT TGACACCTAT CGATGGCAGAGA CCCTTGGAGT ATATCATGGA TGGCAGAT TGGCAGGAGAGAGCCCT TGGAGTTACCAGAATAT CTGGTTCGAT GAAGCTCAC CTACGACCG GAGGCCCAAA CCTACCACCG CAAACTGCCA	CGAGGGCAAG TTCCAGACT CAGCACCAG CTACAGGCCA TTCAAGGCCA ACAGTGGCTG GACCAAGACC ACAGTCTATT CGGATTGTT AGTGCCTCT GGTATTCAGC CTTCAAGTCCA ACAGTCATGA ATCCTTCTA ACATCCAAGA ATCCTTCTG GGGATGACCA TTCTAACTC TTCAATGTTT CATGAGTACC TTCAAGTTCA CATCAAGAA ATCCTTTCTG GGGATGACCA CATTAAAG CCAGGAAAAAA CTCAGCACCG GGCAGAGCCT CTCACAGTCA CATTCATCATGA CTCAGCACCG GGCAGAGCCT CTCACAGTCA CATTCATCAGGCT CTCACAGTCA GCAGAAAGAGT	120 180 240 300 360 420 660 660 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1500 1560
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	1   GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGGG AGAGGGAGCA TGCTGACCAT TGCGAACCAT TGCGAACCAG GCCTTTCCA CGGATCCTTA ATGGACAGAA ATGGAAGAGA TTGCAGTGCA TTGCAGTGCA AGAGGAGAA ATTGCAGAA ATTGCAGAA CTGCTGCTGC CTTTCTCAGA TTTCTCAGAC TATCTCAGAC TATCTCAGAC TATCTCAGAC TATCTCAGAC TATCTCAGAC TATCTCAGAC TATCTCAGAC TATCTCAGAC TATCCAGTGCT ACCAGTGCT TGTACCTGCA ACCTCGGAGAT TGCAGTGCT TGTACCTGCA TGAGCCCGAA	TCAAGCAGAG AGCCAGGGG CCGCTGCCC CCGCTGCCC CCGCTGCCC CACTGCCCC CACTGCCAGGC CACTGCCCC CACTGCCCC CTACGGCAGGC CTCAGAGGGA CTCAGAGGGA CTCAGAGGCAATTCC CTATTTTTT ATCAGGCACA ACGTCTGGTC TGATCAGGTC TGATCAGGTC TCCATCATCT CCGGGTATTC CCGGGTATTC CCGGGTATTC CCGGGTATTC TAAAGGTGGG TCCCATTGAT CAAAAAAGGC CCGTGTACGG CCATTGTAGAC TACCCTGCAGAA CATCCCTGCAGAA CATCGCGGGAG CATCGGGGGAG CATCGGGGGAG CATCATAGTG	21   CCCAGGGGGG GCTGAGCGG GCTGAGCGG ACGCCCGGG CCTGGCCCGG ACGCCCGGG ACGCCCGGG ACGCCCGGG ACGCCCGG ACGCAGACC GGCAAGACAC GGCAAGACAC GGCAAGACAC GGCAAGACAC TAGTACATTT AAGTACATTG ACACTTG ACACTTG CTGCACTTG CTCACACTTG CAGTATTCC CAAGACGGG AAATTGTCC CAAGACGTGG GAGAAAATT ATACAGGCCA CAGGATTATA TCCTCTGTGT ATTGCCACTT ACTCCTCTCT ATTGCCACTT ACTCCTCTCT ACTCCTCTCC ACGCACTTC ACTCCCCCC ACGCATACAC ACGGATAGAC ATTGCCAGTA TCCTCTGCGCCC CAGATAGACC ATTGCCAGTA ACTCGGGCAGA	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC AGCTCGCGGC AGCGCAGGCA GCTTCCCTGG AACCCTGGAA TGCTGCTCAC TCATTAAGAA GAGGAGAGCT TGTATGGAAG GGGTCACAG TGACCAGT ACCAGGGCACACG TGATGACAGT ACCAGGACCTCT CTACAATGGA GGTTGCTTG CTACAATGGA GGTTTGCTTG CTACAATGGA CGTTTGCTTG GGAACCTCTG CTACAATGGA CGTTTGCTTG GGAACCTCTG CTACAATGGA CGTTTGCTTG GGAACCTCTG CTACAATGGA CTGATTACTC CCAACCAGGT TGAACCAGGT TGAACCAGGT TGAACCAGGT TGCACCACAGT TGGAGGACAT	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTOTTCTGG GGCACATCC CCCTGGCCAT CTCTTCTGCC CCAGGACGAG GCATGCTGGG GGCTGATGAA AGGAGGGGT CCTTCACCA TGGATTATT TGACACCAT TGACACTAT TGACACTAT TGACACTAT TGACACTAT TGACACTAT TGACACTAT TGACACTAT TGACACCTAT TGACACCTAT TGACACCTAT TGACACCTAT TGACACCTAT TGACACCTAT TGACACCTAT TGACACCTAC TGAGACTTCAC TAGAGCTCAC CTACGACCG GAGGCCCAAA GGATAATGTACCAC CAAACTGCGC CAAACTGCGC CAAACTGCCC CAAACTGCCAC ATGCTCCCC CAAACTGCCAC ATGCTCCCC CAAACTGCCAC ATGCTCCCC CAAACTGCCAC ATGCTCCCC CAAACTGCCAC ATGCTCCCC CAAACTGCCAC ATGCTCCCCC CAAACTGCCAC ATGCTCCCCC CAAACTGCCAC ATGCTCCCC CAAACTGCCAC ATGCTCCCCC CAAACTGCCAC ATGCTACCCCC CAAACTGCCAC ATGCTACCCCC ATGCTCCCCC ATGCTCCCCC ATGCTCCCCC CAACTGCCAC ATGCTACCCC CAAACTGCCAC ATGCTACCCCC ATGCTCCCCC ATGCTCCCCC CAACTGCCAC ATGCTACCCCC ATGCTCCCCC CAACTGCCAC ATGCTACCCCC ATGCTCCCCC CAACTCCCCCC ATGCTCCCCC CAACTCCCCC CAACTCCCCCC CAACTCCCCC CAACTCCCCCC CAACTCCCCC CAACTCCCCCC CAACTCCCCC CAACTCCCCC CAACTCCCCC CAACTCCCCCCC CAACTCCCCC CAACTCCCCCC CAACTCCCCC CAACTCCCCCC CAACTCCCCCC CAACTCCCCC CAACTCCCCC CAACTCCCCCC CAACTCCCCC CAACTCCCCC CAACTCCCCC CAACTCCCCCC CAACTCCCCC CAACTCCCCC CAACTCCCCCC CAACTCCCCC CAACTCCCCCC CAACTCCCCCC CAACTCCCCCC CAACTCCCCCCCC	CGAGGGCAAG TTCCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCA ACAGTGGCTG GACCAAGACC ACAGTGGTTT AGTGCCTCT GGTATTCAGC CTTGAGTTCAG GTGATTCAGC CTTGAGTTGG GTTCATGTCA AGATCCAAGA ATCCATGTCA AGATCCAAGA ATCCATTTCTAG GCATGAGCAC TTTCTAACTT CATGATAAAG CTCAGGAAAA CTCAGGAACCA GCCAGAGACCT CTCACAGTC CTCACAGTC CATCACGGC GCAGAAGAGT GCAGAAACAC GCAGAAGAGT GCAGAAACAC TTCACAGTCA CAGTCATGGA GCAGAACCAC TTCACAGTCA CAGTCATGGA GCAGAACCAC TTCACAGTCA CAGTCATGGA CTACGGAACCC TTCACAGTCA CAGTCATGGA CTACAGGAACCAC TTCACAGTCA CAGTCATGGA CTACAGGAACCAC TTCACAGTCA CAGTCATGGAACCAC TTCACAGTCA CAGTCATGGAACCAC TTCAGAAACCAC TTCAGAACCAC TTCAGAAACCAC TTCAGAAACCAC TTCAGAAACCAC TTCAGAAACCAC TTCAGAAACCAC TTCAGAAACCAC TTCAGAAACCAC TTCAGAAACCAC TTCAGAAACCAC TTCAGAACCAC TTCAGAAACCAC TTCAGAAACCAC TTCAGAAACCAC TTCAGAAACCAC TTCAGAACCAC TTCAGAAACCAC TTCAGAAACCAC TTCAGAAACCAC TTCAGAAACCAC TTCAGAACCAC TTCAGAACCAC TTCAGAACCAC TTCAGAACCAC TTCAGAACCAC TTCAGAACCAC TTCAGAACCAC TTCAGAAACCAC TTCAGAAACCAC TTCAGAAACCAC TTCAGAAACCAC TTCAGAAACCAC TTCAGAAACCAC TTCAGAAACCAC TTCAGAAACCAC TTCAGAAACCAC	120 180 240 300 360 420 660 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1500 1560 1620 1680
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	1   GAGCTAGCGC GGAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGCGG AGAGGGAGCA TGCTGACCAT TGCGATGCCC ACCATGTGCA CCATCCACAT TGCGAACCGG GCCCTTTCCA ATGGAACCGG ACGATGGCA CAGAAGGAGA ATTGCAGAAG TTGCAGTGAA ATTGCAGAAC TTGCAGTGAA CTGCTGCTGC CTTTGTCCAG TATCCAGAAC TATCCAGAAC TATGCAGTGAT CCATTGACCC AACCTGGAGA TCCAGGTGCT TGTACCTGCA ACCTGGAGA TCCAGGTGCT TGTACCTGCAA TCAGGCGGAA TGAGCCGGAA TGAGCCGGAA TGAGCCGGAA TGAGCCGGAA ACATCTGCAA	TTAAGCAGAG AGCCAGGGG CCGCTGCGC CCGCTGCGCT CACTGCCAGGG CAGCTGGCTC CACTGCAGGC CAGCTGGCTC TGACCAGAGGC CTCAGAGGGA GCACATCCTG GGGCAATTCT ATCAGGCACA ACGTCTGGTC TGATGATTTTTT ATCAGGCACA ACGTCTGGTC TGATGAGGT TGATGAGGT TAAAGTTGGC TCCATCATCT CCGGGTATTC TAAAGTTGGG TCCCATTGAT CAAAAAAGGC CCGTGTACGG TCCCTTGCAGA CATCGGGGGAG CATCGTGGGGAG CATCGTGGGGAGA CATCGTGGGGAGA CATCATAGTG	21   CCCAGGGGGG GCTGAGCGG GCTGAGCGG ACGCCCGGG CCTGGCCCGG ACGCCCGGG ACGCCCGGG ACGCCCGGG ACGCCCGG ACGCAGACC GCAAGACAC GCAAGACAC ACCATCATTT TGGACATTTC GAAAGGGGT TCAGTATTTGA TCTCGAAATC CTGCACCTTG TCAGTATTTCAGTATTTCC CAAGACGTGG GAGAAAATT TTCCTCTGTG AGGACTATT ATACAGGCA ACGCATTAT ATCCTCTGTG AGGACATTAT TCCTCTGTG AGGACATTAT TCCTCTGTG AGGACATTAT TCCTCGTGC CAGGATTATA TCCTGCGCCC GAGATAGACG TTCGGACAC TTCGGACAC TTCGGACAC TTCGGACAC TTCGGACAC TTCGGACAC TTCGTGCCC CAGGATTACAC TCCTGCGCCC CAGGATTACAC TCCTGCGCCC CAGGATTACAC TCCTGCGCCC CAGGATTACAC TCCTGCGCCC CAGGATTACAC TTCGTGCCCC TTCGGTCCC TCGTCGTCC TCCTGTCC TCCTGCCCC TCGTCATCC TCCTGCCCC TCCTGTCC TCCTGCCCC TCCTGTCC TCCTGCCCC TCCTCTCTC TCCTGCCCC TCCTCTCTC TCCTCTCTC TCCTCTCTC TCCTCTCTC TCCTCTCTC TCCTCTCTC TCCTCTCTC TCCTCTCTC TCCTCTCT TCCTCTCTC TCCTCTCT TCCTCT TCCT TCCTCT TCCT	TGCTATCGGA GCCAGGGTCT AGCTCGCGC GAGGGTGAC CTGGGAGGCA GCTTCCCTGG AACCCTGGAA TGCTGCTCAC TCATTAAGAA GAGGAGAGCT TGTATGGAAG GGGTTGGTAA TGACAAGAC GGGCCACCG CTGACCGGTT ACCCGGTTG ACCATATTAAGAC ACCATATTAA ACCATATTGA AGACAGACCTCTG GTGAACGGT CTACAATGGA GGTTTGCTTG GGAACCTCTG GGAACCTCTG GGAACCTCTT TGAACTGGA GGTTTACTC CCAACCAGGT TGAACTGGA CTGCATATCA CTGATTACTC CCAACCAGGT TGCACCAGGT TGAACTAGGA TTGAGCACAA TTGGGGGACAA TTGGGGGACAA	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTOTCTCG GGCCACATCC CCCTGGCCAT CTCTTCTGCC CCACGACGAG GCATCCTGG GGCTGATGAA AGGAGGCGCT TGACTACTC TGACTCACCA TGAGTTATT TGACACCTAG TGAGTATAT TGACACCTAG TGGCAGAAG CCTTGGAGT TATATCATGGA TATATCATGGA TAGACCTCAC CAGAGCCCAAA GGATTAAT CTGGATTAAC CTACGACCG GAGGCCCAAA GGATAATGTA CATGTACCAC CAAAGTTACCAC CAAAGTGCC CATCAAGTT	CGAGGGGAAG TTCCCAGACT CAGCACCAG CTACAGACCC TTCAAGGCCCA ACAGTGGCTG GACCAAGACC ACAGTCTATT AGTGCCTCT GGTATTCAGC CTTCAAGTCCA GGTATTCAGC CTTGAGTTGC GTTCATGTCA AGATCCAAGA ATCCTTTCTA AGATCCAAG TTCTAACTG CATCGAGGCT TTCAATGTTT CATGAGTACCA TTCTAACTG CATCGAGGCT CTCAAGGAAAAA CCTCAGGAAAAAA CCTAGGAGCCT CTCACAGTCA GGCAGAAGAGT GGGAAACCAA GGTTGGGCTTC TTCGAGAACCA GTTGGGCTTC TTCAAGAAACC GCTCTGGGAT	120 180 240 300 360 420 6600 6600 720 780 840 900 1020 1140 1200 1140 1200 1380 1440 1500 1680 1740 1860
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	1   GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGCGG AGAGGGAGCA TGCTGACCACT CTGGGTGCCC ACCATGTGCA CCATCCACAT TGCGAACCCG GCCTTTCCA CGGATCCTTA ATGGACAGAA AAGAGAGGG TGGACCCCAA AAGAGAGGAG TGAAAGGAAA CTGCTGCTGCA TATCCAGTAA TATGCAATCA TATGCAATCA TATGCAATCA TATGCAATCA TATGCAGTCA TATTCAGCAC TATTCAGCA TATTCAGCAC TATTCAGCAC TATTCAGCAC TATTCAGCAC TATTCAGCAC TATTCAGCAC TATTCAGCAC TATTCAGCAC TATCACAC TATGCAGTCT TGACCTGCAA ACATCTGCAA TTAAGGCAGC	TCAAGCAGAG AGCCAGCGG CCGCTGCGC CACTGCCAGG CACTGCCAGG CACTGCCAGG CACTGCCAGG CACTGCCAGG CTCAGAGGC CTCAGAGGGA CTCAGAGGC CTCAGAGGCAATTCC CTATTGTTTTT ATCAGGCACA ACGTCTGGTC TCAATCATCT CCATCATCT TCAATCATCT CCAGGTATTC TCAATCATCT CCAGTTATCT TCAATCATCT CCAGTTATCT CAAAAAAGC CCGTGTACGG CAATGTGAAC CTACTGGTG CAACTGCTC CCGTTATCT TAAAAAAGC CCGTGTACGG CAATGTGAAC CATCGCGGAA CATCCGCGGAAC CATCCGCGGAG CATCATACTG CATCATACTATACT	21     CCCAGGGGGG GCTGAGCGG GCTGAGCGG GCTGAGCGGG ACGCCCGGG CCTGGCCGGG CCTGGCCGGG ACGCCGGG ACGCCGGG ACGCTGAGTTGC GGCAAGACAC GGCAAGACAC GGCAAGACATTC GAAAGGAGTTG GAAAGAGTTG GAAAGAGTTTC GAAATTTCAGAATTT CAGTATTTGAAACG TCAGCACTTG TCAGCACTTG TCAGCACTTG AAATTGTCCAATT ATACAGGCCA AAATTGTCCC CAAGACGTGG GAGAAAATTT ATACAGGCCA CAGGACTGG GAGATATA TTCCTCTGTG ACGCCCTCG GAGATAGACG ATGGGGCAGAC ATGGGCAGAC ATGGGCAGAGC ATGGGATACA TTCCATACC GGCACGGGGCG	TGCTATCGGA GCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGGGAGGCA ACCCTGGAA TGCTGCTCAC TCATTAAGA GAGGAGAGCA TGATGGAAG TGAACAAGAC CGGGCCACCG CTGACCGGTT ACCCGGTGC TGAATGACA ACACATATGA AGACAAGAC CTACATTGA AGACAGACC CTACATTGCA CCATATTGCA CCATATTGCA CCATATTGCA CCATATTGCA CCATATTGCA CCATACTGG CTACATTGCA CCATACTGG CTACACTGG CTACACTGG CTACACTGG CTACACTGG CTACACTGG CTACACTGG CTACACTGG CGGACCTCT GGAACCTGG CGGACCAC TGGAGCACA TGGAGCACA TGGAGCACA TGGAGCACA TTGGAGCACA TGGAGCCATAT	CAGAGCCTGG GAACCCAGAT GCCTGGCGAT CCCTGGCCAT CCCTGGCCAT CCCTGGCCAT CCCACGACAGG GCAGCAGG GCCAGCAGG GCCAGCAGG GCCAGGAAG CCCTTGAGAT ATATCATGGA GAAGCTCAC TGGAGTTAAT TGAGTCAGCG GAGGCCCAAA GGATAATGTA CAAGTTACCAG CAAAGTGGCA GCGGCGGAG ATGCTACCCC CAACAGTGGCAGG CCATCAAGTTG GGAGCCCATCAAGTTG GAGCACCCC CATCAAGTTG GGGCCCAAA	CGAGGGCAAG TTCCAGACT CAGCACCAG CTACAGGCCAG CTACAGGCCCAG CTACAGACCC TTCAAGGCCCA GACCAGACCC ACGGTCTATT CCGATTGTT AGTGCCTCT GGTATTCAGC CTTGAGTTCCA ACATCCAAGA ATCCTTCTCA ACATCCAAGA ATCCTTCTCA CTTCAACTCC CATCGAGGCT CTCAAGACCA CCAGGAAAAA CTCAGCACCG CCTCACAGTCA CATCATGGA CCAGGAAAAA CTCAGCACCG CTCACAGTCA CATCATGGA GCAGAAACCA GCAGGAAACCA GCAGGAAACCA GTTGGGCTTC CTCACAGACCA CTTCACAGACCA CCATCATGGA GCAGAACCAA GCAGAAACCAA CTCACGACCCC CTCACAGTCA CCAGTCATGGA CCAGGAAACCAA CCAGGAAACCAA CCAGGAAACCAA CTCACGGCTCC CTCACAGTCCA CGTCGGGGTTC CTCACAGACCC CGTCTGGGGTTC CTCACGGCTC CTCACAGACCC CGCTCTGGGGTC CTCACGGCTC CTCACGCC CTCTCACGCC CTCTCACGCC CTCTCGCGCTC CTCACGCC CTCTCACGCC CTCCTCC CTCACGCC CTCTCACGC CTCCTCC CTCCC CTCC	120 180 240 300 360 420 540 660 720 780 900 960 1080 1140 1290 1380 1440 1500 1560 1680 1740 1800 1740 1860 1920
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	1   GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGCGG AGACCACT TGCTGACCAT TGCGAACCACT TGCGAACCACT TGCGAACCACT TGCGAACCAG ACGATCCTTAA ATGGAAGAGA AATGGGAAGA AATTGCAGTAC TTTTTCCAG TTTTTCCAG TTTTTCCAGAC TATGCAGTACT AGCTGTTCTA ACCTGGAGTA ACCTGGAGA ACCTGGAGA TCCAGGTGCT TGTACCTGCA ACCTTGCAGA TTGAGCCGAA TTAGGCCGAA TTAGGCCGAA TTAGGCCGAA TTAGGCCGAA TTAAGCCCGAA TTAAGCCCGAA TTAAGCCCGAA	TCAAGCAGAG AGCCAGCGG CCGCTGCGC CCGCTGCGC CCGCTGCGC CACTGCCAG CACTGCAGG CACTGCAG CTACAGAGGA CTCAGAGGGA CTCAGAGGGA CTATCTG AAAGCTCTC CTATTTTTTT TCAGACACAG CACATCAT CAAAAAAGC CCGGTATC CCATTGAT CAAAAAAGC CCCTGTCAGAGGA CCCCTGTCAGAGGT TCACATGAGGT TCAACACTTC CCGGGTATC CAAAAAAGGC CCGTGTACGG CAATGTGAAC CATCCTGGAGG CATCATGAGT TTCCTTCCAGGAG CATCATAGTG TTCCTTCAGAG CATCATAGTG TTCCTTCAGAG CATCATAGTG TTCTTTTAAA CATTCGGGGAG CATCATAGTG TTCTTTTCAC ACACTTTCACAC TCCCTCCAGGAG CATCATAGTG TCCCTTCCAG	21     CCCAGGGGGG GCTGAGCGG GCTGAGCGG GCTGAGCGG ACGCCCGGG CCTGGCCCGG ACGCCCGGG ACGCCGGG ACGCAGCTG ACTCTGAGTTG ACTCTGAGTTG ACTATTACAACG GCAAGACTG ACATCATT CGAAATTC CAGTATTTG CTCACTTG CTCACTTG TCACTGGAAAT CTCGAAATTC CAGCACTTG TCAGTAGTAGAATTC CAGCACTTG TCAGTATTTA ATACAGGCCA CAGGATTATA ATCCTCTGTG AGCACCATTC ATTGCCAGTA TCCTCTGGGAGA ACCCATTC ATTGCCAGTA TCCTCTGGGAGA ACCCATTC ATTGCCAGTA TCCTGGGCAGA ATGGGGAGAG CTGGCCGGGCC CTGGCCGGGCCG	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC AGCTCGCGGC AGCGCAGGCA CCTGCGGAGCA TCCTGCTCAC TCATTAAAGA GAGGAGAGCT TGTATGGAAG CGGGCCACCG CTGACACGTT ACGCGGTCAC AGCACGGT ACCAGTT ACGCGGTCCC TGATGACAGC TGATGACGGA AGTGGACGGA AGTGGACGGA AGTGACCTG CTACAATGGA CGACTTGGACCTT TGAACCTTG CTACAATGGA CGACTTGCTCG CTACAATGGA CGACTTGCACCGT TGAACCTGG TGAACCTGG CTACAACCAGGT TGGAGGACAA TTGGAGGACAA TTGGAGGACAA TTGGAGGACAA TTGGAGGACAA TTGGAGGACAA TTGGAGGACAA TTGGAGGACAA	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTTCTCGG GGCACATCC CCCTGGCCAT CCTCTTCTGCC CCTGGCCAT CCTCTCTGCG GGCTACTAA GGAGCGCAC GGATTATAT TGACACCAT TGACACCAT TGACACCAT TGACACCAT TGACACCTAT TGACACCTAT TGACACCTAT TGACACCTAT TGACACCTAT TGACACCTAT TGACACCTAT TGACACCTAC TGAGATTAT TGACACCTAC TGAGATTACT TGACACCTAC TGAGATTACT TGACACCTAC TAGAGCTCAC CTACGACCG GAGGCCCAAA TGAGCCCAA AAGGGGGGAA ATGCTACCC CATCAAGTTT CATTACCCC CATCAAGTTT CAGGCACAC AAGGGGACAC AAGGGGACACAC AAGGGGACAC AAGGGGACAC AAGGGGACAC AAGGGGACAC AAGGGGACAC AAGGGACAC AAGGGGACAC AAGGGACAC AAGGGGACAC AAGGGGACAC AAGGGGACAC AAGGGACAC AAGGACAC AAGGGACAC AAGGACAC AAGGGACAC AAGGACAC AAGGGACAC AAGGGACAC AAGGGACAC AAGGGACAC AAGGGACAC AAGGGACAC AAGGGACAC AAGGACAC AAGGACAC AAGGACAC AAGGGACAC AAGGACAC AAGGGACAC AAGGGACAC AAGGACAC AAGGACAC AAGGACAC AAGGACAC AAGGACAC AAGGACAC AAGGACAC AAGGACAC AAC A	CGAGGGGAAG TTCCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCA ACAGTGGCTG GACCAAGACC ACAGTGGCTG GACCAAGACC CTGAGTTGTT AGTGCCTCT GGTATTCAGC CTTGAGTTGC GTGATTCAGC GTGATTCAGC GTGATTCAGC GTTCATGTCA AGATCCAAGA ATCCTTTCTG GCGATGACCA TTTCTAATGTTT CATGATAAAG CTCAGCACCG GGCAGAGCCT TCCACAGTCA CAGCACCG GGCAGAGCCT CTCACAGTCA GGGAAACCA GCTGGGCTCC TTCAAGGTCA CTCACAGTCA CTCACAGTCA CTCACAGTCA CTCACAGTCA GCGAAACCAC GCTCTGGGGT TTCAGGACCT TTCAAGGACCT CTCACAGTCA C	120 180 240 300 360 420 540 600 720 780 840 900 960 1020 1140 1260 1320 1380 1440 1500 1620 1680 1740 1800 1740 1800 1920
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	1   GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGCGG AGACGGACCAT TGCGAACCCG ACCATGTGCA CCATCCACAT TGCGAACCCG GCCCTTTCCA ATGGACAGAA CAGAAGGAGA TGCAGACAGA ATTGCAGAC TTGCAGACAGA ATTGCAGAC TTGCAGTGAA CTGCTGCTGA ATTGCAGAC TATTCAGAC ACCTTGGAGA TCCAGGTGCT TGTACCTCCA ACCTTGAGAC TTAAGGCAGA ACATCTCCAA ACATCTCCAA ACATCCCAATACAT CCACATACAT	TCAAGCAGAG AGCCAGGGGCCGCCGCTGCGCC CGCTGCGCT CACTGCCAGGGCCAGCTGGCTC CACTGCCAGGGCCAGCTGGCTC CTATCGGCAGGGCCACATCCTG GGGCAATTTC AAAGCTCTGCAGAGGC CTATTTTTTT ATCAGGCACA ACGTCTGGTC TGATGAAGGT CAAAAAAGCT TCACATCT CAGGTACTGC CAATGTGAAG CATCGCGGAT CAAAAAAGGC CATCGCGGAG CATCGCGGGAG CATCGCGGGAG CATCGCGGGAG CATCGCGGGAG CATCGTGAGC CATCGCGGAG CATCGCGGGAG CATCGTGAGC CATCGCGGAG CATCGCGGGAG CATCATAGTG CAACATTCGAG CATCGCGGGAG CATCATTGAC CAGGGACCTC CAGGGGACCTC CAGGGGACCTC	21   CCCAGGGGGG GCTGAGCGG GCTGAGCGG GCTGAGCGG ACGCCCGGG CCTGGCCCG ACGCCCGG ACGCCCGG ACGCCCGG ACGCAGACAC GGCAAGACAC GGCAAGACAC GGCAACACT TAGTACATT TAGTACATT GAAAGAGGT TCCAGTATTC CAGAATTC CAGAATTT TCCTCTGTG ACGCCCCC GAGATAGACG ATTGCCAGTA TCCTGCGCCC CGGGATAGACC CTGGCGGGGG CTGGCCGGTC CTCCATCCATC TCCATCCATC	TGCTATCGGA GCCAGGGTCT AGCTCGCGC GAGGGTGAC CTGGGAGGCA GCTTCCCTGG AACCCTGGAA TGCTGCTCAC TCATTAAGAA GAGGAGAGCT TGTATGGAAG GGGTTGGTAA TGAACAAGAC GGGCCACCG CTGAACAATTAAGAA ACCATATTGA ACCAGGTGC TGGATGACAT GATTTAGACA ACCATATTGA ACCATATTGA AGACAGAGCA CTGGAACCTCTG GGATGCTTGGACGGT TGAACTTGGA GGTTTGCTTG GGATGACTTT TGAACCTGGA CTGAACCAGGT TGAACCTGGA TTGGAGCACA TTGGAGCACA TTGGAGCACA TTGGAGCACA TTGGAGCACAC ATTGGAGCACAC TTGAACCATGT ATGTAGACCAGGT ATGTAGACCAGGT	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTOTTCTGG GGCCACATCC CCCTGGCCAT CTCTTCTGCC CCAGGACGAG GCATGCTGGG GGCTGATGAA AGGAGGAGT CCTTCACCA TGGAGTTATT TGACACCTAT TGACACCTAT TGACACTAT CATGACCTC CAACACTAT CCACACCGG GAGGCCCAAA TGGACTTACCC CAACACTAT CCATCACCC CAACACTT GGGACACCAC CAACACTC CAACACC CATCAAGTT TCGCTCC TCCCTCC TCCCTC TCCCTCC TCCCTCC TCCCTCC TCCCTCC TCCCTCC TCCCTCC TCCCTCC TCCCTCC TCCCTC TCCCTCC TCCCTC	CGAGGGGAAG TTCCCAGACT CAGCGACCAG CTACAGGCCA ACAGTGGCTG GACCAGACCA	120 180 240 360 420 480 540 660 720 780 840 900 1080 1140 1200 1140 1200 1140 1500 1680 1740 1680 1740 1860 1980 1980 2040
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGGGG AGAGGGAGCA TGCTGACCAT CTGCGACCCAT TGCGAACCCG CGCTTTCCA CGGATCCTTA ATGGACAGAG ACAGGAGGGAG TGCACCCCAA AAGAGAGGGA TTGCAGTGAA AAGTGAA AATTGGAAAG TGAAAGGAA TTGCAGTGAA AAGTGTAA CTTTCCAGAC TATCCAGAC TATCCAGAC TATCCAGAC TATCCAGAC TATCCAGAC TATCCAGAC TATCCAGAC TATCCAGAC TATCAGCAC AACTCGCAA TCAGACCGAAC TTGACCCGAA TTAAGGCAGA TTAAGGCAGA TTAAGCAGA TTAAGCACA ACATTACAAC AGTACCCGAT TTAAGCACA ACATTACAAC AGTACCCCAATACAT	TCAAGCAGAG AGCCAGCGG CCGCTGCCC CCGCTGCCC CCGCTGCCC CACTGCCAGG CCACTGCCAG CCACTGCCAG CTACAGCCAG CTACAGCAG CTCAGAGGA CTCAGAGGA CTCAGAGGA CTCAGAGGA CTATGTCTC CATACTCTC CATACTCTC TCATCATCT TCAACACTC TCATCATCT TCAACACTC TCATCATCT TCAACACTC TCATCATCT TCAACACTC TCATCATCATCT TCAACACTC TCATCATCATCT TCAACACTC TCATCATCATCT TCAACACTC TCAATGTAGAG CACTCCAGAA CATCCGGGAG CATCATACTG TCCCTGCAGA CATCATCACC CACGGGACCTC CCAGGGACCTC CCAGTGTGATC CCAGGACCTC CCAGGACCTC CCAGGACCTC CCAGGACCTC CTTGTTGATC CCAGGACCTC CTTGTTGATC CCAGGACCTC CTTGTTGATC CCAGGACCTC CTTGTTGATC CCAGGACCTC CTTGTTGATC CTAGTGTATC CCAGGACCTC CTTGTTGATC CTTGTT	21     CCCAGGGGGG GCTGAGGGGG GCTGAGGGGG GCTGAGGGGG GCTGAGCGG ACGCCCGGGG ATGGAGCTG ACTCTGAGTTG CGCAAGACAC GGCAAGACAC GGCAAGACAC GGCAAGATTG AAGTACATTG AAGTACATTG GAAAGTTTG GAAAGTTTG GAAAGTTTTGA TCTGAAATT TCAGTATTTGA AATTGTCAATT ATACAGGCA AAATTGTC CAAGACGTGG GAGAAAATTT ATACAGGCCA ATTGCCAGTA TCCTCTGTG AGCACCATTG ATTGCCAGTA TCCTCTGTG AGTACCATTG ATTGCCAGTA ATTGCCAGTA ATTGCCAGTA ATTGGGGGAGA ATTGGGGGAGG CTGGCCGGTTG GGCACGGAGC CTGGCCGGTTG TCCATCCATTC AAGGACCTTC	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGGGTGAC CTGGGAGGCA GCTTCCCTGG AACCCTGGAA TGCTGCTCAC TCATTAAGAA GGGTTGGTAA TGACAAGAC GGGCCACCG CTGACCGGTT ACCCGGTTG ACCATATTAAGACA ACCATATTAGACA ACCATATTAGACA AGACATGGA CTGAACGGTT TGAACTGGA GGTTGCTTG GGAACCTCTG GGAACCTCTG GGAACCTCTG GGAACCTCTG GGAACTTTGCA TGGAACTAGA TGGAACTAGA TGGAACTTACTC CCAACCAGGT TGAACTAGACA TTGGGGGCCAA TTGGGGGCCAA TTGGGGGCCAA TTGGGGGCCAA TTGAGCATAT ATGTAGACAT ATGTAGACAT ATGTAGACAT ATGTAGACAT ATGTAGACTATA	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTOTTCTGG GGCCACATCC CCCTGGCCAT CCCTGGCCAT CCCTGGCCAT CCCTGGCCAT CCCTGGCCAT CCCTGGCCAT CCACGACGAG GCATCCTGG GGCTAATGAA AGGAGGCCTAT TGACACCTAT TGACACCTAT TGACACCTAT TGACACCTAT TGGCAGAG CCCTTGGAGT ATATCATGGA TGGCAGATAT TGGCAATAT TGGCAAGT GAAGCTCAC CTACGACCG GAGGCCCAAA GGATAATGTA CCTACGACCG CAAGTTACCAC CAAGTTACCAC CAAGTGCAC CATCAAGTT GGGCACGAG AGGCGCGAA AAGGGGACGT CATCAGGTACCC CATCAAGTT CGGGCACGC CATCAGGCAC CATCAGGCACC CTCTTTGGGC CTCTTTTGGCC CTCTTTTGCC CTCTTTTTTGCC CTCTTTTTTGCC CTCTTTTTGCC CTCTTTTTGCC CTCTTTTTTTT	CGAGGGCAAG TTCCAGACT CAGCACCAG CTACAGACCC TTCAAGGCCA ACAGTGGCTG GACCAAGACC ACGGTCTATT CGGATTGTT AGTGCCCTCT GGTATTCAG CTTCAAGTCCA GTTCATGCAAGACA ACAGTGCATG GTTCATGCAAGACA ATCCTTCTG CATCGAGTTC CATCGAGTTC CATCGAGGACCA TTCTAACTG CATCGAGGCT TTCAATGTT CATGATAAAG CCAGGAAAAAA CCTAGAGCCC GGCAGAGCCT CTCACAGTCA CATTCATGGAG GGTAGACCA CATTCATGGAG CTTCACAGGCC CTCACAGCACC GGCAGAGCCT CTCACAGGAA CTCACGGCCC CTCACAGGAA CTCACGGCTC CTCACAGGAA CTCACGGCTC CTCACAGGAT CTGGGAAACCA GTTGGGCTTC TTCAGGAT CTGGGGGTC CTCACGGCTC CTCACGGCT CTCACGGCTC CTCACGGCTC CTCACGGCTC CTCACGCACC CCTCTGGGAT CTGGTGGGTC CTGGTGGGTC CTCACGCCCC CCCCTCCCCT	120 180 240 300 360 420 540 660 720 780 840 900 900 1080 1140 1200 1380 1560 1560 1680 1740 1860 1960 1960 1960 2040 2100
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	1   GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCCGGG AGAGGGAGCA TGCTGACCAT TGCGAACCAT TGCGAACCAG TGCGAACCAG TGCGAACCAG TGCGAACCAG TGCGAACCAG AGAGGAGG TCGACCCCAA AAGAGAGGAG TTGCAGTGAA AATTGCAGAAA AATTGCAGAAA TTGCAGTACC TATCCAGAC TATCCAGAC TATCCAGAC TATCCAGAC TATCCAGAC TATCCAGAC TATCCAGAC TCCAGTGCT CCAGTTGCT TGTACCTGCA ACCTCGAGA TCAGACCACAACACACACACACACACACACACACACACAC	TCAAGCAGAG AGCCAGCGG CCGCTGCGC CCGCTGCGCT CACTGCCAGG CAGCTGGCT CACTGCCAGG CAGCTGGCT CACTGCCAGG CTCAGAGGGA CTCAGAGGGA CTCAGAGGGA CTCAGAGGA CTCATCTC CAAAGCTCTC TATCATCT TCAATCATCT CCAGTCTGT TAAACACTTC TCAATCATCT CAAAAAAGGT TCCATTGAT CAAAAAAGGT TCCATTGAT CAAAAAAGGT TCCATTGAT CACCTGGGGAG CACCTTGTTCT TCCTTGCAGA CATCTTGTTGAG CACCTTGGAGA CATCTTGGAGA CATCTTGGAGA CATCTTGGAGA CATCTTGGAGA CACCTTGGAGA CACCTTGGAGA CACCTTGGAGA CACCTTGGAGA CACCTTGGAGA CACCTTGGAGA CACCTTGGAGA CACCTTGGAGA CTCACTTGGAGA CTCACTTGTTGATC CTGGGGGAGCCTC CTTGTTGATC CTGGGGGGGGGG	21   CCCAGGGGGG GCTGAGGGGG GCTGAGGGGG GCTGAGGGGG GCTGAGCGGG ATGGGAGCTG ACTGGGCTGG ACTGTGAGTTG CGGAAGACAC GGCAAGACAC ACTATTT AAGTACATTT GAAAGGAGGT TCTGGAATTC CAGTATTTGAAATTG CAGTATTTGAAATTG TCAGTGGAAATTT ATACAGGCAA AAATTGTCC CAGGACTTGT ATTGCAGTATTT ATTCCAGTTGT ATTGCAGTATTT ATTCCAGTGGAGGAGAAATTT TCTGGAGAGTT CTGGACCATTC ATTGCAGTGG AGGAATACAT TCCTGGGGGGGAGA TTCCATCGGGCG ATGGGGGGGGGAGA TTCCATCCATC CGGACGGGGGGGAGA TTCCATCCATC CGGACGGGGGGAGA TTCCATCCATC CGAGACGTTGGGACGGGGGGGGGAGA TTCCATCCATC AAGGGACGTTC AAGGACGTTC AAGGACGTTC AAGGACGTTC AAGGACGTTC AAGGACGTTC AAGGACGTTC GGAACGCAACC	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGAGGC	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTTCTCGG GGCACATCC CCTGGCCAT CCTGGCCAT CCTGGCCAT CCTGGCCAT CCTGGCCAT CCTGGCCAT CCTGGCCAT CCTGGCACAG GCATGCTGGG GGCTATCAA GGAGGAGGAT TGACACCTAT TGACACCTAT TGACACCTAT ATATCATGGA TGGGGATTAAC TGGGTTCAT CTGAGCTCAG GAAGCTCAC TGGAGTTAAC CTACGACCGG GAAGTTCAC CACAGATT CATGACCAG GAAGCTCAC TGGAGTTAAC CTACAACTTT CATGACCAG AAGGCAAA TGCTACCAC CATCAAGTTT TGGGACAGGCA AAGGGAGGA ATGCTACCC CATCAAGTTT TGGGACAGCAC AAGGGAGGT CCTCTTGGGT CTCTTTGGGC CTGTCTTGGGT CTCTTTGGGC CTGTCTTGGGT CTCTTTGGGC CTCTTTGGGC CTGTCTTGGGC CTGTCTTTGGGC CTGTCTTGGGC CTGTCTTGGGC CTGTCTTGGGC CTGTCTTGGGC CTGTCTTTGGGC CTGTCTTTGGGC CTGTCTTGGGC CTGTCTTGGGC CTGTCTTGGGC CTGTCTTTGGGC CTGTCTTGGGC CTGTCTTGGGC CTGTCTTTGGGC CTGTCTTTGGGC CTGTCTTTGGGC CTGTCTTGGGC CTGTCTTTGGGC CTGTCTTTGGCC CTGTCTTTGGCC CTGTCTTTGGCC CTGTCTTTGGCC CTGTCTTTTGGGC CTGTCTTTGGCC CTGTCTTTGGCC CTGTCTTTGGCC CTGTCTTTGGCC CTGTCTTGGCC CTGTCTTGGCC CTGTCTTGGCC CTGTCTTGGCC CTGTCTTTGGCC CTGTCTTTGGCC CTGTCTTGGCC CTGTCTTTGGCC CTGTCTTGGCC CTGTCTTTGGCC CTGTCTTGGC CTGTCTTGGCC CTGTCTTTGGCC CTGTCTTGGCC CTGTCTTTGGCC CTGTCTTGGCC CTGTCTTGGCC CTGTCTTGGCC CTGTCTTGGCC CTGTCTTGGCC CTGTCTTGGCC CTGTCTTGCC CTGTCTTGGCC CTGTCTTGCC CTGTCTTGCC CTGTCTTGCC CTGTCTTGCC CTGTCTTGCC CTGTCTTGCC CTGTCTTGCC CTGTCTTGCC CTGTCTTTGCC CTGTCTTTGCC CTGTCTCTTGCC CTGTCTTTGCC CTGTCTTCTTGCC CTGTCTTTGCC CTGTCTTTGCC CTGTCTTCTCT CTGTCTCTTTGCC CTGTCTTTGCC CTGTCTTTGCC CTGTCTTTTGCC CTGTCTTTGCC CTGTCTTTGCC CTGTCTTTGCC CTGTCTTTGCC CTGTCTTTTGCC CTGTCTTTTGCC CTGTCTTTTGCC CTGTCTTTTGCC CTGTCTTTTTGCC CTTTTTGCC CTGTCTTTTGCC CTTTTTTGCC CTTTTTTTGCC CTTTTTTTT	CGAGGGGAAG TTCCCAGACT CAGCGACCAG CTACAGGCCA CTACAGGCCA ACAGTGGCTG GACCAAGACC ACAGTGGCTG GACCAAGACC CTGAGTTGTT AGTGCCTCT GGTATTCAGC CCTTGAGTTGC GGTGGCATGG GTTCATGTCA AGATCCAAGA ATTCTATCTG GCATGACCA ATTCTAATGTTC TCAATGTTT CATGATAAAG CTCAGGACCA GGCAGAGCCT CTCACAGTCA CAGTCATGGA GTTGGGCTTCT CTCACAGTCA GGTAGACCA GGTGGCACG GCAGAACCA CTCTCTGGGA GTTGGCTCC CTCACGTCA CAGTCATGGA GTTGGGCTTC TTCAGGACCA CTCTCTGGGAAACC CTCTCTGGGAAACC CTCTGGGGTTC TTCAGGACCA CTTCTGGGGTC TTCAGGACCA CTTCTGGGGTC TTCAGGACCA CTCTGGGGTC TTCAGGTCC CTCACGTCA CTGGTGGGTC TTCAGGCTCC CTCACGTCAC CTCTCTGCGTC CTCTCTCTCACC CACAGTCCATC CCTCTCTGTCA CCTCTCTCTCC CCTCTCTCTCACC CCTCTCTCTC	120 180 240 300 360 420 540 660 720 780 840 900 900 1080 1140 1200 1380 1560 1560 1680 1740 1860 1960 1960 1960 2040 2100
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCGCGGG AGCTACCACT CTGGGTGCCC ACCATGTGCA CCATCCACAT TGCGAACCCG CGCCTTTCCA CGGATCCTTA ATGGACAGAA ACGAAGGAGG TTGCAGAGGAG ACATCGAAA AAGTGAAA AATTGGAAAG TGAAAGGAAA TTGCAGTGAA AAGTGTGAA ACTCTGAGC TATCTCAGAC TGAACCCGAA TCAACATAGCACA ACTCTGAAC TGACCCGAAC TTAAGGCAGAA TTAAGGAACA TCACATACAT CCACATACAT TCACCGAAGAA AGTCTCCAATGGAAA AGTCTCCAATGGAAA AGTCTCAATGGAAAA AGTCTCGAAAA AGTCTCGAAAAAATCCCCAATACATCCCCAATACACATACACTCCAATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACATACAT	TCAAGCAGAG AGCCAGCGG CCGCTGCCC CCGCTGCCCC CCGCTGCCCC CCGCTGCCCC CCGCTGCCCC CCGCTGCCCC CCGCTGCCCAG CCACAGCCAG CCACAGCCAG CCACAGCCAG CCACATCCTC CATAGGCAC ACGTCTGGTC TGACTGGTC TGACTGGTC TGATGATGT TCAACACTTC TCATCATCT TCAATCATCT CCATCATCT TAAAGGTGGG TCCCATTGAT TAAAGGTGGG TCCCATTGAT TCAAAAAGCC CCGTGTACCG CATCATCT TCCCTGCAGA CATCCTGGAC CATCATCT TCCCTGCAGA CATCTTCCAC CAGGACCTC CCGGGACCT CCTGCTGCAG CCTCTTCCAC CCGGGACCTC CCTCCTCCCCC CGGGTACAT	21     CCCAGGGGGG GCTGAGGGGG GCTGAGGGGG GCTGAGGGGG GCTGAGGGGG GCTGAGCTG ACTGCAGTTG CCTGAGTTG CGCAAGACAC GGCAAGACAC GGCAAGACAC GGCAAGACAC GTCATTT AAGTACATTG CAAGTATTT CAGTATTTGAAATC CTGCACTTG TCAGTAGTATT ATACAGGGAA AAATTGTTCC CAAGACGTGG GAGAAAATTT ATACAGGCCA ATTGCCAGTA TTCCTCTGTG AGCACCATTG ACTGCACCTG CAGGACGTGG CTGGCCCTG CTGCACCTG CTCGTCCCCC GAGATAGACG TTCGTACCTTG TCCTGCGCCC GAGATAGACG TTCGTACCTT ATTGCCAGTC ATTGCGATCCT CTCATCCATC AAGGACCTTC TCCATCCATC TCCATCCATC TCCATCCATC TCCATCCA	TGCTATCGGA GCCAGGGTCT AGCTCGCGC GAGGGTGAC CTGGGAGGCA GCTTCCCTGG AACCCTGGAA TGCTGCTCAC TCATTAAGAA GAGGAGAGCT TGTATGGAAG GGGTTGCTAC CTGACCGGTT ACGCGGTGCA ACCATATTAAGAC ACCATATTAA ACCATATTGA AGACAGACTCTG GAACCTCTG GAACCTCTG GAACCTCTG CTACAATGGA GGTTGCTAC CTACAATGGA GGTTGCTTG GGAACCTCTG TGAACTGGA CTGAACTGGA CTGAACTGGA CTGAACTGGA CTGAACTGGA CTGAACTTGC CCAACCAGGT TGAACCTGT TGAACCTGT TGAACCTGT TGAACCTAC TTGAGCACA TTGGAGCATAT TGGAGCATAT ATGTAGACCG TTGAACCAGGT TGGAGCATAT ATGTAGACCA TTGGAGCATAT ATGTAGACCA TTGGAGCATAT ATGTAGACCA TTGGAGCATAT ATGTAGACCA TTGGAGCATAT ATGTAGACCA TTGAGCATAT ATGTAGACCA TTGGAGCATAT ATGTAGACCA TTGGAGCATAT ATGTAGACCA ACACCAAGAT ACACCAAGAT ACACCAAGAT	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTOTTCTGG GGCCACATCC CCCTGGCCAT CCCTGGCCAT CCCTGGCCAT CCAGACGAG GCATCCTGG GGCTACTGA GGCTACTGA GGCTACTGAC CCTGGCCAT TGAGTATAT TGACACCTAT TGACACCTAT TGACACCTAT TGAGATTAT TGACTCAGA GGCTACAGAG CCTTGGAGT TATATCATGGA TATATCAGA TATATCAGAC GAAGATTAC CTAGACCGG GAGGCCAAA GGATTAAC CTAGACCGG GAGGCCCAAA GGATAATGTA CATGTACCC CAACAGTT GGGACAGCAG AAGGGAGGT CTCTTTGGGC CTCTTTTGGGC CTGTCTTTGGGC CTGCAACACT CTGACCTGT CTGCTGTT CTGCTGTC CTGCTGTCTTGGGC CTGTCTTTGGGC CTGTCTTGGGC CTGCAACACT CTGACCTGT CTGCTGTT	CGAGGGGAAG TTCCAGACC TTCAAGGCCA TCAAGACCA TCAAGACCA TCAAGACCA TCAAGACCA ACAGTGGCTG GACCAAGACC ACGGTCTATT AGTGCCCTCT GGTATTCAGC CTTGAGTTGC GTTCATGCAAGACCA AGATCCAAGA ATCCATTCTA GCATCATGCA TTCTAACTG CATCGAGGCT TTCAAGGCT CATCAAGACCA GGCAGAAAAA CCATCAAGGA GGCAGAAGACT CTCACAGTCA GGCAGAAGACT CTCACAGGAA GCTGGGGT CTCACAGGAA CCTGGGCTC CTCACAGGAA CCTGGGAT CTGGGGTC TTCGGGTGC CTCACAGGAA CCTCGTGGAT CTGGGGGTC TTCGGGGTC CTCTGGGAT CTCACAGCAC CCTCTGGGAT CTCACAGCAC CCTCTTGTCA CACAGCACG ACAGTCCATG CTCCTTGTCA ACACTCCATG CTCCTTGTCA ACACTCCATG TCCACAGGAG TCCACCTTCT	120 180 240 300 360 420 6600 6600 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1500 1560 1860 1740 1800 1800 1920 1980 2040 2100 2220 2280
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCCGGG AGAGGGAGCA TGCTGAACCAT TGCGAACCAT TGCGAACCAT TGCGAACCAG CCATTCCACAT TGCGAACCAG AGAGGAGG TCGGATCCTTA ATGGACAGAA AAGAGGAGG TTGCAGTGAA AAGAGGAGA TGCAGTGAA AATTGCAGTGAA ACTTGCAGC TATTCAGAC ACCTTGAGAC ACCTTGAGAC ACCTTGAGAC TGAGCCGGAA ACATCTCCAA TGAGCCGGAAGA ACTCCTACC GGATCGGAAGA AGTCTCGAAC ACTCCTACC GGATCGCAAC ACTCCTACC GGATGGCCAAC ACTTCCTACC GGATGGCCAAC ACTTCCTACC GGATGGCCAAC ACTTCCTACC GGATGGCCAAC ACTTCCTACC GGATGGCCAAC ACTCCTACC GGATGGCCAAC ACTTCCTACC GGATGGCCAAC ACTTCCTACC GGATGGCCAAC ACTCCTACC GGATGGCCAAC ACTCCTACC GGATGGCCAAC ACTCCTACC GGATGGCCAAC ACTCCTACC GGATGGCCAAC ACTCCTACC GGATGGCCAAC ACTCTCTACC GGATGGCCAAC ACTCTCTACC GGATGGCCCAAC ACTCTCTACC GGATGGCCCAAC ACTCTCTACC GGATGGCCCAAC ACTCTCTACC GGATGGCCCAAC ACTCTCTACC GGATGGCCCAAC ACCTTCTACC ACCTCTACC AC	TCAAGCAGAG AGCCAGCGG CCGCTGCCC CCGCTGCCC CCGCTGCCC CCGCTGCCC CACTGCCAGG CAGCTGCCC TGACCAGAGC CTATCGCCAG CTCAGAGGGA CTCAGAGGGA CTCAGAGGCAATTCC CTATTTTTT ATCAGGCACA ACGTCTGGTC TCAATCATCT CCAGCTATCATCT CCAGCTATCATCT CAACACTTC TCCATCATCATCT CCAGTATCC CCGGTTATCC CCGGTTATCC CCGGTTATCC CCGGTTATCC CCGGTTATCC CCGGTTATCC CCGTGTACGG CAACACTC CCATCAGTC CCATCAGTC CCATCAGTC CCGTGTACGG CACCTTCCTCCCC CCGGGCACTC CCTCCTCCCCC CCGGGGACCTC CCTCCTCCCCC CGGGGTACATC CCGGGGACCTC CCTCCTCCCCC CCGGGGACCTC CCTCCTCCCCC CGGGGTACATC CCGGGGACCTC CCTCCTCCCCC CGGGGTACATC CCGGGGGACCTC CCTCCTCCCCC CGGGGTACATC CCGGGGTACATC CCGGGGGACATC CCTCCTCCCCC CGGGGTACATC CCGGGGGACATC CCCGGGGACACAC CTCCCTCCCCC CGGGGTACATC CCGGGGTACATC CCCCAACAACACAC	21   CCCAGGGGGG GCTGAGCGG GCTGAGCGGG GCTGAGCGGG ACGCCCGGG CCTGGCCCGG CCTGGCCCGG ACGCCCGGG ACGCCAGCGG ACTGCAGCTG ACTCTGAGTTG CGCAAGACAC GGCAAGCTG ACTACATT AAGTACATTG AAAGAGGTG TCAGTACATT CAGTATTTGAAATC CTGCACCTTG TCAGTGGAAA TTCCTGAAATT ATACAGGCA AAATTGTCC CAAGACATTA ATTCCCAGTA ATTCCCAGTA ATTCCCAGTA TCCTCGGCC GAGATAGACG CTGGCCGGGG CTGGCCGGGG CTGGCCGGGG CTGGCCGTG CTCACCCTC AAGGACGTAC AAGGACGTAC CTGGCCCGTG CTCCATCCATC AAGGACGTAC CCCAAGCCCC AACCTCATCC	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGAGGC	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTTCTCGG GGCACATCC CCTGGCCAT CCTGGCCAT CCTGGCGAGAG GCATCCTCG CCCAGGACGAG GCATCCTCG CCAGGACGAG GCATCCTCG CCAGGACGAG GCATCCTCG CCAGGACGAG GCATCACCA TGAGTTATAA CCTACCAA TGACCACAT TGACACCTAT TGACACCTAT TGACACCTAT TGACACCTAT TGAGACTTAC TGAGATTAAC TAGAAGTTCAA TGAGACCAA GGATAATTA CATGACCAG CAGCAGAAG CCATCAAGTTT CATGACCAG CAGCAGAAG TCGCTCACCAC ACAGCTCAC ACAGCAGCAG AAGGGAGGAG ATGCTACCC CATCAAGTTT CTCTTTGGC CTGCTCTTGGC CTGCAGATAT CAATTCTGGAC CAGCAGAAG TCGCACGAT CCATCAAGTTT CTCTTTGGC CTGCAGATC CATCAAGTTC CATTCTGGC CTGCAGATC CAATCAGTCC CATCAAGTT CTCTTTGGC CTGCAGATC CAATCAGTCC CAATCAGTCC CTGCAGAGT CCAAGTT CAATCAGTC CA	CGAGGCGAAG TTCCAGACT CAGCACCAG CTACAGACCC TTCAAGGCCA TCAAGACCC ACAGTGGCTG GACCAAGACC ACAGTGGCTG GACCAAGACC ACAGTCTATT AGTGCCCTCT GGTATTCAGC CTTGAGTTGC GTTCATGCAAGACCA ACAGTCCAAGA ATCCATTCTA ACATCCAAGA ATCCATTCTT CATGATTACT CATGAGACCA TTCTAACTG GCAGAAGACCA TTCAAGGCCT CTCACAGGAAGAC GCAGAAGACCT CTCACAGTCA GGCAGAAGACT CTGCAGGACCA CAGTCATGGA CGCTCTGGGAT CTGGGGGTC TTCGGGGTC CTCACAGGACCA CGCTCTGGGAT CTCACAGGAC CTCACAGGACCA CCTCTGCGAT CTCACAGGAC CTCACAGGAC CTCCTGGGAT CTCACAGGAC CTCCTGGGAT CTCCTTGTCA CACAGTCCATG CTCCTTGTCA ACAGTCCATG CTCCTTGTCA ACAGTCCATG CTCCTTGTCA ATCACAGAGG TCCACCTTCT	120 180 240 360 420 540 660 720 780 900 960 1020 1140 1260 1320 1380 1440 1500 1560 1740 1800 1920 1980 2040 2160 2220 2280 2340

	GTTATTCAGA	CCA CA TTOOL	TARASSOC	тстатаасаа	CCGACCACAT	TOTALOTACE	2460
	GGGCTGGCAT	CATCATACAC	CIGGGAAAA	AAACCACCGA	GCCTCTCCC	ADGGACAAGC	2520
	GGCCGTTCCT	CTCDATCATA	TAGACOCACAT	ACAGCCCTCA	CCAGGACGCC	GACCCCCTGA	2580
	AGCCCCGGGA	CLCCCLCATC	ATCAGACACT	TCATTGCCTA	CAAGAACCAG	GACCACGGGG	2640
5	CCTGGCTGCG	CCCCCCCATC	CACACACACACA	ACAGCTGCCG	GTTTGCTGAC	AATGGCATTG	2700
9	GCCTGACCCT	GGCCAGTGGT	CCAACCTTCC	CGTATGACGA	CGGCTCCAAG	CAAGAGATAA	2760
	AGAACAGCTT	CTTTCTTCCC	CAGACTGGCA	ACGTGGGGAC	GGAAATGATG	GACAATAGGA	2820
	TCTGGGGCCC	TECCECTURE	CACCATAGOG	GAAGGACCCT	CCCTATAGGC	CAGAATTTTC	2880
	CAATTAGAGG	AATTCAGTTA	TATGATGCCC	CCATCAACAT	CCAAAACTGC	ACTITCCGAA	2940
10	AGTTTGTGGC	CCTGGAGGGC	CCACACCA	GCGCCCTGGC	CTTCCGCCTG	AATAATGCCT	3000
10	GGCAGAGCTG	CCCCATAAC	AACGTGACCG	GCATTGCCTT	TGAGGACGTT	CCGATTACTT	3060
	CCAGAGTGTT	CTTCGGAGAG	CTEGGCCCT	GGTTCAACCA	GCTGGACATG	GATGGGGATA	3120
	AGACATCTGT	CTTCCATGAC	CTCCACCCCT	CCGTGTCCGA	GTACCCTGGC	TCCTACCTCA	3180
	CGAAGAATGA	CAACTGGCTG	GTCCGGCACC	CAGACTGCAT	CAATGTTCCC	GACTGGAGAG	3240
15	GGGCCATTTG	CAGTGGGTGC	TATGCACAGA	TGTACATTCA	AGCCTACAAG	ACCAGTAACC	3300
10	TGCGAATGAA	GATCATCAAG	AATGACTTCC	CCAGCCACCC	TCTTTACCTG	GAGGGGGCGC	3360
	TCACCAGGAG	CACCCATTAC	CAGCAATACC	AACCGGTTGT	CACCCTGCAG	AAGGGCTACA	3420
	CCATCCACTG	GGACCAGACG	GCCCCCCCCC	AACTOGCCAT	CTGGCTCATC	AACTTCAACA	3480
	AGGCGACTG						3540
20	CGGATGTTCA	CAATCGCCTG	CTGAAGCAAA	CGTCCAAGAC	GGGCGTCTTC	GTGAGGACCT	3600
	TGCAGATGGA	CARAGTGGAG	CAGAGCTACC	CTGGCAGGAG	CCACTACTAC	TGGGACGAGG	3660
	ACTCAGGGCT	GTTGTTCCTG	AAGCTGAAAG	CTCAGAACGA	GAGAGAGAAG	TTTGCTTTCT	3720
	GCTCCATGAA	AGGCTGTGAG	AGGATAAAGA	TTAAAGCTCT	GATTCCAAAG	AACGCAGGCG	3780
	TCAGTGACTG	CACAGCCACA	GCTTACCCCA	AGTTCACCGA	GAGGGCTGTC	GTAGACGTGC	3840
25	CGATGCCCAA	GAAGCTCTTT	GGTTCTCAGC	TGAAAACAAA	GGACCATTTC	TTGGAGGTGA	3900
	AGATGGAGAG	TTCCAAGCAG	CACTTCTTCC	ACCTCTGGAA	CGACTTCGCT	TACATTGAAG	3960
	TGGATGGGAA	GAAGTACCCC	AGTTCGGAGG	ATGGCATCCA	GGTGGTGGTG	ATTGACGGGA	4020
	ACCAAGGGCG						4080
						ATGGCATCAA	4140
30	AGGGAAGATA	CGTCTCCAGA	GGCCCATGGA	CCAGAGTGCT	GGAAAAGCTT	GGGGCAGACA	4200
	GGGGTCTCAA						4260
	TCTGGGTGAC						4320
	CTGTGGTGAA	GAAGAAGAAG	TTGTGAGGAC	AGCTGCCGCC	CGGTGCCACC	TCGTGGTAGA	4380
	CTATGACGGT	GACTCTTGGC	AGCAGACCAG	TGGGGGATGG	CTGGGTCCCC	CAGCCCCTGC	4440
35	CAGCAGCTGC	CTGGGAAGGC	CGTGTTTCAG	CCCTGATGGG	CCAAGGGAAG	GCTATCAGAG	4500
	ACCCTGGTGC	TGCCACCTGC	CCCTACTCAA	GTGTCTACCT	GGAGCCCCTG	GGGCGGTGCT	4560
	GGCCAATGCT	GGAAACATTC	ACTTTCCTGC	AGCCTCTTGG	GTGCTTCTCT	CCTATCTGTG	4620
						ACAGCAAAGA	4680
40	TCCACTTTGG						4740
40	GATCCCCATG						4800
	CTTAAGGAAA	TCTTTACTCC	TGTAAGCAAG	AGCCAACCTC	ACAGGATTAG	GAGCTGGGGT	4860
	AGAACTGGCT						4920
				TAGATGACTC			4980
4.5	GAGATTCCAG	AAATCTGCTG	CATTTCACAT	GGTACCTGGA	ACCCAACAGT	TCATGGATAT	5040
45	CCACTGATAT	CCATGATGCT	GGGTGCCCCA	GCGCACACGG	GATGGAGAGG	TGAGAACTAA	5100
				GGGCAGGCAG			5160
						CAGAGGGGAG	5220
				AAGGCTGGGG			5280
50				AGCCCTCCCT			5340
50	GTGACTACGG	GGTCGCCCTT	TGCTCACGTC	TCTCTGGCCC	ACTCATGATG	GAGAAGTGTG	5400
				ATGAGCACAG			5460
				CCACAGAAGT			5520
	CATTTGCTCT	TCATCCAGGG	AACTGAGCAC	AGGGGGCCTC	CAGGAGACCC	TAGATGTGCT	5580
55				GGAAATATAG			5640
33				CCAAGATGGG			5700
	GAGGGCCTGG	GGAGCCCCAC	CCTAGCCCTT	GCTGCCACAC	CACATTGCCT	CAACAACCGG	5760
	CCCCAGAGTG	CCCAGGCACT	CCTGAGGTAG	CTTCTGGAAA	TGGGGACAAG	TCCCCTCGAA	5820
				CTAGCAGATC			5880
60				GCGGTCCCTG			5940
00	ACCTGTCAGC	CCAGCCTGGG	TGCACAGTAG	CTGCAACTCC	CCATTGGTGC	TACCIGGCIC	6000
	TCCTGTCTCT	GCAGCTCTAC	AGGTGAGGCC	CAGCAGAGGG	AGTAGGGCTC	GCCATGTTTC	6060
				CTGAACAGCT			6120
	TTTCAGCTGC	TGCTTAATGC	CCTGCTCTCT	CCCTGGCCCA	CCTTATAGAG	AGCCCAAAGA	6180
65	GCTCCTGTAA	GAGGGAGAAC	TCTATCIGIG	GTTTATAATC	TIGCACGAGG	CACCAGAGIC	6240
05						CAAACTCTTT	6300 6360
				CAGGGAGGTC		CTCGGTCCAA	6420
						CAAAGGCCAG	6480
						GTTAAAATGA	6540
70	CCTC ACCOUNT	Under CT I CT I	CONTRACTOR	CACHALLAC	TCTTCTAATC	CAAGGGTCTC	6600
70	ACACTETEAA	CCACTTAGGA	TOTCATCACT	TTCACCTCCC	CAGGAATGTT	GAATGTCTTT	6660
						CATATGTTTC	6720
						AGCCAATATC	6780
						TCCTTGTTAT	6840
75						CTCTGAAATG	6900
. •						TGTATAGAGT	6960
						TTCTATTTAT	7020
						CITAAATGTC	
80	Seg ID NO:	95 Protein	sequence				
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	1	11	21	31	41	51	
	Ī	I	1	1			
	MGAAGRQDFL					DODHHVHIGO	60
85						SALCPFQGNF	120
					2.4	77	

85							
				TGTTGCTATG			
						GGTTGTGACC	
						ACTTGCGTGG AGAACTCATC	
οU						CCCAAACACC	
80						GATGGCTCCC	
						ACCCTCCCGG	
						AATGGCGGTC	
						ATCCTGGCCC	
75						AACACCATGG	
75						TACATGACAC	
						CCTTTTGTGT	2760
	CAGCCCAGCC	ACGCCGACAG	GCCAAGCAAC	ATGGCTGCAC	ACGGTGTGGG	AAGAACTTCT	2700
						CCTTTGTTAG	
70						GTCAAGGTTG	
						ACTGAGATGG	
						AGCATCAAGT	
						CCAGATATCC	
00						GATGGCTTGA	
65						GGTCCTGCCC.	
						TOGGCATCAC	
						AGCTCCCAGG	2160
				CAATGACCGT			2100
00				GCGGTCAGAA			2040
60				TCTGCCAGAA			1920
				AGACACACCT			1920
				GGGAGAGACC			1860
				AATTGCAGCA TTTGCCACCG			1740 1800
"				CCCCAAGGGC			1680
55				GGCCTTCTCC			1620
				CTTCGGGGAC			1560
				TTTCTTTAGA			1500
				CGGCCGGCAA			1440
50	CCACCAAGGG	CAACCTCAAG	GTGCACTTTC	ACCGACATCC	CCAGGTGAAG	GCAAACCCCC	1380
50	ACCTCCGCTC	CCACACTGGA	GAGAGACCCT	TCGTGTGCTC	TGTCTGTGGT	CATCGCTTCA	1320
						TTGCAGATCC	
				ATGTCAAACC			1200
				CTGTGGCGCT			1140
45				TCCCGAGCGC			1080
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	TITUIGRADE	GIGEDFAIGP	KIIGAGVOOV	TETHIOGUALS	MILTWEITHE	GGPPEGGIFF	100

TIILYGRADE GIQPDPYYGL KYIGVGKGGA LELHGQKKLS WTFLNKTLHP GGMAEGGYPF

		97 Proteir					
	Protein Acc	ession #: 1 11	IP_065169.1 21	31	41	51	
_	Ī	Ĩ	ī	Ī	i .	Ī	
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                                                                                           360
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30	Seq ID NO:	106 DNA 500	nance				
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33	· Gr 2 ADMMAN	CATUL ELLING		- PREPARTEDI	Tryvinski.		-00

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                                                                                   360
        GGCAGAAGAC AAATGGTGTC CACAAAATAC ACAGTACTGT TTGACAGTTC ATCACTTCAC
                                                                                   420
        CAGCCACGGA AGAAGCACAT CCATCACCAA AAAGTGTGCC TCCAGAAGTG AATGTCATTT
60
        TGTCGGTTGC CACCACAGCC GAGATTCTGA ACATACGGAG TGTAGGTCTT GCTGTGAAGG
                                                                                   540
       AATGATCTGC AATGTAGAAT TACCACCAA TCACACTAAT GCAGTGTTTG CCGTAATGCA
CGCTCAGAGA ACATCTGGCA GCAGTGCCCC CACACTCTAC CTACCAGTGC TTGCCTGGGT
                                                                                   600
                                                                                   660
        CTTTGTGCTT CCATTGCTGT GATGCCACCA TTCCTAGGAG AGGCAGAGAC CAGCCTCTAA
       AGCACAAGCC AAAAACTGTG TGAACGGTGA ACTTTGGAGT GAAGATCAAT CTTGCACTTG
                                                                                   780
65
        GTGAAGAGTG CACATTGGAC CTCAAGGCGA AAGCCAGTGG TTTGCTTGGA TAAAATGTTC
                                                                                   840
        CCGCATGAGG CCACAGGACT GAGGATGGGA ATTTGGCAGG GCCTGAGAAG ATGGTCTGAC
                                                                                   900
        TTCCAGGCTT CCTGGTCAAA GAGAGCTACG TTTGGGCAGT TCTGCAGAGA GGATCCTGGC
        AACTAGTCCC ACCTGACTAG GCCTTTAGCT GAAAGGATTT CTTGACCTCC TTGACTGCCT
                                                                                  1020
       CAGAGGCTGC CAGGTCAAAC CCTCTTGTTT ATGTGATTAG CTCAGAGCAT CTCTATGAAA
TCTAACCCTT CCCCTCATGA GAAAGCAGTT TTCCCCACCA ACAGCATAGT CAATGAGAAA
                                                                                 1080
70
                                                                                 1140
        GGCAACTGTA CGAAGAAAC TTCCAGTGGA ACTAATATGA AATCTATTTG CAAATTATGG
        GGGGAAATAA AGCTTTTAAA TTATACAATG T
        Seg ID NO: 111 Protein seguence
75
        Protein Accession #: AAM20908.1
                               21
                   11
                                            31
        MLYKSSDRPA HKVSMLLICH ALAIAVVQIV IPSESWAFAK NINFYNVRPP LDPTPPPNSF
                                                                                    60
        KCFTCENAGD NYNCNRWAED KWCPONTOYC LTVHHFTSHG RSTSITKKCA SRSECHFVGC
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        HHSRDSEHTE CRSCCEGMIC NVELPTNHTN AVFAVMHAQR TSGSSAPTLY LPVLAWVFVL
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        Nucleic Acid Accession #: Eos sequence
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        Coding sequence: 228-884
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GEOCOCIOGIS   COCCAGGOS GEOGRAGICA CITCHOTOCA   GEOGRACITA MAGNOTISTIC   60		1	11	21 	31 I	41 I	51 1	
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5 TITICAGCT GCTTTAMAG TRANTISMA GARGOGSCIT TRANSATAR COCACTTCT 180 ANTACTOR GSTEARACCT TITICACHTY CAGAGAGGA GCTGACAC GARTISTCTC 180 ANTACTOR GSTEARACCT TITICACHTY CAGAGAGGA GCTGACAC GACTTCTC 180 ANTACTOR GSTEARACCT TITICACHTY CAGAGAGGA GCTGACAC GACTTCTC 180 TITICACAGGT GAGGAGGAC CACCAGGAGGAGGA GCTGACACAC GACTTCTC 180 CACACAGGT CAGAGAGTCT CACCAGGAC TAGAGATAT TAGAGATTCG GACCACCAG TTACTTCT AGAAGACTG COCTACTOR AGACTTCAC ATTACTTY TOCAGATC 480 TACATTCT AGACTACAG TOGGCAGAGA GACAAACCT TAGAGATTCT GACAGAGAG ATAATTATAA CTGCATACA TOGGCAGAGA ACAAATGGT TCCACAAAAT ACACATCACT ATTACTAGT TACACTCTAC GAGGAGAGAGA CACAAAGGT TAGAGATTCT GAACATACG GTTGACACT CACACAGGAG GAGAAAGGAC ACCACACAG CACAAAATGGT TACACACTCT AGACATACGG ATTACACATT CACACACCAGG GAGAAAGACA ACAAAATGGT CAACACACACAG AACACACACAG AACACACACAG AACACACAC	_							
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TICTCHASGT GIGGITCHTA CTGGGCAGGC TARACAGIATA TARAGISTITOS GACOGCCAG 360 CACAGAGGT CAGANACTICS CANTIFICORA AGACATCAS CITCTATRAT GIRAGOCCT CAGACAGTAT CORANGET TRACTIFICATA GIRAGOCCT CAGACAGTAT CORANGET TRACTIFICATA ARCCAGGGGGGGGGGGGGGGGGGGGGGGCGGGGGCTGCACTATACTATA GIRAGOCCT CAGACAGTAC TOCAGAGAGA CAGACAGTAC TAGACAGTAC TOCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG								240
CACACAGAGO CAGCATGCTC CTCCTCTOTC AGGCTCTOG TATACCTOTT GTCAGAATCT 480 CTCTCGACCC TACACCATT CAAATAGCT TCAAGTGCT TATAGCTATA GTGAGGCCT 480 CTCTCGACCC TACACCATT CAAATAGCT TCAAGTGCT TACACTATATA GTGAGGCCT 480 CTCTCGACCC TACACCATT CAAATAGCT TCAAGTGCT TACACTATATA GTGAGGCCT 480 CTCTCGACCC TACACCATT CAAATAGCT TCAAGTGCT TACACTATATA GTGAGGCCT 480 CTCTGACAGT TACACTATCA TOGGCCAGAGA GCAAATAGTG TCACCAAATATA CACAGCTACT 600 GTTTGACGT TCATCATTATA CACCACCACG GAAGAAGCA CATCACTACCA CAAAAAATCT 600 CTCTGAGAGT TACACTATA GAATAAACT GTGACACTA GAACAACTA 780 AGCACGAGT TACACTATA GAACACTACA GAACAACTA 780 AGCACGAGAGA ACACGCCTC AAAGCACAAG CAAAAACTG GTAAAAAATG TACACACTA 780 AGCACGAGAAAAAATG TCCCCACTAG GACCACCAGG CACAGAGTA GAACACCTA 780 GGGTTGACTAG GAACAACTAG CAAAAACTG TTCTACACTA 600 GGGTTGACAAGAACTA ACCTCTCTACACT GGTGAAAGAAC ACCTCTCTAG CAGAAGACA 780 GGGCTCAAAAACTG TCCCCACTAG GCCCACCAGAC ACCTCACTAC COTTAGCACA ACCTCACTACAC CATCACCTAC GAACACCTAC CACACCACCACAC ACCTCACACAC ACCTCACACACA								
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GGTTTGCTGG GATAMANTST TCCCGCATGA GGCCACGGA CTGAGGATGG GATTTGCAA GGGCTGGAG AGAGTCCGG GCACTAGTG CCACCTGCT AGAGGATGG CATGTGGCA GTTCTGCAGA GAGGATCCGG GCACTAGTG CCACCTGACT AGGCCTTTG CTGAAAGGAT TCTGACAC ATCTCATGA AATCTAACCC TTCCCCTCAT GAGAAGGAT GTTTCCCCAC AGCTCAGAGG ATCTCATGA AATCTAACCC TTCCCCTCAT GAGAAGGAT TTTCCCCAC  25 CAACAGCATA GTCATACAA AATCTAACCC TTCCCCTCAT GAGAAGGAT TTTCCCCAC  30 AAATCTATT TGCAAATTAT GGGGGGGAAAT ÄAAGCTTTTA AATTATAAA  Seq ID NO, 111 Protein sequence Protein Accession #: Eos sequence Protein Accession #: Eos sequence  Protein Accession #: Eos sequence Protein Accession #: Eos sequence  Protein Accession #: Eos sequence  Protein Accession #: Eos sequence  Protein Accession #: Eos sequence  Protein Accession #: Eos sequence  Protein Accession #: Eos sequence  ATTATATAAA  Seq ID NO: 114 PROTEINITY NUPPULDIPTF PERSEKFETC ENAGDIYMCH READBACHCPO 120  MTQYCLTVHH FTSHGRSTSI TEXCASSISSE HEVGCHISKD SEHTECRSCC EGHICNVELP 180  THITHAVYAV MEAQRTSGSS AFTLYLPVLA WOFVLPLL  Seq ID NO: 114 DR Sequence  Nucleic Acid Accession #: EOS sequence  Coding sequence 402-1025  1 11 21 1 41 51  ACTTCCTGAG CCGGGGCCGC GGGGCTCC CTTGCAACCT CGTGGTGGGA CCCTGGGCTGG CACCTACCACA CTGCCGCCCC GGGCTCCC CTTGCAGCTC GCGCCGCGCC		AGAGGCAGAG	ACCAGCCTCT	AAAGCACAAG	CCAAAAACTG	TGTGAACGGT	GAACTTTGGA	960
GGGCTCAGA AGATGGTCTG ACTTCCAGGC TTCCTGGTCA AAGAGAGCTA GOTTTGGCA TTCTTGACTG CCTGACTGC CTGAGAGGCT GCCAGGTGAA AACCTCTTG TTATGTGATT 1260 AGCTCAGAGC ATCTCTATGA AATCTAACC TTCCCCTCAT GGGAAGCAGT TTATGTGATT 1260 AGCTCAGAGC ATCTCTATGA AATCTAACC TTCCCCTCAT GGGAAGCAGT TTATGTGATT 1260 CAACAGCATA GTCAATGAGA AAGGCACTG TACGAAGAAA ACCTCTTGT TTATGTGATT 1260 CAACAGCATA GTCAATGAGA AAGGCACTG TACGAAGAGAA ACCTCCAGTG GAACTAATAT 1380  Seq ID NO; 113 PTOLEIN SEQUENCE PROLEIN ACCESSION #: EOS SEQUENCE 1 1 11 2 1 31 41 51	~~							1020
GITCTGCAGA GAGGATCCTG GCAACTAGTC CCACCTGAT AGGCCTTGAC CTAAAGGAT 1200 TTCTTGACTC CCTTGACTGAC CTAGAAGAGC GCACGAGGTAA ACCCTCTGT TATATGTAAT 1200 AGCTCAGAGA ATCTCTATA AATCTAACC TTCCCCTCAT GAGAAAGAGT TTTCCCCCAC 12120 AGCTCAGAGA ATCTCATATA AATCTAACC TTCCCCTCAT GAGAAAGAGT TTTCCCCCAC 12120 GAAATCTATT TGCAAATTAT GGGGGGAAAT AAAGCTTTA AATTATAAA  Seq ID NO, 113 Protein sequence Protein Accession #: Eos sequence 1	20							
25 AGCTGAGGG ATCTGTAGA ATCTAGAC TYCCCCCTAT GAGANAGGG TYTCCCCAGA GAAACAGCATA GYCAATGAGA AAGCGAACTA TACCAGAGAAA ACTTCCAGGG GAAACATATA 1380  Seq ID NO:, 113 Protein sequence  Protein Accession #: Eos sequence  MOYALVSECK PHCSREED MILLLENVEC LIBELTRYKS SDEPAHKYSM LLICHALATA 60  WOIVUTYSES WAFANINEY NVRPILDETT FENSEYCCTC ENAGENYNCH RUMEEKKCPO 120  MOYALVSEN WAFANINEY NVRPILDETT FENSEYCCTC ENAGENYNCH RUMEEKKCPO 120  MOYALVSTA WAFANINEY NVRPILDETT FENSEYCCTC CHARGACCTC CAGCACCTCC CAGCACCACACACACACACACACACACACACACACAC								
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CAACAGCATA GICAATGAGA AAGGCAACTA TACGAAGAAA ACTITCAGTG GAACTATAT 1380 GAAATCATT TGCAAATTAT GGGGGAAAT AAAGCTTTA AATTATAAA  Seq ID NO:, 113 Protein sequence Protein Accession #: Eos sequence Protein Accession #: Eos sequence 1								
GAANTCHATT TGCAAATTAT GGGGGGAAAT AAAGCTTTA AATTATAAA  Seq ID NO. 113 Protein sequence Protein Accession #: Eos sequence 1	25							
Seq ID NO: 113 Protein sequence Protein Accession #: Eos sequence 1 1 11 21 31 41 51	43						GAACTAATAT	1380
1 11 21 31 41 51  MOVADYSECK PFECSREEPD NHILLLKAVE LLERLTRYKS SDRPAHKVSM LLLCHALAIA 60  WOUTUISSES WARANINHY NURPPLDPTP FRISKRCTC ENAGMYNCH REARDINGED 120  NTOYCLTVHH FTSERGSTSI TIKKCASRSEC HPVGCEHSRD SEHTECRSCC EGMICNVELP 180  THETRAVPAN WHAQRISGSS APTLYLPVLA WVFVLPLL  Seq ID NO: 114 DNA sequence Nucleic Acid Accession #: EOS sequence  Coding sequence: 402-1025  1 11 21 31 41 51  ACTICCTGAG CCGGGCTGGC TGGGTGGGAA CAGGCTTCTT GCCGGCCTCCC CAGGGCTGGC CACTACCACA CTGCGGCCC CGTGGGCCTC CTTCAAACT GTGGTGGGG CCCTGGGGT 120  ACTICCTGAG CCGGGCTGGC TGGGTGGGAA CAGGCTTCTT GCCGGCCTCCC CAGGGCTGGC CACTACCACA CTGCGCCCC GGGGCTGC CTTCAAACT GTGGTGGAG CCCGGCGGT 120  TCCCAGGGAG GCGGGCCCG GGGTTGCTC CTTCGAGGGC AGGCTCACCT GTCCCGGCCC 180  GGGCCCCTCC GGGCCCCA GGGTTGCTC CTTCGAGGGC AGGCTCACCT GTCCCGGCCC 240  GTAGCAGCA ACGCGGCCC CAGGCGGGG GCGAGATATC CCACATTTCT GCCTGCTGTT 360  GGGCCCGAG GGCCCCACA GGCCGGGG GCCAGGAGA GCCGCCGCGGC 240  GTAGCAGCCA ACGCGGCCC CAGGCGGGG GCCAGAACAC CACATTCCT GCTCCTGTT 360  GGGAAACCT TTTCACTGTT CCAAGAGGG GCCTGACAC CACATTCCT GCTCCTGTT 360  GGCAAACCT TTTCACTGTT CCAAGAGGG GCCTGACAC CACATTCCC TTCTCAAAGT 480  ATTAGAGAGTT GGACCGCCA GCACAGAGGG GCCTGACAC CACATTCCC TTCTCAAAGT 480  ATTACTGTA AAACGCAGGG GATAATTATA ACTGCAAAC CACATTCCC TTCTCAAAGT 480  ATTACTTGTA AAACGCAGGG GATAATTATA ACTGCAAATC GCCACAGATC CACATTCCC CACAAAAGTG GCCACAAAATGT 720  GCCACAAAA TACACACTA TTTTTGACAG TTCACACATT TCCAAATAGC 170  GCCACAAAT TACACAGTA TTTTTTGACAG TTCACACATT TCCAAATAGC 170  GCCACAAAT CACACATC AATCCACAT TTTGCTGTTAT GCACACACAC GCCACACAC 660  GTTCAACGC CAATCCACACT AATCCACATT TTGCACTTAT TCCAATAGC GTTCACACACT TTCAATAGC 170  AATTACCACA CAATCCACAT AATCCACATT TTGCACTTAT TCCAATAGC GTTCATCTTC 1020  ACTGCAGGG GGAACATCA GGGTGAGAGG GCCTGCCTCG GAGAAAACT 1080  GCCACAGATC TACACACAT GAGGGCAGA GACCAGCCT TTAAAGCCATA GCCACACAC TACACCACT TTTGCACTGTA GCTCACTCAC GAGACACT 1020  ACTGCACAGC CAATCCACAC AATCCACACA TACTCACCAC GCCACAGG GCCACAGG GCCACAGG 1020  ACTGCACGG GGACAAAT TGCAACACG GCCTCACACC TACACCACT 1020  ACGCCACAGC CAACACT AATCCACAT TTCCACAGA GGCCACAACT 1020  GCCACACTCA		GAMATCIATI	IGCAAATTAT	GGGGGAAAT	AAAGCIIIIA	WITHIAM		
1 11 21 31 41 51  MOVADYSECK PFECSREEPD NHILLLKAVE LLERLTRYKS SDRPAHKVSM LLLCHALAIA 60  WOUTUISSES WARANINHY NURPPLDPTP FRISKRCTC ENAGMYNCH REARDINGED 120  NTOYCLTVHH FTSERGSTSI TIKKCASRSEC HPVGCEHSRD SEHTECRSCC EGMICNVELP 180  THETRAVPAN WHAQRISGSS APTLYLPVLA WVFVLPLL  Seq ID NO: 114 DNA sequence Nucleic Acid Accession #: EOS sequence  Coding sequence: 402-1025  1 11 21 31 41 51  ACTICCTGAG CCGGGCTGGC TGGGTGGGAA CAGGCTTCTT GCCGGCCTCCC CAGGGCTGGC CACTACCACA CTGCGGCCC CGTGGGCCTC CTTCAAACT GTGGTGGGG CCCTGGGGT 120  ACTICCTGAG CCGGGCTGGC TGGGTGGGAA CAGGCTTCTT GCCGGCCTCCC CAGGGCTGGC CACTACCACA CTGCGCCCC GGGGCTGC CTTCAAACT GTGGTGGAG CCCGGCGGT 120  TCCCAGGGAG GCGGGCCCG GGGTTGCTC CTTCGAGGGC AGGCTCACCT GTCCCGGCCC 180  GGGCCCCTCC GGGCCCCA GGGTTGCTC CTTCGAGGGC AGGCTCACCT GTCCCGGCCC 240  GTAGCAGCA ACGCGGCCC CAGGCGGGG GCGAGATATC CCACATTTCT GCCTGCTGTT 360  GGGCCCGAG GGCCCCACA GGCCGGGG GCCAGGAGA GCCGCCGCGGC 240  GTAGCAGCCA ACGCGGCCC CAGGCGGGG GCCAGAACAC CACATTCCT GCTCCTGTT 360  GGGAAACCT TTTCACTGTT CCAAGAGGG GCCTGACAC CACATTCCT GCTCCTGTT 360  GGCAAACCT TTTCACTGTT CCAAGAGGG GCCTGACAC CACATTCCC TTCTCAAAGT 480  ATTAGAGAGTT GGACCGCCA GCACAGAGGG GCCTGACAC CACATTCCC TTCTCAAAGT 480  ATTACTGTA AAACGCAGGG GATAATTATA ACTGCAAAC CACATTCCC TTCTCAAAGT 480  ATTACTTGTA AAACGCAGGG GATAATTATA ACTGCAAATC GCCACAGATC CACATTCCC CACAAAAGTG GCCACAAAATGT 720  GCCACAAAA TACACACTA TTTTTGACAG TTCACACATT TCCAAATAGC 170  GCCACAAAT TACACAGTA TTTTTTGACAG TTCACACATT TCCAAATAGC 170  GCCACAAAT CACACATC AATCCACAT TTTGCTGTTAT GCACACACAC GCCACACAC 660  GTTCAACGC CAATCCACACT AATCCACATT TTGCACTTAT TCCAATAGC GTTCACACACT TTCAATAGC 170  AATTACCACA CAATCCACAT AATCCACATT TTGCACTTAT TCCAATAGC GTTCATCTTC 1020  ACTGCAGGG GGAACATCA GGGTGAGAGG GCCTGCCTCG GAGAAAACT 1080  GCCACAGATC TACACACAT GAGGGCAGA GACCAGCCT TTAAAGCCATA GCCACACAC TACACCACT TTTGCACTGTA GCTCACTCAC GAGACACT 1020  ACTGCACAGC CAATCCACAC AATCCACACA TACTCACCAC GCCACAGG GCCACAGG GCCACAGG 1020  ACTGCACGG GGACAAAT TGCAACACG GCCTCACACC TACACCACT 1020  ACGCCACAGC CAACACT AATCCACAT TTCCACAGA GGCCACAACT 1020  GCCACACTCA		Sea ID NO:	113 Proteir	secuence				
1 1 1 21 31 41 51   MOVADYSECK PPHCSEREPD NHILLLKWIC LLERLTRYKS SDRPARKYSM LLLCHALAIA 60   WOUTISES HAPAKHINFY NURPELIDER PROSECTED CERRODBYNON REARDINGED 120   MTOYCLTVHH FISEGRSTSI TRKCASRSEC HFVGCHISRD SEHTECRSCC EGMICNVELP 180   TRHTRAVFAN MEAGRESGSS APTLYLFVIA WVFVLPLL   Seq ID NO: 114 DNA sequence   Nucleic Acid Accession 8: EDS sequence   Coding sequence: 402-1025     1					3			
VVQIVIFEES WARANINTY NVRPPLIPTF PRISTRETS ENAGENTHON RWAEDENCED  NTOTALITHE TESTEGRETS IT KEKCASSES ENFUGENERS SEHTECRSCC EGHICNVELP  Seq ID NO: 114 DNA sequence Nucleic Acid Accession #: EDS sequence Coding sequence: 402-1025  1 11 21 31 41 51  ACTICCTGAG COGGCTGGC TOGGTGGGAA CAGGCTCCTT GCGCCTCCC CAGGCTGGC CAGGCTGGC CAGGCTGGC CTTCCAACCT COTGGTGGGA CCCACACACACA CAGGCCCCCC CCTGGCCCCC CTTCCAACCT COTGGTGGGA CCCACGCGGCCCC CTTCCAACCT COTGGTGGGA CCCCCCCGG GGCTCCCC CAGGCCGCCC CAGGCCGCCC CAGGCCGCCC CAGGCCCCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCCCCC CAGGCCGCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCGCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCGCCC CAGGCCGCCCC CAGGCCACACACCCCCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCCCCCC CAGGCCCACCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCACCCCCCCC	30	_				41	51	
VVQIVIFEES WARANINTY NVRPPLIPTF PRISTRETS ENAGENTHON RWAEDENCED  NTOTALITHE TESTEGRETS IT KEKCASSES ENFUGENERS SEHTECRSCC EGHICNVELP  Seq ID NO: 114 DNA sequence Nucleic Acid Accession #: EDS sequence Coding sequence: 402-1025  1 11 21 31 41 51  ACTICCTGAG COGGCTGGC TOGGTGGGAA CAGGCTCCTT GCGCCTCCC CAGGCTGGC CAGGCTGGC CAGGCTGGC CTTCCAACCT COTGGTGGGA CCCACACACACA CAGGCCCCCC CCTGGCCCCC CTTCCAACCT COTGGTGGGA CCCACGCGGCCCC CTTCCAACCT COTGGTGGGA CCCCCCCGG GGCTCCCC CAGGCCGCCC CAGGCCGCCC CAGGCCGCCC CAGGCCCCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCCCCC CAGGCCGCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCGCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCGCCC CAGGCCGCCCC CAGGCCACACACCCCCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCGCCCC CAGGCCCCCCC CAGGCCCACCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCCCCC CAGGCCCACCCCCCCC		1	1	1	1			
TOUCLIVEH PTSEGRSTSI TRICASRSE HPUGCEHSRD SEHTECRSCC EGHIONVELD 180  THETRAVEAV MEAGRISGS APPLYLPULA WYFULPLL  Seq ID NO: 114 DNA sequence Nucleic Acid Accession #: EDS sequence Coding sequence: 402-1025  1 11 21 31 41 51   ACTICCITAG COGGCTGGC TEGGTGGAA CAGGCTCCTT GCCGCCTCC CAGGCTGGC 60 CACTACCACA CTGCCGCCC CTGGGCTC CTTTCAACCT CGTGGTGGAG CCCTGCGGT 120  TCCCAGGGAG CCGGGCCCC GGGCTGCTC CTTGGAGGA GCCGGCCCC GCCCCCGGG 240 GTAGCAGCCA ACGCCGGCC CAGGCGGGG CAGGGAGGAG GCCGGCCCC GCCCCCGGG GGGAGAGCAGG GCAGGCAG								
Seq ID NO: 114 DNA sequence Nucleic Acid Accession #: EDS sequence  Ociding sequence: 402-1025  1 112 13 41 51  ACTICCTORA COGGCTGGC TEGGTGGAA CAGGTCCTT GCOSCTCCC CAGGCTGGC CACTACCACA CTGCCCCCG CCTGGGCTC CTTTCAACCT CGTGGTGGAG CCCTGCGGCT 160  ACTICCTCAGG GCCGGGCTGG GTGGTTCAGG GCAGGCTGGT GCCGGCTGCC CAGGCTGGC GTGGTACACACACA CTGCCGCCG GGGGTTCAGG GCAGGAGGA GAGGTCACT GTCCCAGCGCG 180  GGCCCCCTCC CGCCCCCCG GGGTGTTCAGG GCAGGGAGG AGCGTCACCT GTCCCAGGCGGC GTGGTCAGG GCAGGAGGAG AGCGGCCCC GCCCCCCGG GGGGAGAAACT GCACACTTC GCCGGCGGTG AGCGGCACCAC GTGAGCAGGAG GCGGCCCCAGGGGGG GGGAGAATAT CAGACACT TTCACTGTT CAGGAGAGGA GCCTGACAC CACATTCTC TTTCAAGAT 420  GTGCAAACCT TTTCACTGTT CCAGAGAGGA GCCTGACAC CACATTCT GCCTGCTGTT GCGCACACCT CTGAGATAGG CCTGACAAGG GCACCTCC TTTCAAGAT 420  ATAAGAGATTC GACCCCCCA GCACCAAGG TAGACACCT GCTCCTGTT ATACCACAT GATTTCTCA ATTCACATT TCCAAGAACT TTCCAAGAT TTCTCAAGAT 480  ATAAGAGATTC GACCCCCCA GCACCACAGG TCAGCACCT GCTCCTTGT CACGCTCCCG CACACCACGCACG GAAAACTTC GCTCCTGTT TCCAAGATAC TTTCTCAAGAT ACTCCAATC ACTCTGTAA TCTGAAGA GTAATATATA ACTGCAATC AGACCATT TCCAAGAAG GAAAAAATGT 720  GCCACAAAA TACACAGTAC TTTTTGCAGA TTCTCTCAT ATGCCAGAA GACAAAATGT 720  GCCAGAGTC CCCCACACCT TTCACAGTC TTTGCTGTG AGGAACACCA GCCAAGAAACT AGGCCAAGA GAAAAATGT 720  GCCAGAGTC CCCCCACACT TTCACACTAC TTGCTGTGT TCCCACACA 840  GCCGAGGTGC CCCCCACACT TACCACGTCT TTGCTGTGA AGGAACATCG GCAAGAACCT GCCCACACCT TACCACCAT TTCCCACACA AGGAAAAACT 180  GCCGAGGTGC CCCCCACACCT TACCACAGGT TTGCTGTGT TCCCCACACA 840  GCCGAGGTGC CCCCCACACCT TACCACAGGT TTGCTGTGT TCCCCACACA GCCAAAAAACT 180  GCCGAGGTGC CCCCCACACCT TACCACAGGA AACCACCAT TTGCTGAGA GGGAAAAACT 180  GCCGAGGTGC CCCCCACCT TACCACAGGA TACCACACCAT TTGCCAAGAG GCCAAAAACT 180  GCCGAGGTGC CCCCACACCT TACCACAGGAT AGCACACCT TAAACCACAA GCCACACACACACACACACACACACACACA								
Seq ID NO: 114 DNA sequence Nucleic Acid Accession #: EDS sequence Coding sequence: 402-1025  1 11 21 31 41 51    ACTICCTGAG CGGGGCTGCC TGGGTGGGAA CAGGCTCCTT GCGGCCTCCC CAGGCTGGC GCACACACAC CTGCCGCCCC CCTTCAACCT CGTGGTGGAGA CCAGCTCCCC CAGGCTGGCT TCCCAGGGGAG GCCCCCCCCC CGGGCCTCC CTTCAACCT CGTGGTGGAG CCCTGGGGTT 120  TCCCAGGGGA GCCGGGCCCC GGGCTGCCC CTTCAACCT CGTGGTGGAG CCCTGCGGTC 180 GGCCCCCCCC CGGCCCCCCAG GTGGTTCAGG GCAGGGAGAG GCCCGCCCCC GCCCCCCCGC GGGCCCCCAGGGGAGAGCCCC CAGGCCCCCAG GTGGTAGAGG CCCGGGGAGAGCCCC CAGGCCCCCAG GGGCCCCCAGGGGAGAGCCCCC CAGGCCCCCAGGGGAGAGCCCCC CAGGCCCCCAGGGGAGAGCCAGGCCCCC CAGGCCCCAGGGGAGAGCCCCC CAGGCCCCAGGGAGAGCCCCCCAGGCCCCAGGGAGAGCCAGGCCAGAGAGCCAGGAGACCAGGAGCCAGAGCCAGGAGACCCACATCCTC GCCTCCTGTT 360 GGCAACCCTTTCACAGTT CAGAGAGGGA GCCCGAGAACACCAATTCCTC CCTCCTCTGT AAAACAGTTC CACAAACACCACTTCCTTCCAGATT CAGAAACACACACACCACTCC TTCACAACACACACCACTCCCCTTTCCAGATT CAGAAACACCACATCCCTCTTCCAGAACACACCACAC	35					SEHTECRSCC	EGMI CNVELP	180
Nucleic Acid Accession #: EOS sequence  Coding sequence: 402-1025  1 11 21 31 41 51    ACTTCCTGAG CCGGGCTGGC TGGGTGGGAA CAGGCTCCTT GCCGCCTCCC CAGCGCTGGC CACTACCACA CTGCCGCCG CCTGGGCTC CTTCAACCT CGTGGTGGAG CCCTGCGGCT 120  TCCCAGCGAG GCCGGCCCG GGGTCGTCC CTTGCAGGG AGCCTCACCT GCCCGGCCC 120  GCGCCCCTCC CGCGCCCCAG GTGGTTCAGG GCAGGAGGA GGCCTACCT GTCCGGGCT 120  GGGCCCCACA CAGCCCGCCC CAGCGGGTG GCTGGGAGG CAGCCGGGGA GGCCCGGCCG 240  GTAGCAGCCA AGGCTCGGTG GGGCCGGGG GCAGGAATAG CCCACATTCT GCCTCATT 360  GGGCCCCAC AGGCCCAGGCC CAGCGGGTG GCAGGAATAG CCCACATTCT GCTCACTGTT 360  GGCACCCTC CTGGACTAGG CTGTTCTTG TAATCACATG GATGTTGCTG ATTACTCTG 420  GTCAAACCT TTTCACTGTT CAGAGAGGAG GCCTGACAAC CACATTCTC CTTCTCAAGAT 480  ATAAGAGTTC GGACCGCCA GCACACAAGG TCAGCACAC CACATTCTC CTTCTCAAGAT 480  ATTACTTTTCA TATCCAGATC CTCTCGAC CTACACACAT GCCATTCCC TTCCAAGACTG ACTTCATACTTT AACACATCA CACATTCTCATACTTCC AGGCACACA ACTTCATACTTTCAAATAGA TCCACATACA CTCATTCATACAT GCAAAAGTGT TCCAAAATAGC TCCACAAATAGC TTACATTCATA AACACAGAGA CACAATAGT TCCAAAATAGC TCCACAAAATAGC TTACATTCAAAAAAACACACACAATAGAACACACA AACACAATAGA TTACACAATACA CACAATAGA TTACACAATACA AACACACACA TATTCAATACAATACA TGTTTCACAGA TTACACATACA TACACAGTAC TGTTTCACAGA TTACACATACA TACACAGTAC TATTCCACACA TACACACTA TATCACAGTTC TACCACACAC AACACACACA AACACACACA TACACACTA AATCACAGTTA TTTCACTGTGA AACACACACA GCCAAACACACA GCCAAACACAA GCAAAATAGC GCAACACACAC CAATCACACAT AATCACAGTTA TTTCACTGTGTA AGGAACATAC GAACACACACA GACCAAGCCAA GCCAAAACACACA GCCAACACACA GCCAACACACAA GCAAAACACACA GCACAACACACA GCACAACACACA GCACAAACACACA GCACACACA	55	INHINAVFAV	MHAQKISGSS	APTLILIPVLA	MALAPPP			
Nucleic Acid Accession #: EOS sequence  Coding sequence: 402-1025  1 11 21 31 41 51    ACTTCCTGAG CCGGGCTGGC TGGGTGGGAA CAGGCTCCTT GCCGCCTCCC CAGCGCTGGC CACTACCACA CTGCCGCCG CCTGGGCTC CTTCAACCT CGTGGTGGAG CCCTGCGGCT 120  TCCCAGCGAG GCCGGCCCG GGGTCGTCC CTTGCAGGG AGCCTCACCT GCCCGGCCC 120  GCGCCCCTCC CGCGCCCCAG GTGGTTCAGG GCAGGAGGA GGCCTACCT GTCCGGGCT 120  GGGCCCCACA CAGCCCGCCC CAGCGGGTG GCTGGGAGG CAGCCGGGGA GGCCCGGCCG 240  GTAGCAGCCA AGGCTCGGTG GGGCCGGGG GCAGGAATAG CCCACATTCT GCCTCATT 360  GGGCCCCAC AGGCCCAGGCC CAGCGGGTG GCAGGAATAG CCCACATTCT GCTCACTGTT 360  GGCACCCTC CTGGACTAGG CTGTTCTTG TAATCACATG GATGTTGCTG ATTACTCTG 420  GTCAAACCT TTTCACTGTT CAGAGAGGAG GCCTGACAAC CACATTCTC CTTCTCAAGAT 480  ATAAGAGTTC GGACCGCCA GCACACAAGG TCAGCACAC CACATTCTC CTTCTCAAGAT 480  ATTACTTTTCA TATCCAGATC CTCTCGAC CTACACACAT GCCATTCCC TTCCAAGACTG ACTTCATACTTT AACACATCA CACATTCTCATACTTCC AGGCACACA ACTTCATACTTTCAAATAGA TCCACATACA CTCATTCATACAT GCAAAAGTGT TCCAAAATAGC TCCACAAATAGC TTACATTCATA AACACAGAGA CACAATAGT TCCAAAATAGC TCCACAAAATAGC TTACATTCAAAAAAACACACACAATAGAACACACA AACACAATAGA TTACACAATACA CACAATAGA TTACACAATACA AACACACACA TATTCAATACAATACA TGTTTCACAGA TTACACATACA TACACAGTAC TGTTTCACAGA TTACACATACA TACACAGTAC TATTCCACACA TACACACTA TATCACAGTTC TACCACACAC AACACACACA AACACACACA TACACACTA AATCACAGTTA TTTCACTGTGA AACACACACA GCCAAACACACA GCCAAACACAA GCAAAATAGC GCAACACACAC CAATCACACAT AATCACAGTTA TTTCACTGTGTA AGGAACATAC GAACACACACA GACCAAGCCAA GCCAAAACACACA GCCAACACACA GCCAACACACAA GCAAAACACACA GCACAACACACA GCACAACACACA GCACAAACACACA GCACACACA		Seg ID NO:	114 DNA sec	nience				
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CACTACACA CRECCECCO CCTGGGCCTC CTTCAACCT GTCCCGGCC 180  TCCCAGGGGA GCCGGCCCC GGGGTGCTCC CTCGCGGGC AGGCTCACCT GTCCCGGCCC 180  GGCCCCCCCCC CGCGCCCCAG GTGGTTCAGG GCAGGGAGA AGCCCGCCCC GCCCCGGCGC 240  GTAGCAGCCA AGGCCGGCCC CAGGCGGTG CGCTGGGAGC GCGCGCCCC GCCCCGGCG GGGGGGGGAAGA AGGCCGGTG GGGCGGGAAAAAAAAAA	40	1	11	21	31	41	51	
CACTACACA CRECCECCO CCTGGGCCTC CTTCAACCT GTCCCGGCC 180  TCCCAGGGGA GCCGGCCCC GGGGTGCTCC CTCGCGGGC AGGCTCACCT GTCCCGGCCC 180  GGCCCCCCCCC CGCGCCCCAG GTGGTTCAGG GCAGGGAGA AGCCCGCCCC GCCCCGGCGC 240  GTAGCAGCCA AGGCCGGCCC CAGGCGGTG CGCTGGGAGC GCGCGCCCC GCCCCGGCG GGGGGGGGAAGA AGGCCGGTG GGGCGGGAAAAAAAAAA		1	1		1	1		
TCCCAGGGA GCCGGGCCC GGGCTGCTCC CTCGGGGGC AGGCTCACCT GTCCCGGCC 240 GGCCCCCTCC CGGGCCCCAG GTGGTCAGG GCAGGGAGGA GCCGGGCCC GCCCGCGCG 240 GTAGCAGCCA ACGCCGGCCC CAGGGGGGG GCAGGAGGAGCCGGAGA 300 GGGCGCCGAA AGGCCGCGCG GGGGGGGGG GCGAGATATG CCACACTTCT GCCTGCTGTT 360 GGCACCCCTC CTGGACTAGG CTGGCTCTTG TAATCACATG GATGTGCTG ATTACTCTGA 420 GTGCAAACCT TTTCACTGTT CCAGAGAGGA GCCTGACAAC CACATTCTC TTCTCAAGAT 480 ATAAGAGTTC GGACCCCCA GCACACAAGG TCAGCATGCT GCTCCTCTGT CAGGCCTCG ACTATAGCTGT TGTCCAGATTC GTTATCTTCT CAGAAACCT GCCTCTCTGT CAGGCCTCG 540 ATTACTTGTA TGTCCAGATT GTTCTTCTTC TCAGAAACCT CACCACTT TCCAAGATAGC ACTTCTATAA TGTGAGGCCT CTCTGGACC ACTTCATAAA TACCACGTAC TGTTTTGACAG TTCATCACCATT TCCAAATAGC TACAACAGTAC TACACCACT TACACCACACA ACGACACTC CAGAACATCA GCCCACACAC CAACAACACT CACAACACAC CAACAACACC CAACAACACT TGTACACACAT TTTTGCCGTAA GACACACACA 840 GCCGGAGATC TGAACATACG GAGTGTAGGT CTTCCTGTGA AGGAATGAC TGCCACCACA 840 GCCGGAGTC TGAACATACG GAGTGTAGGT CTTGCTGTGA AGGAATGAC TGCCACCACA 840 GCCGGAGAGTC TGAACATACG GAGTGTAGGT TTGCCGTGAA AGAACACTC TACCTACACCAT TTTGCCGTAAT GCACCCCTCA AGAACACTC GACCACACC CAATCACACCT AATCCACT TTGCCGTGAA GCACACCTC TACCACACAT ACCTACCAG TCTTGCTGTGA AGGAATGAC TGCCACCACA CATTCACACCA TACCACCAC TACCACCAC TTTGCCTGTGA AGGAATGAC TGCCACCACA CATTCACACAC AATCACCAC AATCACCAC TACCACCAC TACCACCACACC TTGCTTGCTG GGTCTTTGTG GTCCACCACA GCCACAACACT 1080 ACTGGAGGATG GGAAACCAC TGGTTTGCTT GGATAAAAACCAC AGCCAAAAACT 1080 ACTGGAGGATG GGAACCAC TGGTTTGCTT GGATAAAAACCAC AGCCAAAAACT 1080 ACTGAGGATG GGAACCAC AGGCCACAGAGAC CACTCCTCAGAGG CTCCCTCAGAGG CTCCTCAGAGGA TTCCTCAGGC TACCACAGGA TACCTTTGCC ACCACACGCT TACCACACGCT TACCACACGAC TACCTCCTCA AGCCACAGGG CTCCCCCCACAGC TACCACACAGAACAT TTCCTCAGAGAA TTCCTCAGAGAA TTCCTCAGAGAACAT TTCCCCCCA AACCACCACACACACACACACACA								
GCCCCCCCC CGGGCCCCAG GRGGTTCAGG GCAGGGAGGA GCCGGGCCCC GCCCCGGGGCGCCCCGGA AGCCCGGCCCCCCCC								
GTAGCAGCCA ACGCCGGCCC CAGGCGGGTG CGCTGGGAGC CTCGGCCGGG AGCCGGTGA 300 GGGCGCGAG AGCCTCGGTG GGGCGGGGG GCGAGATATG CCACACTTCT GCTGCTGTT 360 GGCAACCCTC CTGGACTAGG CTGCTCTTT TAATCACATG GATGTTGCTG ATTACTCTGA GTGCAAACCT TTTACTGTT CCAGAGAGGA GCCTGACAAC CACATTCTC TTCTCAAGAT 480 ATAAGAGTTC GGACCGCCCA GCACACAAGG TCAGCATGCT GCTCCTCTGT CACGCCTCTCG 540 CTATAGCAGT TGTCCAGATC GTTATCTTCT CAGAAAGCT GCACATTTCC CAGAAACACTAC 600 ACTTCTATAA TGTGAGGCCT CCTCTCGACC CTACACCATT TCCAAATAGC TCCAGATGCT 660 ACTTCTATAA TGTGAGGCCT CCTCTCGACC CTACACCATT TCCAAATAGC TCCAGATGCT 720 GTCCACAAAA TACACAGGAC TGTTTGACAG TTCATCACCTT TCCAAATAGC TCCACACAGT 720 GTCCACAAAA TACACAGTAC TGTTTGACAG GTGAATGTCA TTTTGTCGGT TGCACCACAA 660 GCCGGGAGATTC TGAACATACA GGAGTAGGGT TGCCACCACA 840 GCCGGAGATTC TGAACATACA GAGTGATGGGT TTTGTGTGTA AGGAACGAT TGCAATGTAG 900 AATTACCCAC CAATCACACT AATGCAGTT TTTGCCGTAAT GCACACCACA 840 GCCGGAGATC CCACACCT TACCTACCAG TGCTTGCTGTGA AGGAACACTC 960 AATTACCCAC CAATCCACT AATGCAGTT TTTGCCGTAAT GCACGCTCT GAAACACCAA 900 AATTACCCAC CAATCCACT AATGCAGGTT TTTGCCGTAAT GCACGCTCT TAAAGCCAAA GCCAAAAACT 1080 GTGTGAACGG TGAATTTGG AGGGGGAGA GACCAGCTC TAAAGCCAAA GCCAAAAACT 1080 GTGTGAACGG TGAATTTGG AGGGGCAGA GACCAGCTC TAAAGCCAAA GCCAAAAACT 1080 GTGTGAACGG TGAATTTGG AGGGGCAGA GACCAGCTC TAAAGCCAAA GCCAAAAACT 1080 ACTGAGGATG GGAATTTGG AGGGCCTGA AGGAACACTC GACTTCCAGG CTTCCCAGG CTCCTAAGGCCAT AGGCCACAGG 1200 ACTGAGGATG GGAATTTGGC AGGGCCTGA AGGAGATCT GACTTCCAGG CTTCCCTGCT 1260 AAAGAAGAG TGTTTTGGC AGGGCCTGA AAGAGATGTC TGCCTCCAGAG CTTCCCTGCT 1260 AAACCCCTTG TTTATGTGAT TAGCTCAGAG CATCTCTAGT GACTTCCAGG CTTCCCTGAC 1320 AACCCCCTTG TTTATGTGAT TAGCTCAGAG CATCTCTAGT GACTTCCAGG CTTCCCTGAC 1320 AACCCCTTG TTTATGTGAT TAGCTCAGAG CATCTCTAGT AAATCTAAAT CCACCTGAC 1380 AACCTCCCTG TGAAAGAA TTTCTTGACC TCCTTGACTG CCTCAGAGGC TTCCCTGAC 1380 AACCTCCCTTG TTTATGTGAT TAGCTCAGAG CATCTCTATG AAATCTAAAT CCACCTGAAC  Seq ID NO: 115 Protein sequence Protein Accession #: EOS sequence 1 11 21 11 11 11 11 11 11 11 11 11 11 11	15							
GGGGCGCGAA AGGCTCGGTG GGCGCGGGG GCGAGATATG CACACTTCT GCTGCTGTT 350 GGCAACCTC CTGGACTAGG CTGCTCTTGT TAATCACATG GATGTTGCTG ATTACTCTGA 420 GTGCAAACT TTTCACTGTT CCAGAGAGGA GCCTGACAAC CACATTCTCT TTCTCAAGAT 420 ATAAGAGTT GGACCGCCCA GCACACAAGG TCAGCATGCT GCTCCTTGT CAGGCTCTG 540 CTATAGCTGT TGTCCAGATC GTTATCTCT CAGAAAGCTG GGCACTTGCC AAGAACATCA 600 ACTTCTATAA TGTGAGGCCT CCTCTGGAC CTACACCATT TCCAAATAGG TCAGAGATGGT 650 TTACTTGTGA AAACGCAGGG GATAATTATA ACTGCAATCG ATGGCCAGAAA GACAAATGGT 720 GTCCACAAAA TACACAGTAC TGTTTGACAG TTCATCACTT CACCAGCAC GGAAGAAGACA 780 GCCGAGATTC TGAACATGG GAGTGTAGCT CTTGCTGTGA AGGAAATGGT 720 GCCGAGATC CAAAAAGGTT GCCTCCAGAA GTGAATGCA TTTTGTGGGT TGCCACCAC 840 GCCGAGATCC CAACAACACT AATGCAGTGT CTTGCCTGTGA AGGACAATCT GCCACACCAC 840 GCAGCAGTGC CCCCACACT TACCTACCAG TTGCCTGTGAA GGCAATGACT 950 GCAGCAGTGC CCCCACACT TACCTACCAG TGCTTGCCTG GGTCTTTGTG CTTCCATTCC 950 GCAGCAGTGC CCCACACTC TACCTACCAG TGCTTGCCTG GGTCTTTGTG CTTCCATTCC 1020 ACTGGAGGG TGAACTTTGG AGGAGGACAA GACCAGCCTC TACAGCACA GCCAAAAACT 1080 GTGTGAACGG TGAACTTTGG AGTGAAGATC AATCTTGCC TAAAACCACAA GCCAAAAACT 1080 GTGTGAACGG TGAACTTTGG AGTGAAGATC AATCTTGCC TTAGATGACG CTCCACTTGC 1140 GACCTCAAGG CGAAAACCAG TGGTTTGCTT GGATAAAATG TTCCCCCATG AGGCCACAGG 1200 ACTGAGGATG GGAATTTGGC AGGCCTGGA AGAGGATCCT GACTCCAGG CTTCCTGGTC 1260 AAACCCTCTTG GTTTAGTGT TTGCTGCAG AGAGGATCCT GCCACTAGG CTCCCTGTC 1260 AACCCCTCTTG TTTATTGTAT TTGCTAGAC TCCTTTGACT CCCTCCTAACACCT TACAGGC TTCCCTGTC 1260 AACCTCCACT GAAAGGA TTTCTTGAC TCCTTGACT GCCACCTAGG CTCCCCTCACAGGAC AACCCACTATG TTCCTCCCTCC CCACACAGCAT AGTCAATGAG CATCTCTATG AAATCTAACC CTTCCCCTCA 1440 GGAGAAAGGA GTTTTCCCCA CCAACACACAT AGTCAATGAG AAAGGCAAC TGACGAAGAA TAAACCTTTT 1560 AACCTTCAGT GGAACTAATA TGAAATCTAT TTGCAAATTA TGGGGGGAAA TAAAGCTTTT 1560 AACCTTCAGT GGAACTAATA TGAAATCTAT TTGCAAATTA TGGGGGGAAA TAAAGCTTTT 1560 AACCTCTCAG GGAACTAATA TGGAACCAGCAT AGTCATCAGA AAAGGCAAC TGTACCAAGAA 1500 AACTTCCAGT GGAACTAATA TGGAACCAG AAGGACCC GMICNVELPT NHTNAVFAVM 180 HAQRISAGSA PTILPULAW VPVLP   Seq ID NO: 115 DNA Sequence Nucleic Acid Accession #: EO	43							
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ATARGAGTTC GGACCGCCA GCACACAGG TCAGCATGCT GCTCCTCTGT CACGCTCTCG CTATAGCTGT TGTCAGATC GTTATCTTCT CAGAAAGCTG GGCATTTGCC AAGACATCA 600 ACTTCTATAA TGTGAGGCT CCTCTGGACC CTACACCATT TCCAAAATAGC TCAAAGGGCT CTACACATAA TACACAGTAC TGTTTGACAG TTCATCACTT TCCAAAATAGC TTCAAGTGCT 660 TTACTTGTGA AAACGCAGGG GATAATTATA ACTGCAATCG ATGGGCACA GACAAATGGT 720 GTCCACAAAA TACACAGTAC TGTTTGACAG TTCATCACTT CACCAGCCAC GAACAAGCA 780 GCCGAGATTC TGAACATAC GAGTGTAGGT CTTGCTGTGA AGGAATGATC TGCACCACCAC 840 GCCGAGATTC TGAACATACG GAGTGTAGGT CTTGCTGTGA AGGAATGATC TGCAATGTAG 900 AATTACCAC CAATCACACT AATGCAGTGT TTGCCGTAAT GCACGCCCAC GAGACAACAC GCACACACCC CAATCACCAC TACCCAG TGCTTGCCTG GGTCTTTGTG CTTCCATTGC 1020 GCAGCAGTGC CCCCACACTC TACCTACCAG TGCTTGCCTG GGTCTTTGTG CTTCCATTGC 1020 ACTGCAAGGC CCACACTC TACCTACCAG TGCTTGCCTG GGTCTTTGTG CTTCCATTGC 1020 ACTGCAAGGC CCACACTC TACCTACCAG TGCTTGCCTG GGTCTTTGTG CTTCCATTGC 1020 ACTGCAGGTG CCACACTC TACCTACCAG TGCTTGCCTG GGTCTTTTGTG CTTCCATTGC 1020 ACTGCAAGGC CCAACACCAG TGGTTTGCTC GGTCTTTGTG CTTCCATTGC 1020 ACTCCAAGG GGAAAGCCAG TGGTTTGCTT GGAAAAACT 1080 ACTTCCAAGG GGAAAGCCAG TGGTTTGCTT GGAAAAACT TCCCGCATG AGGCCCAAGG AAAGAGAGCT ACGTTAGGC AGTCTCTAGA AGAGAGTCT GACTTCCAGG CTTCCTGGTC 1260 AAACAGAAGCA GTTTTCCCA AGGGCCTCAG AGAGAGTCT GACTTCCAGG CTTCCTGGTC 1260 AACCCTCTTG TTTATGTGAT TAGGTCAAGGA ATTCTTGACT CCTCTAAGAGC CTCCCCTCA 1340 TGAGAAAAGCA GTTTCCCCA CCAACAGCAT AGTCAATAGA AAAGGCAACT GTACCAAGAA 1500 AACTTCCAGT GGAACTAATA TGAAATCTAT TTGCAAATTA TGGGGGGAAA TAAAGCTTTT 1560 AAACTATACA ATGT  70 Seq ID NO: 115 Protein sequence Protein Accession #: EOS sequence  1								
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ACTICIATAA TETGAGGCCT CCTCTGGACC CTACACCATT TCCAAATAGC TTCAAGTGCT 660 TTACTTGTAA AAACGCAGGG GATAATTATA ACTGCAATCG ATGGGCAGA GACAAATGGT 720 GTCCACAAAA TACACAGTAC TGTTTGACAG TTCATCACTT CACCAGCCAC GGAAGAAGCA 780 CATCCATCAC CAAAAAGTGT GCCTCCAGAA GTGAATGTCA TTTTGTCGGT TGCCACCACA 840 GCCGAGATTC TGAACATACG GAGTGTAGGT CTTGCTGTGA AGGAATGAT TGCAATGTAG 900 AAATTACCCAC CAATCACACT AATGCAGTGT TTGCCGGTAA AGGAATGATC 960 GCAGCAGTGC CCCCACACTC TACCTACCAG TGCTTGCCTG GGTCTTTGTG CTTCCATTGC 1020 TGTGATGCAC CCATCCTAG GAGAGGCAGA GACCAGCCTC TAAAGCACAA GCCAAAAACT 1080 GTGTGAACGG TGAACTTGG AGTGAAGATC AATCTTGCAC TTGGTGAAGA GCCAAAAACT 1140 GACCTCAAGG CGAAAGCCAG TGGTTTGGTT GGATAAAAAG TTCCCCACCATG AGGCCACAGG 1200 ACTGAGGATG GGAATTTGG AGTGAAGATC AATCTTGCAC TTGCTGAGG GTGCACATTG 1140 GACCTCAAGG CGAAAGCCAG TGGTTTGGTT GGATAAAAAG TTCCCACACTAGG CTACCATGC 12200 ACTGAGGATG GGAATTTGGC AGGGCCTGAG AAGAGGATCT GACTTCCAGG CTTCCTGGTC 1260 AAAGAGAGCT ACGTTTGGGC AGTTCTGCAG AGAGGATCT GACTTCCAGG CTTCCTGGTC 1260 AAAGAGAGCT ACGTTTGGGC AGTTCTGCAG AGAGGATCT GGCAACTAGT CCCACCTGAC 1380 AACCCTCTTG TTTATGTGAT TAGCTCAGAG CATCTCTATG AAATCTAACC CTTCCCCTCA 1440 TGAGAAAAGCA GTTTTCCCCA CCAACAGCAT AGTCAATGAG AAAGGCAACT GTACGAAGAA 1500 AACTTCCAGT GGAACTAATA TGAAATCTAT TTGCAAATTA TGGGGGGGAAA TAAAGCTTTT 1560 AAAATTATACA ATGT  70 Seq ID NO: 115 Protein sequence Protein Accession #: EOS sequence 1								600
STCCACAAAA TACACAGTAC TGTTTGACAG TTCATCACTT CACCAGCCAC GGAAGAGCA								660
CATCCATCAC CAAAAAGTGT GCCTCCAGAA GTGAATGTCA TTTTGTCGGT TGCCACCACA GCCGAGATTC TGAACATACG GAGTGTAGGT CTTGCTGTGTA AGGAATGAT TGCAATGTAG 900  AATTACCCAC CAATCACACT AATGCAGTGT TTGCCTGTGA AGGAATGATCT 960  GCAGCAGTGC CCCCACACTC TACCTACCAG TGCTTGCCTG GGTCTTTGTG CTTCCATTGC 1020  TGTGATGCCA CCATTCCTAG GAGAGGCAGA GACCAGCCTC TAAAGCACAA GCCAAAAACT 1080  GTGTGAACGG TGAACTTTGG AGTGAAGATC AATCTTGCAC TTGGTGAAGA GCCAAAAACT 1080  ACTGAGGATG GGAATTTGGA GTGGATGATAG CACCTCCAGA GGCCACAGG 1200  ACTGAGGATG GGAATTTGGC AGGGCCTGA AAGATGTT GACTTCCAGG CTTCCTGGTC 1260  AAAGAGAGCT ACGTTTGGC AGGGCCTGA AAGATGTCT GACTTCCAGG CTTCCTGGTC 1260  AAAGAGAGCT ACGTTAGGC AGTTCTGCAG AGAGGATCCT GGCAACTAGT CCCACCTGAC 1320  AACCCTCTTG TTTATGTGAT TAGCTCACGA GAGAGGATCCT GCCAAGTGC TGCCAGGTCA 1380  AACCTCCTTG TTTATGTGAT TAGCTCACAG CATCCTCATG CACTCCACC TACA 1320  AACTTCCAGT GGAACTAATA TGAAATCTAT TTGCAAATTA TGGGGGGAAA TAAAGCTTTT 1560  AAATTATACA ATGT  70  Seq ID NO: 115 Protein sequence  Protein Accession #: EOS sequence  1		TTACTTGTGA	AAACGCAGGG	GATAATTATA	ACTGCAATCG	ATGGGCAGAA	GACAAATGGT	720
GCCGAGATTC TGAACATACG GAGTGTAGGT CTTGCTGTGA AGGAATGATC TGCAATGTAG 900 AATTACCCAC CAATCACACT AATGCAGTGT TTGCCGTAAT GCACGCTCAA AGAACATCTG 960 GCAGCAGTGC CCCCACACTC TACCTACCAG TGCTTGCCTG GGTCTTTGTG CTTCCATTGC 1020 TGTGATGCCA CCATTCCTAG GAGAAGCACA GACCACTC TACCTACCAG TGCTTGCCTG GGTCTTTGTG CTTCCATTGC 1020 TGTGATGCCA CCATCCTAG GAGAAGCACA GACCACCTC TAAAGCCACA GCCAAAAACT 1080 GTGTGAACGG TGAACTTGG AGTGAAGATC AATCTTGCAC TTGGTGAAGA GTGCACATG 1140 GACCTCAAGG CGAAAGCACA TGGTTTGCTT GGATAAAATG TTCCCGCATG AGGCCACAGG 1200 ACTGAGGATG GGAATTTGGC AGGCCTCGAA AAGATGGTCT GACTTCCAGG CTTCCTGGTC 1260 AAAGAGAGCT ACGTTTGGC AGGCCTCGAA AAGATGGTCT GCCAACTAGT CCCACCTGAC 1320 TAGGCCTTTA GCTGAAAGGA TTTCTTGACC TCCTTGACTG CCTCCAGGGC TGCCAGGTCA 1320 TAGGCCTTTA GCTGAATA TAGCTCAGAG CATCTCTATG AAATCTAACC CTTCCCCTCA 1440 TGAGAAAGCA GTTTTCCCCA CCAACAGCAT AGTCAATGA AAATCTAACC CTTCCCCTCA 1440 TGAGAAAGCA GTTTTCCCCA CCAACAGCAT AGTCAATGAG AAAGGCAACT GTACGAAGAA 1500 AACTTCCAGT GGAACTAATA TGAAATCTAT TTGCAAATTA TGGGGGGGAAA TAAAGCTTTT 1560 AAATTATACA ATGT  70  Seq ID NO: 115 Protein sequence Protein Accession #: EOS sequence  Protein Accession #: EOS sequence  1								780
AATTACCCAC CAATCACACT AATGCAGTGT TTGCCGTAAT GCACGCTCAG AGAACATCTG GCAGCAGTGC CCCCACACTC TACCTACCAG TGCTTGCTG GGTCTTTGTG CTTCCATTGC 1020 TGTGATGCCA CCATTCCTAG GAGAGCAGA GACCAGCCTC TAAAGCACAA GCCAAAAACT 1080 GTGTGAACGG TGAAACTTTGG AGTGAAGATC AATCTTGCAC TTGGTGAAGA GTGCACATTG 1140 GACCTCAAGG CGAAAGCCAG TGGTTTGCTT GGATAAAACT TTGCCACTAG AGGCCACAGG 1200 ACTGAGGATG GGAATTTGGC AGGCCTGAG AAGATGGTCT GACTTCCAGG CTTCCTGGTC 1260 AAAGAGAGGT ACGTTTGGGC AGGTCTGGAG AGAGAGTCCT GACTTCCAGG CTTCCTGGTC 1260 AAAGACAGCT TTGTTGGC AGTTCTGCAG AGAGGATCCT GACTTCCAGG CTTCCTGGTC 1260 AACCCCTTTA GCTGAAAGGA TTTCTTGACC TCCTTGACTG CCTCAGAGGC TGCCAGGTCA 1320 TAGGACATGA GTTTCCCCA CAACAGCAT AGTCAATGAG AAAGCAACT GTACGAAGAA 1500 AACCTCCTGT TTTATGGAT TAGGTCAGAG CATCTCTATG AAATCTAACC CTTCCCCTCA 1440 AACTTCCAGT GGAACTAATA TGAAATCTAT TTGCAAATTA TGGGGGGAAA TAAAGCTTTT 1560 AAATTATACA ATGT  70 Seq ID NO: 115 Protein sequence Protein Accession #: EOS sequence 1 11 21 31 41 51	22							
GCAGCAGTGC CCCCACACTC TACCTACCAG TGCTTGCCTG GGTCTTTGTG CTTCCATTGC   1020								
TGTGATGCCA CCATTCCTAG GAGAGGCAGA GACCAGCCTC TAAAGCACAA GCCAAAAACT 1080 GTGTGAACGG TGAACTTTGG AGTGAACATC AATCTTGCAC TTGGTGAAGA GTGCACATTG 1140 GACCTCAAGG CGAAAGCCAG TGGTTTGCTT GGATAAAATG TTCCCGCATG AGGCCACAGG 1200 ACTGAGGATG GGAATTTGGC AGGGCCTCAG AAGATGGTCT TCCCCGCATG AGGCCACAGG 1200 ACTGAGGATG GGAATTTGGC AGGGCCTCAG AAGATGGTCT GACTTCCAGG CTTCCTGGTC 1260 AAAGAGAGCT ACGTTTGGC AGTTCTGCAG AGAGGATCCT GGCAACTAGT CCCACCTGAC 1320 AACCTCTTTA GCTGAAAGGA TTTCTTGACC TCCTTGACG CTCCACAGGC TGCCAGGTCA 1380 AACCTCTTG TTTATGGAT TAGCTCAGAG CATCCTATAG AAATCTAACC CTTCCCCTCA 1440 TGAGAAAGCA GTTTTCCCCA CCAACAGCAT AGTCAATGAG AAAGGCAACT GTACGAAGAA 1500 AACTTCCAGT GGAACTAATA TGAAATCTAT TTGCAAATTA TGGGGGGAAA TAAAGCTTTT 1560 AAATTATACA ATGT  70 Seq ID NO: 115 Protein sequence Protein Accession #: EDS sequence 1								
GTGTGAACGG TGAACTTTGG AGTGAAGATC AATCTTGCAC TTGGTGAAGA GTGCACATTG 1140 GACCTCAAGG CGAAAGCCAG TGGTTTGGCT GGATAAAATG TTCCCGCATG AGGCCACAGG 1200 ACTGAGGATG GGAATTTGGC AGGGCCTGAG AAGATGGTT GACTTCCAGG CTTCCTGGTC 1260 AAAGAGAGCT ACGTTTGGC AGGGCCTGAG AAGATGGTCT GGCTACAGG CTTCCTGGTC 1260 AAAGAGAGCT ACGTTTGGC AGTTCTGCAG AGAGAGTCCT GGCAACTAGT CCCACCTGAC 1320 TAGGCCTTTA GCTGAAAGGA TTTCTTGACC TCCTTGACTG CCTCAGAGGC TGCCAGGTCA 1320 AACCTCTTG TTTATGTGAT TAGCTCAGAG CATCCTATG AAATCTAACC CTTCCCCTCA 1440 TGAGAAAGCA GTTTTCCCCA CCAACAGCAT AGTCAATGAG AAAGGCAACT GTACGAAGAA 1500 AACTTCCAGT GGAACTAATA TGAAATCTAT TTGCAAATTA TGGGGGGAAA TAAAGCTTTT 1560 AAATTATACA ATGT   Seq ID NO: 115 Protein sequence Protein Accession #: EOS sequence  1								
GACCTCAAGG CGAAAGCCAG TGGTTTGCTT GGATAAAATG TTCCCGCATG AGGCCACAGG 1200 ACTGAGGATG GGAATTTGGC AGGGCCTCAG AAGATGGTCT GACTTCCAGG CTTCCTGGTC 1260 AAAGAGAGCT ACGTTTGGGC AGTTCTGCAG AGAGGATCCT GGCACTAGT CCCACCTACA 1320 TAGGCCTTTA GCTGAAAGGA TTTCTTGACC TCCTTGACTG CCTCAGAGGC TGCCAGGTCA 1380 AACCTCCTG TTTATGTGAT TAGCTCAGAG CATCTTATG AAATCTAACC CTTCCCCTCA 1440 TGAGAAAGCA GTTTTCCCCA CCAACAGCAT AGTCAATGAG AAAGGCAACT GTACGAAGAA 1500 AACTTCCAGT GGAACTAATA TGAAATCTAT TTGCAAATTA TGGGGGGAAA TAAAGCTTTT 1560 AAATTATACA ATGT  70 Seq ID NO: 115 Protein sequence Protein Accession #: EOS sequence 1 11 21 31 41 51	60							
ACTGAGGATG GGAATTTGGC AGGGCCTGAG AAGATGGTCT GACTTCCAGG CTTCCTGGTC 1260 AAAGAAGAGC AGGTTCTGCAG AGAGGATCCT GGCAACTAGT CCCACCTGAC 1320 TAGGCCTTTA GCTGAAAGGA TTTCTTGACC TCCTTGACTG CCTCAGAGGC TGCCAGGTCA 1380 AACCCCCTTG TTTATGTGAT TAGGTCAGAG CATCTCTATG AAATCTAACC CTTCCCCTCA 1440 TGAGAAAGCA GTTTTCCCCA CCAACAGCAT AGTCAATGAG AAAGGCAACT GTACGAAGAA 1500 AACTTCCAGT GGAACTAATA TGAAATCTAT TTGCAAATTA TGGGGGGAAA TAAAGCTTTT 1560 AAAATTATACA ATGT  70 Seq ID NO: 115 Protein sequence Protein Accession #: EDS sequence 1 11 21 31 41 51	00							
AAAGAGAGCT ACGTTTGGGC AGTTCTGCAG AGAGGATCCT GGCAACTAGT CCCACCTGAC 1320 TAGGCCTTTA GCTGAAAGGA TTTCTTGACC TCCTTGACTG CCTCAGAGGC TGCCAGGTCA 1380 AACCTCTTG TTTATGTGAT TAGCTCAGAG CATCTCTATG AAATCTAACC CTTCCCCTCA 1440 TGAGAAAGCA GTTTTCCCCA CCAACAGCAT AGTCAATGA AAAGGCAACT GTACGAAGAA 1500 AACTTCCAGT GGAACTAATA TGAAATCTAT TTGCAAATTA TGGGGGGAAA TAAAGCTTTT 1560 AAATTATACA ATGT  70 Seq ID NO: 115 Protein sequence Protein Accession #: EOS sequence 1 11 21 31 41 51								
TAGGCCTTTA GCTGAAAGGA TTTCTTGACC TCCTTGACTG CCTCAGAGGC TGCCAGGTCA 1380  ACCCTCTGT TITATGTGAT TAGGTCAGAG CATCTCTATG AAATCTAACC CTTCCCCTCA 1440 TGAGAAAGGA GTTTTCCCCA CAACAGCAT AGTCAATGAGA AAAGGCAACT GTACGAGAGAA 1500 AACTTCCAGT GGAACTAATA TGAAATCTAT TTGCAAATTA TGGGGGGAAA TAAAGCTTTT 1560 AAATTATACA ATGT   70 Seq ID NO: 115 Protein sequence Protein Accession #: EOS sequence 1 11 21 31 41 51								
AACCICITE TITATGRAT TAGCICAGAG CATCICTATG AAATCIAACC CITCCCCTCA 1440 TGAGAAAGCA GITTICCCCA CCAACAGCAT AGTCAATGAG AAAGGCAACT GTACGAAGAA 1500 AACTICCAGT GGAACTAATA TGAAATCTAT TTGCAAATTA TGGGGGGAAA TAAAGCTTTT 1560 AAATTATACA ATGT  70 Seq ID NO: 115 Protein sequence Protein Accession #: EOS sequence 1 11 21 31 41 51								1380
AACTTCCAGT GGAACTAATA TGAAATCTAT TTGCAAATTA TGGGGGGAAA TAAAGCTTTT 1560 AAATTATACA ATGT   Seq ID NO: 115 Protein sequence Protein Accession #: EOS sequence  1 11 21 31 41 51	65							1440
AAATTATACA ATGT  70 Seq ID NO: 115 Protein sequence Protein Accession #: EOS sequence  1 11 21 31 41 51                           MILLITLSANL FTVPERSLIT TFSFSRYKSS DRPAHKVSML LLCHALAIAV VQIVIFSESW 60 APAKNINFYN VRPPLDPTPF ENSKCFTCE NAGDNYNCNR WAEDKWCPON TOYCLTVHHF 120 TSHGRSTSIT KKCASRSECH FVGCHHSRDS EHTECRSCCE GMICNVELPT NHTNAVFAVM 180 HAQRISGSSA PTLYLPVLAW VPVLP  80 Seq ID NO: 116 DNA sequence Nucleic Acid Accession #: Eos sequence Coding sequence: 1-1059 1 11 21 31 41 51   ATGGTATGGC AGCAAGATTA TGGAACCAGG AGAGAGCACC ATGGCTGCCG TCTGGAATTC 60								
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75  MILITISANI FTVPERSLTT TFSFSRYKSS DRPAHKVSML LICHALAIAV VQIVIFSESW APAKNINFYN VRPPLDPTPF PNSFKCPTCE NAGDNYNCNR WAEDKWCPQN TQYCLTVHHF 120 180 HAQRTSGSSA PTLYLPVLAW VPVLP  Seq ID NO: 116 DNA sequence Nucleic Acid Accession #: Eos sequence Coding sequence: 1-1059 1 11 21 31 41 51 1 1 1 21 31 41 51 1 1 1 1 60 ATGGTATGGC AGCAAGATTA TGGAACCAGG AGAGAGCACC ATGGCTGCCG TCTGGAATTC 60						41	51	
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	GGTGCTGATG	AAGAAGCTGC	AGCAAGTGAT	CCAGAAGATC	TAGCTAAGAT	CATTGATGAA	300
				AGAATCACAG			360
5				AATGTAAAAT			420
9							
	ATTATCCGAG	CICAGACTIG	GGMAAIAGIC	ATGCTTCTGG	ACCAMBIGCC	MGG1CC1GGC	480
				TTGGATAATG			540
	AAACACAAAC	CCACTGATGT	AAATATAAA	GAAACTGAAC	CAGTGTGTCT	TTTCACCATA	600
	GATATAAGAG	TTCGGACCGC	CCAGCACACA	AGAATAAAAC	AGAAAGTCTC	CATTACTTCT	660
10				TGCTTTACTT			720
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				TGGTGTCCAC			780
	ACAGTTCATC	ACTTCACCAG	CCACGGAAGA	AGCACATCCA	TCACCAAAAA	GTGTGCCTCC	840
	AGAAGTGAAT	GTCATTTTGT	CGGTTGCCAC	CACAGCCGAG	ATTCTGAACA	TACGGAGTGT	900
	VINCENTAL STATE CAL	CTCLACCAAT	GATCTGCAAT	GTAGAATTAC	CCACCAATCA	CACTAATGCA	960
15				TCTGGCAGCA			1020
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				TTGCTGTGAT			1080
	CAGAGACCAG	CCTCTAAAGC	ACAAGCCAAA	AACTGTGTGA	ACCGTGAACT	TTGGAGTGAA	1140
	GATCAATCTT	GCACTTGGTG	AAGAGTGCAC	ATTGGACCTC	AAGGCGAAAG	CCAGTGGTTT	1200
	COTTCCATAA	AATCTTCCCC	CATGAGGCCA	CAGGACTGAG	GATGGGAATT	TGGCAGGGCC	1260
20				GGTCAAAGAG			1320
20							
				TGACTAGGCC			1380
	GACCTCCTTG	ACTGCCTCAG	AGGCTGCCAG	GTCAAACCCT	CTTGTTTATG	TGATTAGCTC	1440
	AGAGCATCTC	TATGAAATCT	AACCCTTCCC	CTCATGAGAA	AGCAGTTTTC	CCCACCAACA	1500
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				SPLTSLVIVS			60
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		TGGGCAGGAG	CCAGTGATGA	CGGWWIGGCW	WICHCHIIIG	ACCICIGATO	60
15	TGTTTATTTC	CTCCTCCTTG	ACGTCTCCAT	ATAAATGTTA	CACGGGCATC	CCCACACTCG	120
45	TGTTTATTTC GATACGCACC	CTCCTCCTTG CACAGTGGCT	ACGTCTCCAT GATTCGGGGG	ATAAATGTTA TAACCGTGTC	CACGGGCATC ATTTGCTTGC	CCCACACTCG AACACTGGCA	120 180
45	TGTTTATTTC GATACGCACC CCTCTGCCCT	CTCCTCCTTG CACAGTGGCT GCACCCCGGG	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT	ATAAATGTTA TAACCGTGTC GAGTGAGGCT	CACGGGCATC ATTTGCTTGC CGGGTCTGGG	CCCACACTCG AACACTGGCA CGCTGGCTCC	120
45	TGTTTATTTC GATACGCACC CCTCTGCCCT	CTCCTCCTTG CACAGTGGCT GCACCCCGGG	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT	ATAAATGTTA TAACCGTGTC	CACGGGCATC ATTTGCTTGC CGGGTCTGGG	CCCACACTCG AACACTGGCA CGCTGGCTCC	120 180
45	TGTTTATTTC GATACGCACC CCTCTGCCCT GAATCTTCGG	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT	ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGCGG	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT	120 180 240 300
45	TGTTTATTTC GATACGCACC CCTCTGCCCT GAATCTTCGG GTCTTCCTGC	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG	ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGCGG CGAGTCTCCG	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CCGCGAGAGG	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC	120 180 240 300 360
	TGTTTATTTC GATACGCACC CCTCTGCCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CTCGCCGCCG	ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGCGG CGAGTCTCCG CCTCGGGCAC	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CCGCGAGAGG TGCCCCAGGT	CCCACACTOG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CTTGCTGCAG	120 180 240 300 360 420
45 50	TGTTTATTTC GATACGCACC CCTCTGCCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CTCGCCGCCG CGCAGACCCG	ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGCGG CGAGTCTCCG CCTCGGGCAC GTCCACACGG	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CCGCGAGAGG TGCCCCAGGT CCAGGGGCTA	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CTTGCTGCAG CGACCCTTGG	120 180 240 300 360 420 480
	TGTTTATTTC GATACGCACC CCTCTGCCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCCT	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CCGCTCAGCT	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CTCGCCGCCG CGCAGACCCG CGAGCTTCCC	ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGCGG CGAGTCTCCG CCTCGGGCAC GTCCACACGG TCGTGGCCGA	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CCGCGAGAGG TGCCCCAGGT CCAGGGGCTA CGGAACAATG	CCCACACTOG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CTTGCTGCAG CGACCCTTGG AAGGATTGCA	120 180 240 300 360 420 480 540
	TGTTTATTTC GATACGCACC CCTCTGCCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCCT	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CCGCTCAGCT	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CTCGCCGCCG CGCAGACCCG CGAGCTTCCC	ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGCGG CGAGTCTCCG CCTCGGGCAC GTCCACACGG TCGTGGCCGA	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CCGCGAGAGG TGCCCCAGGT CCAGGGGCTA CGGAACAATG	CCCACACTOG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CTTGCTGCAG CGACCCTTGG AAGGATTGCA	120 180 240 300 360 420 480
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	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGACCGC GATCTGCCCT GTAACGGATG TTAAGGCTAA	CTCCTCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CCGCTCAGGT CTCCGCAGAG AGACCTAATA	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CTCGCCGCCG CGAGACCCG CGAGACCCG CGAGACCCG CGAGACCCG CGACACCAG GTCACACCAG	ATAAATGTTA TAACCGTGTC GAGTGAGGCTG CTGGGGGGCG CCAGTCTCCG CCTCGGGCAC GTCCACACGG TCGTGGCCGA AAGGAGGATC CTACCATTT	CACGGGCATC ATTTGCTTGC CGGGTCTTGG CCTGGGGAG CCGCGAGAGG TGCCCCAGGT CCAGGGGCTA CGGAACAATG AAAAGAGGTG AAAGGAAAAA	CCCACACTOG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CTTGCTGCAG CGACCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA	120 180 240 300 360 420 480 540 600
50	TGTTTATTTC GATACGCACC CCTCTGCCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCCT GTAACGCATG TTAACGCATA ATAATCTGGT	CTCCTCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CTCCGCAGGA TTTTGGAACT TTTTGGAACT	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CTCGCCGCC CGCAGACCCG CGAGCTTCCC TGTACCGGAG GTCACCCAG GTCACCCAG GTGTTCACCG	ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGGGG CCACTCCGGCAC GTCCACACGG TCGTGGCCGA AAGGAGGATC CTIACCATTTT ATCATATGCT	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CCGCGAGAGGG TGCCCCAGGT CCACGGGCTA CGGAACAATG AAAAGAGGTG AAAGAGGTG AAAGGAAAAA GACGGTGGAG	CCCACACTOG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CTTGCTGCAG CGACCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG	120 180 240 300 360 420 480 540 600 660 720
	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCCT GTAACGGATG TTAAGGCTAA ATAATCTGGT AGTTTGGATG	CTCCTCTTG CACAGTGGCT GCACCCCGG GCTGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CCGCTCAGCT CTCCGCAGAG AGACCTAATA TTTTGGAACT GGAGAAACCT	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CTCGCCGCCG CGAGACCCG CGAGCTCCC TGTACCGGAG GTCTACACCAG GTGTTCACGG CATATCAAGC	ATAAATGTTA TAACGGTGTC GAGTGAGGCT CTGGGGGCGC CGAGTCTCCG GTCCACACGG TCGTGGCCGA AAGGAGGATC CTACCATTTT ATCATATGCT CTCTCAGAA	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CCGCAGGGT CCACGGGCTA CCACGGGCTA CAGAGACAATG AAAAGAACAA AAAAGAAAAA CACGTGGAG CCTGTCATTG	CCCACACTOS AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CGACCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCCTGGC CACCCTGGCT	120 180 240 300 360 420 480 540 600 660 720 780
50	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGACCGG GATCTGCCCT GTAACGGATG TTAAGGCTAA ATAATCTGGC AGTTTGGATG CATCAGCTTT	CTCCTCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CCGCTCAGCT CTCCGCAGAG AGACCTAATA TTTTGGAACT GCAGAAACT GCACTATGCA	ACGTCTCCAT GATTCGGGGG ACTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGACCCG CGAGACCCG CGAGCTCCC TGTACCGGAG GTCTTCACCAG GTGTTCACAG GTGTTCACAG CATATCAAGC GTGGAATTAT	ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGCGG CGAGTCTCCG GTCCACACGG TCGTGGCCGA AAGGAGGATC CTACCATTT ATCATATGC TCTCTCAGAA TTGAAGGATT	CACGGGCATC ATTTGCTTGC CCGGGTCTGGG CCTGGGGGAG CCGCAGAGG TGCCCCAGGT CCAGGGGCTA CAAAAAAAA AAAGAGTG AAAAGAAAA ACGGTGGAG CCTGTCATTG GAAGGCATTT	CCCACACTOG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCOGGTCTGC CGACCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCA TGGTCCTCA TGGTCCTCA CACCCTGGCT CCAGGGAGTAG	120 180 240 300 360 420 480 540 600 660 720 780 840
50	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGACCGG GATCTGCCCT GTAACGGATG TTAAGGCTAA ATAATCTGGC AGTTTGGATG CATCAGCTTT	CTCCTCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CCGCTCAGCT CTCCGCAGAG AGACCTAATA TTTTGGAACT GCAGAAACT GCACTATGCA	ACGTCTCCAT GATTCGGGGG ACTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGACCCG CGAGACCCG CGAGCTCCC TGTACCGGAG GTCTTCACCAG GTGTTCACAG GTGTTCACAG CATATCAAGC GTGGAATTAT	ATAAATGTTA TAACGGTGTC GAGTGAGGCT CTGGGGGCGC CGAGTCTCCG GTCCACACGG TCGTGGCCGA AAGGAGGATC CTACCATTTT ATCATATGCT CTCTCAGAA	CACGGGCATC ATTTGCTTGC CCGGGTCTGGG CCTGGGGGAG CCGCAGAGG TGCCCCAGGT CCAGGGGCTA CAAAAAAAA AAAGAGTG AAAAGAAAA ACGGTGGAG CCTGTCATTG GAAGGCATTT	CCCACACTOG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCOGGTCTGC CGACCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCA TGGTCCTCA TGGTCCTCA CACCCTGGCT CCAGGGAGTAG	120 180 240 300 360 420 480 540 600 660 720 780
50	TGTTTATTTC GATACGACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCC CCGGGACCGC GATCTGCCCT GTAACGGATG TTAAGGGTAA ATAATCTGGT AGTTTGGATG CATCAGCTTT ATAATAAAAT	CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGCT CTCCGCAGAG AGACCTAATA TTTTGGAACT GGAGAAACCT TCGCACTAGCA TCCACTAGCA TCCACTATGCA TCCACTAGTACT TCCACTAGTACT TCCACTAGTACT TCCACTAGTACT TCCACTAGTACT	ACGTCTCCAT GATTCGGGGG ACTCACCAT CGCTAGGTCG CTCGCCGCCC CGCAGCCCC CGAGCTTCCC GTTACCGGA GTCACCCAG GTGTTCACGG CATATCAAGC CTTATCAAGC CTGGAATTAT CAGCCAAACC	ATAAATGTTA TAACCGTGTTC GAGTGAGGCG CGAGTCTCCG CCTCCGGGCAC GTCCACACGG TCGTGGCCGA AAGGAGGATTTC ATCATATGCT CTTCTCAGAA TTGAAGGATT TCAACATGGA	CAOGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CGCGGAGAGG TGCCCCAGGT CCAGGGCTA CGGAACAATG AAAGAGGTG AAAGAGAGAAAA GACGGTGGAG CCTGTCATTG TAGAATGTATT	CCCACACTOS AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CAGCCCTTGC AAGGATTGCA GTGGGACCTT CCAGACCCCA TGGTCCTCAG CACCCTGGCT CCAGGAGTAG CACCCTGCT CCAGGAGTAG CGCTCTGCTG CGCCTCTGCTG	120 180 240 300 360 420 480 540 600 660 720 780 840
50	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC GATCTGCCCT GTAACGGATGG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTTT ATAATAAAAT TGAGGGCAAC	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CTCCGCAGAG AGACCTAATA TITTTGGAACT GGAGAAACCT GGAGAAACCT GCACTATGCA TCGCACTGTTT TCTGCCGGTA	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CTCGCCGCCG CGAGCCTCC CGAGCCTCC GTACCAGGG GTCACACCAG GTGTTCACAGG CATATCAAGC CTGGAATTAT CAGCCAAACC TTTGACAAAAG	ATAAATGTTA TAACGTGTC GAGTGAGGCT CTGGGGGCG CGAGTCTCCG CCTCCGGCCA AGGAGGATC CTACCATTT ATCATATGCT CTCTCAGAA TTGAAGGATT TCAACATCT TCAACATCT TCAACGAT AAGAGCTCTT	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CGCCAGGT CCACGGGCTA CCGAACAATG AAAAGAGGTAA AAAGAGAAAA AACGGAAAA AACGGAGTAA CCTGTCATTG GAAGGCATTT TAGAATGTAT AGAGTGTATT	CCCACACTOS AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CGACCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCCTGGCT CGAGGGGTT CGAGGGGTT CGAGCACTTGCT CAACACCTTGCT CAACACCTTGCT CAACACCTTGCT CAACACCTTGCT CAACACCTTG	120 180 240 300 360 420 480 540 660 720 780 840 900 960
50 55	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCCT GTAACGGATG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA	CTCCTCTTG CACAGTGGCT GCACCCCGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CTCCGCAGAG AGACCTAATA ATTTTGGAACT GGAGAAACCT GCACTATGCA TCCACTGTTT TCTGCCGGTA TCAAGAATGG	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CTCGCCGCCG CGAGACCCG CGAGACCCG GTGTACCGGAG GTCTACACCAG GTGTACACGG CATATCAAGC GTGGAATTAT CAGCCAAACC TTTGACAAAG GTCCCATATT	ATAAATGTTA TAACGGTGTC GAGTGAGGCT CTGGGGGGCG GTCCACACGG TCCTGGCCGA AAGGAGGATC TATCAATATGCT ATCAATATGCT TCAACATGGA AAGAGGATT TCAACATGGA AAGAGGATT CAACATGGA AAGAGCTCTT CAACATCGC	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CCCCCAGGT CCAGGGCTA CCAACAATG AAAAGAAAAA AAAGGAAAAA CACGTGGAG CCTGTCATTG GAAGGCATT TAGAATGTAT TAGTCTGTAT TAGTCTGTAT	CCCACACTOS AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC GCACCCTTGC AAGGATTGCA GTGGGGACTT CCAGACCCCA CACCCTGGCT CGAGGGTAG CGCCTCTGCT CGAGGGTAG CACCCTGCCT CGAGGGTTAG CGCTCTGCTC ATTCGTCCTA ATTCGTCCTA	120 180 240 300 360 420 480 540 600 660 720 780 840 900 900 960 1020
50	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCT GTAACGATA ATAATCTGGT AGTTTGGATG CATCAGCTTI ATAATAAAAT TGAGGCCAAC TGAAATTGGA CATTAGTAGATTGATTGATTGATTGATTGATTGATTGATT	CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG TGATGCAATC GCCCTGCAGCT CTCCGCAGAG AGACCTAATA TTTTGGAACT GGAGAAACCT TCTGCCGGTT TCTGCAGTT TCTGCCGGTT TCTGCCGGTT TCTGCCGGTT TCTAGCGGTT TCTAGCGGTT TCAGCAGTTT TCTAGCAGCT TCAGCAGCT	ACGTCTCCAT GATTCGGGGG ACTCACCAT CGCTAGGTCG CTCGCCGCC CGCAGACCCG CGCAGACCCG GTCACCCAG GTCTACCGAG GTCTACCAGG CATATCAAGC CTGGAAATTAT CAGCCAAACC TTTGACAAAG GTCCCATATT TCTCTTGGAG	ATAAATGTTA TAACCGTGTTC GAGTGAGGCG CGAGTCTCCG CCTCGGGCAC GTCCACACGG TCGTGGCGA AAGGAGGATC CTACCATTTT ATCATATGCT CTCTTCAGAG TTCAACATGGA AAGAGCTCTT CAACATGGA AAGAGCTCTT CAACATCGC TCAAGAAGCCC TCAAGAAGCCC TCAAGAAGCCC	CAOGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CGCGGAGAGG TGCCCCAGGT CCAGGGCTA CGGAACAATG AAAAGAGGTG AAAGAGGTG AAGGGAAAAA GACGTGGAG GAAGGAATT TAGAATGTAT TAGAATGTAT TAGATCTGTAT TACCAAAGCC	CCCACACTOS AACACTGSCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CGACCCTTGCTGCAG CGACCCTTGG AAGGATTGCA GTGGGACCTC CGGTCCTCAG CACCCTGGCT CGAGGAGTAG CGCTCTGCTG CAACAGCTTG CAACAGCTTG CATCGTCCTA CTGCTCTTG CTGCTCTTTG CTCCTTTTTG	120 180 240 300 360 420 480 600 660 720 840 900 960 960 1020
50 55	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC GATCTGCCCT GTAACGGATGG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA CATTCATTGG TACTCTTGAG TACTCTTGAG TACTCTTGAG TACTCTTGAG	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACTGTTA GCTCTGCAGAG TCTCCGCAGAG AGACCTAATA TITTTGGAACT GCAGTATACA TCGACTGTTT TCTGCCGGTA TCAAGAATGGA ACACTATGCA ACACTATGCA TCAAGAATGGA ACTGAGCT CCCAGTGGGA ACTGAGCCT	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGACCCG CGAGCTTCCC TGTACCGGAG GTCACACCAG GTGTTCACCGG CATATCAAGC CTGGAATTAT CAGCCAAACC TTTGACAAAG GTCCCATATT TCTCTTGGAG CCTTATTTT	ATAAATGTTA TAACGGTGTC GAGTGAGGCTG CTGGGGGCG CCACGGGGA TCGTGGCCGA AAGGAGGATC CTACCATTTT ATCATATAGCT CTCTTCAGAA TTCAAGGAT TTCAACGATTT CAACATCTGC AAGAGCTCTT CAACATCTGC CTACAGAA CAACATCTGC CAACATCAGC CAACATCGAACA	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CGCGAGAGGG TGCCCCAGGT CCAGGGGCTA AAAGAGGTAA AAAGAGAAAA AACGGAGAAA AACGGTGGAG CCTGTCATTG GAAGGCATTT TAGAATGTAT AGAGTGTATT TAGCTCTGTAT TACCAAAGCC CTTTAATCCA	CCCACACTOS AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CAGCCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCCTGGCT CGAGGAGTTG CACCCTGGCT CAACACCTTGCT CAACACCTTG CACCTTGCT CAACACCTTG CACCTTGCT CAACACCTTG CATTCGTCCTA CTGCTCTTTTG CTGTCCTTTTTG GTGTCCCTTTT	120 180 240 300 360 420 480 540 660 720 780 900 960 1020
50 55	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC GATCTGCCCT GTAACGGATGG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA CATTCATTGG TACTCTTGAG TACTCTTGAG TACTCTTGAG TACTCTTGAG	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACTGTTA GCTCTGCAGAG TCTCCGCAGAG AGACCTAATA TITTTGGAACT GCAGTATACA TCGACTGTTT TCTGCCGGTA TCAAGAATGGA ACACTATGCA ACACTATGCA TCAAGAATGGA ACTGAGCT CCCAGTGGGA ACTGAGCCT	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGACCCG CGAGCTTCCC TGTACCGGAG GTCACACCAG GTGTTCACCGG CATATCAAGC CTGGAATTAT CAGCCAAACC TTTGACAAAG GTCCCATATT TCTCTTGGAG CCTTATTTT	ATAAATGTTA TAACGGTGTC GAGTGAGGCTG CTGGGGGCG CCACGGGGA TCGTGGCCGA AAGGAGGATC CTACCATTTT ATCATATAGCT CTCTTCAGAA TTCAAGGAT TTCAACGATTT CAACATCTGC AAGAGCTCTT CAACATCTGC CTACAGAA CAACATCTGC CAACATCAGC CAACATCGAACA	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CGCGAGAGGG TGCCCCAGGT CCAGGGGCTA AAAGAGGTAA AAAGAGAAAA AACGGAGAAAA AACGGTGGAG CCTGTCATTG GAAGGCATTT TAGAATGTAT AGAGTGTATT TAGCTCTGTAT TACCAAAGCC CTTTAATCCA	CCCACACTOS AACACTGSCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CGACCCTTGCTGCAG CGACCCTTGG AAGGATTGCA GTGGGACCTC CGGTCCTCAG CACCCTGGCT CGAGGAGTAG CGCTCTGCTG CAACAGCTTG CAACAGCTTG CATCGTCCTA CTGCTCTTG CTGCTCTTTG CTCCTTTTTG	120 180 240 300 360 420 480 540 660 720 780 900 960 1020
50 55	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCT GTAACGGTAA ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA CATTCATTGG TACATCTTTGG TGCATCATCTTGG GGGCCAATCC	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGCT CTCCGCAGAG AGACCTAATGCA TTTTGGAACT GGAGAAACCT GCACTATTCC GCACTGTTT TCTCCCGGTA TCAAGAATGG AACTGAGGCT ACCAGTGGGA CCAGTGGGA CCAGTGGGA CAAGTATGTA	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT CGCTAGGTCG CTCGCCGCCG CGAGCTCCC TGTACCGGAG GTCACACCAG GTCTACACAG GTATCAAGC CATATCAAGC CATATCAAGC CTTGACAAACC TTTGACAAACC TTTGACAAAC CTTTGACAAAG GTCCCATATT TCTTTGGAG CCTTATTTT AGAGCCTGGA	ATAAATGTTA TAACGGTGTC GAGTGAGGCGC CCTCGGGCAC CCTCCGGCAC CTCCTCGCCAA AGGAGGATC CTACCATTT ATCATATGCT CTCTCAGAA TTCAAGGATTCAGAA ATCAACATGC TCAACATGCT CAACATCTC CAACATCTC CAACATCTC CAACATCTC CAACATCTC CAACATCTAACAAGCC CAACGGAAC AAGGTGGAAC	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CCCCAGGT CCAGGGGCTA CCGAACAATG AAAAGAAATG AAAAGAAAAA GACGATATG GAAGGCAATT TAGAATGTAT TAGAATGTAT TAGATGTATT TAGTCTGTAT TAGCAAAGCC CTTTAATCCA TGGGGACTGC TGGGGACTGC TGGGGACTGC TGGGGACTGC TGGGGACTGC TGGGGACTGC TGGGGACTGC	CCCACACTOS AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CAGCCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCTGGCT CGAGGAGTTAG CACCTTGGTCTCAG CACCTTGCTCTCAG CACCTTGCTCTCAG CACCTTGCTCTCTCAG CACCTTCTTTC ATTCGTCCTA ATTCGTCCTTA AGATGGAG AAGATGGAG	120 180 240 300 360 480 540 660 660 720 780 840 990 1020 1080 1140
50 55	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CGGGACCGC GATCTGCCCT GTAACGGATG TTAACGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTTT ATAATAAAAT TGAGGGCAAT CTGAAATTGGA CATTCATTGG TACTCTTGAG GGGCCAATCC GGAATTACGG	CTCCTCTTG CACAGTGGCT GCACCCCGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CTCCGCAGAG AGACCTAATA TTTTGGAACT GCACTATGCA TCCACTGTTT TCTGCCGGTA TCAAGAATGGA ACTGAGCCT CCCAGTGGGA ACTGAGCCT CCCAGTGGGA ACTGAGATATGGA CAGTATGTA CCAGTATGTA CCAGTATGTA CCAGTATGTA CCAGTATGTA CCAGTATGTA CCAGTATGTA CCAGTATGTA CCAGTATGTA CCACTCTCTT	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT CGCTAGGTCG CTCGCCGCCG CGAGACCCG CGAGACCCG GTGTACCGGAG GTCTACACCAG GTGTACAGG GTGTACAGG CATATCAAGC GTGGAATTAT CAGCCAAACC TTTGACAAAG GTCCCATATT TCTCTTGGAG CCTTATTTTT AGAGCCTGAA TTTGCCCAAT TTTGCCCAAT	ATAAATGTTA TAACGGTGTC GAGTGAGGCT CTGGGGGGCG GTCACACGG TCCTGGGCAC GTCACACTGT ATCATATGCT ATCATATGCT CTACAATTGT TCAACATGGA AAGAGGATT CAACATGGA AAGAGCTCTT CAACATGGC TCAACATGGA CAAGTGGAAC GTGAAGAGCC CAAGTGGAAC GTGAAGCAGT	CACGGGCATC ATTTGCTTGC CCGGTCTGGG CCGGGGGAG CCCCCAGGT CCACGGGCTA CCGAACAATG AAAAGAGAAAAA GACGTGGAG CCTGTCATTG GAAGGCATT TAGAATGTAT TAGATGTAT TAGCAAAGCC CTTTAATCCA AGGGGACTGC AGATTAATGGG	CCCACACTOS AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCOGGTCTGC GCACCCTTGC AAGGATTGCA GTGGGGACTT CCAGACCCCA GTGGGGACTT CCAGACCCCA CACCCTGGCT CGAGGGGTAG CGCCTCTGCT CAACAGCTTG ATTCGTCCTA CTGCTCTTTG GTGTCCCTTG AAGATTGCGCA AAGATGGGAG TGTCAGCAGG TGTCAGCAGG	120 180 240 360 420 480 660 720 840 900 1020 1080 1140 1200 1260
50 55 60	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTCGG GTCTTCCTGC AATCCAGCC CCGGGACCGC GATCTGCCT GTAACGGTAA ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAAC TGAAATTGGG TACTCTTGAG GGGCCAATCCG GGAATTACG GTCTTTGGGT GGGAATTACGG TCCTTGTGGCT TCCTTGGGT TCCTTGGGT TCCTTGGGT TCCTTGTGGCT TCCTTGTGGCT	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGT GCCCTCAGCG TCTCCGCAGAG AGACCTAATA TTTTGGAACT GGAGAAACCT TCTGCAGGT TCAAGAATGCA TCGACTGTTT TCTGCCGGTA TCAAGAATGG AACTGATGCA CCCAGTGGGA CAAGTATGTA CTCATCTTT CTATGGAGAG	ACGTCTCCAT GATTCGGGGG ACTCACCAC ACTCACCAC CGCAGCCCC CGCAGCCCC CGCAGCCCC CGAGCTTCCC TGTACCGGAG GTCTACCACAG GTGTTCACCGG CATATCAAGC CTTGACAAACC TTTGACAAACC TTTGACAAACC TTTGACAAAC GTCCCATATT TCTCTTGGAG CCTTATTTT AGACCTGGA TTTCCCCAAT TTCCCCAAT GCCCAAACC CCTTATTTT AGACCTGGA TTTCCCCAAT GACCATAGA	ATAAATGTTA TAACCGTGTC GAGTGAGGCG GAGTGAGGCG CCTCGGGGCC CCTCCGGGCAC CTGCGCCGAAAGGATCTCAGAAAACATTTAATCATATGCT CTCTTCAGAA TTCAACATCTGC CAACATCTGC CAACATCTGC CAACATCTGC CAAGTGGAAC AAGGTGGAAC AAGGTGGAAC AAGGTGGAAGT TCAACAGTT	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CCGCGAGAGG TGCCCCAGGT CCAGGGGCTA CGGAACAATG AAAAGAGGTG AAGGGAAAAA GACGGTGGAG CCTGTCATTG GAAGGCATTT TAGAATGTAT AGAGTGTATT TAGATGTATT TAGCTGTAT TACCAAAGCC CTTTAATCCA TGGGGACTGC AGATAATGGG AGGATAATGGG AGGATAATGGG	CCCACACTOS AACACTGGCA CGCTGGCTCGC CAGCCTTAGT GCCGGTCTGG CAGCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCCTGGCT CGAGGAGTAG CACCCTGGCT CGAGGAGTAG CCCTTGGTG CAACAGCTTG ATTCGTCCTA TTGGTCCTTG GTGTCCTTTTG GTGTCCCTGT AAGATGGGAG TGTCAGCAG TGTCAGCAG TGTCAGCAG AATCTTTTTC	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1140 1200 1220
50 55	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCT GTAACGGTTA TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTTT ATAATAAAAT TGAGGGCAAC CATTCATTGG TACTCTTGAG GGGCCAATCC GGAATTACGG GGAATTACGG TCTTGGGTT TTTACTGGAT	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACTGTTA GCTCTGCAGAG AGACCTAATA TITTTGGAACT GCACTATGCA TCGACTGTT TCTGCCGGTA TCAAGAATGGA ACTCAGCT TCCTGCTGGAAC CCACTATGCA CCACTATGCA CCACTATGCA ACTGAGCCT CCCAGTGGGA CAAGTATGTA CTCATCTCTT CTATGGAGAG AAATGAGAGA	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGCCCC CGAGCCTCC GGAGCCCG GTCTACCGGAG GTCATCACACCAG GTGTTCACAGC CATATCAAGC CTGGAATTAT TCTCCTAGAG GCCTATATTTT AGAGCCTGGA TTTGCCCAAT TTTGCCCAAT GCCATAGA GGAGAAGAGAG	ATAAATGTTA TAACGGTGTC GAGTGAGGCTG CTGGGGGCG CGAGTCTCCG CCTCCGGGCA AGGAGGATC CTACCATTT ATCATATGCT CTACCATTT TCAACGATT TCAACGATT CAACATCTC CTACATGGA AAGAGCTCTT CAACATCTGC TCAAGAAC CAAGTGGAAC AAGGTGGAAC AAGTGGAAC AACTGGCAA	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CGCGAGAGGG TGCCCCAGGT CCAGGGGCTA CGGAACAATG AAAGAGGTA AAAGAGAAA AAGGCATTT TAGAATGTAT TACCAAAGC CTTTAATCCA TGGGGACTGC AGATAATGGG AGATAATGGG GGGAACTATG TCCTCCACTA	CCCACACTOS AACACTGGCA CGCTGGCTCGC CAGCCTTAGT GCCGGTCTGC GCAGCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCCTGGCT CACACCTGGCT CAACACCTTG CACCCTGGCT CAACACCTTG ATTCGTCCTA ATTCGTCCTA CTGCTCTTTG GTGTCCCTTTT AGATGGCAG AATCTTTTTTC GATGGCATCA	120 180 240 300 360 480 540 660 660 720 780 840 900 960 1020 1080 1140 1200 1320 1380
50 55 60	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCT GTAACGGTAA ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA CATTCATTGG GGGCCAATCC GGAATTACTGGT TTTACTGGAT TTTTCAGGT TTTTCAGGT TTTTCAGGT TTTTCAGGT TTTTTCAGGT TTTTTCAGGT TTTTTCAGGT TTTTTCAGGT	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGCT CTCCGCAGAG AGACCTAATC GGAGAAACCT GGAGAAACCT TCTGCAGCT TCTGCAGTT TCTGCAGTT TCTCCCGGTA TCAAGAATGG AACTGAGCCT ACTGATCT CCCAGTGGGA CAAGTATGTA CTCATCTCTT CTATCGAGAAG AAATGAAGAT AAGTGAAGAT AAGTGAAGAT	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT CGCTAGGTCG CTCGCCGCCG CGAGACCG CGAGACCG GTCACACCAG GTCACACCAG GTCTACAGCAG GTCTACAGCAG CATATCAAGC CATATCAAGC CTTGACAACC TTTGACAAACC TTTGACAAACC TTTCTTGGAG CCTTATTTT AGAGCCTGAA TTTGCCCAAT GACCATCAGA CGCGTACATCAGA CGGGGAATAC	ATAAATGTTA TAACGGTGTC GAGTGAGGCGC CCTCGGGCAC CGTCCACACGG TCGTGGCCGA AAGGAGGATC CTACCATTT ATCATATGCT CTCTCAGAA TTCAACATGT TCAACATGCT TCAACATCTC CAACATCTC CAACATCTGC TCAAGAAGCC TCAAGAAGCC AAGGTGGAAC AAGGTGGAAC AAGGTGGAAC TCAACTAGGA TCACCTGAGT TAACTAGGA TCACTGAAGT TAACTGCGAAC TCACCTGAGT TCACCTGAGT TCACCTGAGT TCACCTGAGT TCACCTGAGT TCACCTGAGT TCACCTGAGT	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGAG CCCCAGGT CCAGGGGTA CAGACAATG AAAGGACAA GACGTGGAG CCTGTCATTG GAAGGATAT TAGAATGTAT TAGAATGTAT TACAAAGCC CTTTAATCA TGGGGACTGC AGATAATGGG GGGAACTATG GAGACTATG AGATAATGCA TGGGGACTGC AGATAATGGG GGGAACTATG ACATCAGTGG ACATCAGTGG	CCCACACTOS AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CAGCCTTGG AAGGATTGCA GTGGGACTTCA GTGGGACTCA GCACCCCA TGGTCCTCAG CACCTGGCT CAACAGCTTCA ATTCGTCCTA ATTCGTCCTA ATTCGTCCTA ATTCGTCCTTA CTGCTCTTTTC AGAGTGGAG TGTCAGCAGG AATCTTTTTC ATTCAGCAGG AATCTTTTTA CAGCAGCAAC GATGGCATCA GGTGAATTTA	120 180 240 360 420 480 540 660 660 720 780 840 900 1020 1020 1140 1200 1260 1320 1380 1440
50 55 60	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCT GTAACGGTAA ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA CATTCATTGG GGGCCAATCC GGAATTACTGGT TTTACTGGAT TTTTCAGGT TTTTCAGGT TTTTCAGGT TTTTCAGGT TTTTTCAGGT TTTTTCAGGT TTTTTCAGGT TTTTTCAGGT	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGCT CTCCGCAGAG AGACCTAATC GGAGAAACCT GGAGAAACCT TCTGCAGCT TCTGCAGTT TCTGCAGTT TCTCCCGGTA TCAAGAATGG AACTGAGCCT ACTGATCT CCCAGTGGGA CAAGTATGTA CTCATCTCTT CTATCGAGAAG AAATGAAGAT AAGTGAAGAT AAGTGAAGAT	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT CGCTAGGTCG CTCGCCGCCG CGAGACCG CGAGACCG GTCACACCAG GTCACACCAG GTCTACAGCAG GTCTACAGCAG CATATCAAGC CATATCAAGC CTTGACAACC TTTGACAAACC TTTGACAAACC TTTCTTGGAG CCTTATTTT AGAGCCTGAA TTTGCCCAAT GACCATCAGA CGCGTACATCAGA CGGGGAAGAGAG	ATAAATGTTA TAACGGTGTC GAGTGAGGCGC CCTCGGGCAC CGTCCACACGG TCGTGGCCGA AAGGAGGATC CTACCATTT ATCATATGCT CTCTCAGAA TTCAACATGT TCAACATGCT TCAACATCTC CAACATCTC CAACATCTGC TCAAGAAGCC TCAAGAAGCC AAGGTGGAAC AAGGTGGAAC AAGGTGGAAC TCAACTAGGA TCACCTGAGT TAACTAGGA TCACTGAAGT TAACTGCGAAC TCACCTGAGT TCACCTGAGT TCACCTGAGT TCACCTGAGT TCACCTGAGT TCACCTGAGT TCACCTGAGT	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGAG CCCCAGGT CCAGGGGTA CAGACAATG AAAGGACAA GACGTGGAG CCTGTCATTG GAAGGATAT TAGAATGTAT TAGAATGTAT TACAAAGCC CTTTAATCA TGGGGACTGC AGATAATGGG GGGAACTATG GAGACTATG AGATAATGCA TGGGGACTGC AGATAATGGG GGGAACTATG ACATCAGTGG ACATCAGTGG	CCCACACTOS AACACTGGCA CGCTGGCTCGC CAGCCTTAGT GCCGGTCTGC GCAGCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCCTGGCT CACACCTGGCT CAACACCTTG CACCCTGGCT CAACACCTTG ATTCGTCCTA ATTCGTCCTA CTGCTCTTTG GTGTCCCTTTT AGATGGCAG AATCTTTTTTC GATGGCATCA	120 180 240 360 420 480 540 660 660 720 780 840 900 1020 1020 1140 1200 1260 1320 1380 1440
50 55 60	TGTTTATTTC GATACGACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCC CCGGGACCGC GATCTGCCT GTAACGACTA ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA TGATCATTGG TACTCTTGAG GGGCCAATCC GGAATTCGG TCCTGTGGCT TTTACTGGGT TTTCTTCAGG	CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG TGATGCAATC GCCCTCAGCT CTCCGCAGAG TTTTTGGAACT TTTTGGAACT TCTGCCGTTA TCTGCCGGTA TCAGAGATGCA TCAGAGATGCA TCAGAGATGCA TCAGAGATGCA TCAGAGATGCA AACTATGTA CTCATCTTT CTATGGAGAG AAATAAGAA AGTGACAGAG AAATAAGAA AGTGACAAGAG AGAATACCTC	ACGTCTCCAT GATTCGGGGG ACTCACCAT CGCTAGGTCG CGCAGACCCG CGCAGACCCG CGCAGCTTCACCGC GTTACCGGA GTCTACCACA GTGTTCACAG GTGTTCACAG GTGTTCACAG GTGTCACAG GTCCAAAT TCTCTTGGAG CCTTATTTT AGACCTAGA GTCCCATATT AGACCTAGA GCATCAGA GCATCAGA GCATCAGA GCATCAGA CCGTGCATTC ACCATTGATT ACACTAGAT CACCTAGAT CACCATAGAT CACCATTAGAT CACCATTAGAT CACCATTAGAT CACCATTAGAT CACCATTAGAT CACCATTAGAT CACCATTCAGAT CACCATTCAGAT CACCATTCAGAT CACCATTCAGAT CACCATTCAGAT CACCATTCAGAT CACTAGAT CACCATTCAGAT CACCATT	ATAAATGTTA TAACCGTGTTC GAGTGAGGCG CGAGTCTCCG CCTCGGGCAC GTCCACACGG TCGTGGCGAA AAGGAGGATC CTACCATTTT ATCATATGCT CTCTTCAGAG AAGAGCTCTT TCAACATGGA AAGAGCTCTT CAACATCTGC CAACATCTGC CAACATCTGC CAAGTGGAAC AAGGTGGAAC AAGTGGAAC AAGTGGAAC TCACTGAAGT TCACTGAAGT TCACTGAAGT TCACTGAAGT AACTGCAAC AACTGCAAC AACTGCAAC AACTGCAAC AACTGCAAC AACTGCAAC AACTGCAAC AACTGCAAC AACTGCAAC	CAOGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CGCGGAGAGG TGCCCCAGGT CCAGGGCTA CGGAACAATG AAAGAGGTG AAAGAGGT GAAGGAAAAA GACGTGGAG GAAGCATT TAGAATGTAT TAGATGTAT TAGATCTATT TACCAAAGCC CTTTAATCCA TGGGGACTAT TGCGACTAT TGCTCCACTA TCCTCCACTA ACATCAGTGGA ACATCAGTGGA ACATCAGTGGA	CCCACACTOS AACACTGSCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CAGCCTTGCTGCAG CGACCCTTGG AAGGATTGCA TGGTCCTCAG CACCCTGGCT CAGCACCTTGGTCCTCAG CACCCTGGCT CAGCAGGTAG CACCCTGCTT CAGCAGGTAG ATTCGTCCTA TGGTCCTAT TGGTCCTTTG GTGTCCTGTT AAGATGGCAG AATCTTTTC GATTGGCAGG AATCTTTTTC GATTGGCATCA CGGTAAATTTA GGGAACAGAG	120 180 240 300 360 420 540 660 720 780 960 1020 1140 1200 1320 1320 1320 1440 1500
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCT GTAACGGTTG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAAC TGAAATTGGG TACTCTTGAG GGGCCAATCC GGAATTACG GTCCTTGGGT TCTTCTGGGT TCTTCTCAGG AGGTGTCAGA AGGTGTCAGA ATGACAGAT	CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG GCACGTGTA GCTCTGCAGAG AGACCTAATA TITTGGAACT GCACTAGTA TCTGCAGAG AGACCTAATA TCTGCAGAG ACACTATCA TCAAGAATGCA TCCACTAGTCA TCAAGAATGCA ACTGATGCA TCAAGAATGCA ACTGATGCA CAAGTATGTT CTCTGCAGGA AAATGAAGATA CTCATCTTT CTATGGAGAG AAATGAAGAT AGTGACAAGG GGAGTACCTC GTTTGGCTCT GTTTGGCTCT GCACTCTCT GTTTGGCTCT GTTTGGCTCT GCACTCTCT GCACTCTCT GCACTCTCT GCACTCTCT GTTTGGCTCT GCACTCTCT GCACTCT GCACT GCACT GCACT GCACT GCACTCT GCACT	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGCCCC CGAGCTTCCC TGTACCGGAG GTCTACCGGAG GTCTACCACAC GTGTTCACCGGAG CATATCAAGC CTTGACAAAC TTTGACAAAC TTTGACAAAC CTTTGACAAAC CTTTTGCCAAT TTCTCTTGGAG CCTTATTTT AGAGCCTGGA TTTGCCCAAT CACCTGGAG CGGGACAGAGAGAG CGGTGCATCC ACCATGGAT GGCATACC ACCATGGAT GGTACACCCT ACCATGGAT GGTACACCCT ACCATGGAT GGTACACCCT ACCATGGAT GGTACACCCT ACCATGGATG GGTACACCCT	ATAAATGTTA TAACGGTGTC GAGTGAGGCG CCTGGGGCGC CCTCCGGGCAC GTCCTCACACGG TCGTGGCCGA AAGGAGGATC CTACCATTTT ATCATATGCT CTCTTCAGAA TTGAAGGAT TCAACATCTGC CAACTACGGA AAGAGCTCTT CAACATCTGC CAAGTGGAAC AAGGTGGAAC GTGAAGCAGT TCACTGAGAGT TCACTGAGAGT TCACTGAGAGT ACTGGCAAGT ACTGGCAAGT ACTGGCAAC GTGACCTGGCAAC GTGTGAACAC GTGTGACAC GTGTTGACAAC GTGTTGACAAC GTGTTGACAAC GTGTTGACAAC	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCGGGTCTGGG CCCCAGGT CCAGGGGCTA CGGAACAATG AAAAGAGGTG AAGGGAAAAA GACGGTGAG CCTGTCATTG GAAGGCATTT TAGAATGTATT AGAGTGTATT TAGCCTATAT CCACAAGCC CTTTAATCCA TGGGGACTGC AGATAATGGG AGGAACTATG TCCTCCACTA ACATCAGTGG AGCCCTGGAG CCCAGGTTCCT	CCCACACTOS AACACTGGCA CGCTGGCTCGC CAGCCTTAGT GCCGGTCTGG CAGCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCCTGGCT CGAGGAGTTAG CACCCTGGCT CAACAGCTTG CAACAGCTTG ATTCGTCCTA GTGTCCTTGT GAGAGTGGA TTTTGTCCTTTTG GTGTCCTTTTG GTGTCCTTTTTC GTGTCCTGTT AAGATGGGA TGTCAGCAG AATCTTTTTC GATGGCATCA GGTGAATTTA GGGAACAGAG GATATACTGT	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1140 1200 1240 1320 1380 1440 1500 1500
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCT GTAACGGTAA ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA TACTTGAT GGGCCAATCC GGAATTACCG TCTTTGGT TTTTACTGGAT TTTTACTGGAT TCTTCCAGG AGGTGTCAGG AGGTGTCAGA TGAGAGGAT TGAGAGAGAT ACAAAGGCGA	CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGT CTCCGCAGAG AGACCTAATG TTTTGGAACT GGAGAAACCT GGAGAAACCT TCTCCGCGTA TCAGCTGTT TCTCCGGTA TCAAGATGG AACTGAGCT CCCAGTGGGA CAGTGGGA AATTAAGAAGAT AGTGACAAGG AAATTAAGAAG GGATATCT CTATCTCTT CTATGGAGAG AATTAAGAAGG GAGATACCTC GTTTGGCTCT GACAATACAC	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGACCCG CGAGCCTCCC TGTACCGGAG GTCACACCAG GTCTACAGAG GTCTACAGAG CATATCAAGC CATATCAAGC CATATCAAGC TTTGACAAAAG GTCCCATATT TCTCTTGGAG TTTGCCCAAT GACCATCAGA GACCATCAGA GACATCAGA GGAGAAGAAG CGGTGCATTC ACCATGAT ACCATCAGA CGGTGCATTC ACCATGATG CGGTACAGCC ATTCCAACTA	ATAAATGTTA TAACGGTGTC GAGTGAGGCG CGAGTCTCCG CCTCCGGGAC CGTCCACACG TCGTGGCCGA AAGGAGATC CTACCATTT ATCATATGCT CTCTCAGAA TTCAAGAA TTCAACATCT CAACATCTC CAACATCTC CAACATCTC CAAGTGGAAC AAGGTGGAAC GTGAAGCACT TCACAGAA TCACAGAA CGTGAACCACT TCACTGAAGT	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCGGGGGGGG CCCCAGGGT CCAGGGGCTA CCGAACAATG AAAAGAATG AAAAGGAAAA AAGGAAAA AAGGAATAT TAGAATGTAT TAGAATGTAT TAGAATGTAT TACCAAAGC CCTTTAATCCA TGGGGACTGC AGATAATGGG GGGAACTATG ACATCAGTGG AGCCTTGCATA ACATCAGTGG AGCCCTGGAG ACCCTGGAG ACCCTTGAAGCC TCCCACTTAACCCT TCCTAAGCTG ACCCTTGAAGC CCCAGTTTCT TCCTAAGCTG	CCCACACTOS AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CAGCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCCTGGCT CAACAGCTTGCT CAACAGCTTG ATTCGTCCTA ATTCGTCCTTA ATTCGTCCTT AAGATGGAG TGTCCCTGTT CAGCAGG AATCTTTTT CATGGCAGG AATCTTTTTT GGGAACAGAGT GGTGAATTTA GGGAACAGAG GGTAATTTTA GGGAACAGAG GATATACTGT GCAAGCCCCA	120 180 240 300 360 480 540 660 660 720 780 840 990 1020 1140 1200 1320 1380 1440 1560 1560 1620
50 55 60	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCT GTAACGATA ATAACGCTA ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGCCAAC TGAAATTGGA CATTCATTGG TACTCTTGAG TCCTGTGGCT TTTACTGAT TTCTTCAGGA AGGTGTCAGA AGGTGTCAGA AGGAGAGAT ACAAAGGCA ACAAAGGCA ACAAAGCGAA TCTTGAGCAA	CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG TGATGCAATC GCCCTGCAGCT CTCCGCAGAG AGACCTAATA TTTTGGAACT TCTGCAGT TCGACTGTT TCTGCCGGTA TCAAGAATGC AACTATGCA CCCAGTGGGA CAAGTATGTA TCAAGAATGG AACTATGTA CTCATCTTT CTATGGAGAG AAATCAAGAT AGTGACAAGG GAGATACTC GTTTGGCAGTA GAGATACTC GTTTGGCAAGG GAGATACTC GTTTGGCAAGAG GAGATACTC GTTTGGCAAGAG GAGATACTC GTTTGGCAAGAG AAATCAAGAT AGTAGCAAGAG GAGATACTC GTTTGGCTCTT GACAATACACA	ACGTCTCCAT GATTCGGGGG ACTCACCAT CGCTAGGTCG CGCAGACCCG CGCAGACCCG CGCAGACCCG CGCAGACCCG CGCAGACCCG CGTTACCGGG GTCACACCAG GTGTTCACAG CATATCAAGC CTTGACAAAC TTTGACAAAC TTTGACAAAC CTTATTTT ACGCCATATT TCTCTTGGAG CCTTATTTT AGACCTAGA GACCATCAGA GACAATCAGA GACAATCAGA CGGTGCATTC ACCATGGATG ACCATGGATG ATTCCAACTA ATTCCAACTA ATTCCAACTA	ATAAATGTTA TAACCGTGTTC GAGTGAGGCG CGAGTCTCCG CCTCGGGCAC GTCCACACGG TCGTGGCGAA AAGGAGGATC ATCATATGCT CTCTTCAGAA TTCAACATGGA AAGAGCTCTT CAACATCGC TCAACATGGA AAGAGCTCTT CAACATCTGC TCAAGAAGCC CAAGTGGAAC AAGTGGAAC AAGTGGAAC ATCACTGCACTCTCAACATCTGACTTCAACATCTGCACTCTCAACATCTGACTCTCAACTCTCTTTTCTTC	CAOGGGCATC ATTTGCTTGG CGGGTCTGGG CCTGGGGGAG CGCGAGAGAG CGCACAGT CCAGGGCTA CGGAACAATG AAAAGAGGT AAAGAGGT AAAGAGGT TAGAATGTAT TAGATGTAT TAGATGTAT TACCAAAGCC CTTTAATCA TGGGGACTGC AGATAATGGG GGGAACTATG TCCTCACTA ACATCACTGGAG ACCCTGGAG ACCCTGGAG ACCCTGGAG ACCCTGAAGCT CCCAGTTTCT CCCAGTTGCT GAGCCACTGG	CCCACACTOS AACACTGSCA ACACTGSCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CGACCCTTGG AAGGATTGCA GTGGGACCTCA TGGTCCTCAG CACCCTGGCT CGAGCAGCTTG CAACAGCTTG CAACAGCTTG CAACAGCTTG ATTCGTCCTA CTGCTCTTTG GTGTCCCTGT AAGATGGGAG ATCTTTTTC GATTGGCATC GATTGGATTA GGGAACTTG AAGATGGAG AATCTTTTT GGGAACAGAG GATATACTGT GCAAGCGCA ACAATTGTGC AACAGCGCA ACAATTGTGC	120 180 240 360 420 480 660 660 720 780 840 900 1020 1140 1200 1260 1380 1380 1440 1500 1620 1680
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTCGG GTCTTCCTGC AATCCAGCC CCGGGACCGC GATCTGCCT GTAACGGTA ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA GGGCCAATCC GGAATTACGG TCCTTGAG GGAATTACG GAATTACG TCCTTGAG TCTTCACGAT TTTACTGAT TTTACTGAT TTTACTGAT TTTTCACGAT TTTTCTCAGG ACGTGTCAGA TCTTGAGGAT ACAAAGGCGAA TCTTGAGGAT TCTTGAGGAT TCTTGAGGAT TCTTGAGGAT TCTTGAGGAATTACCGAAT TCTTGAAT	CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG GCTGGCAGTG CCGCTCAGCT CTCCGCAGAG AGACCTAATA TTTTGGAACT GGAGAAACCT TCTGCCGGTA TCTACGAGT TCAAGAATGCA TCGACTGTTT TCTGCCGGTA TCAAGAATGGA AACTATGCA CCAGTGGGA CAAGTATGTA CTCATCTT CTATCGAGAG AATGAAAGAT AGTGACAAGG GGAGAACCTC GTTTGGCTCT GACAATTACAGA ATTAACTGA ATTAACTGA	ACGTCTCCAT GATTCGGGGG ACTCACCAC ACTCACCAC CGCTAGGTCG CGCAGACCCG CGCAGCCCG CGCAGCCCG CGCAGCCCG CGCACCCG CGCACCCG CGCACCCG CGCACCCG CTTTCACCGGA GTGTTCACGG CATATCAAGC TTTGACAAAG CTCCCATATT TCTCTTGGAG TTTCCCCAAT TTGCCCAAT TTGCCCAAT GACCATCAGA CGGTGCATTC ACCATGGAT ACCATGGAT ATTCCACTAC ATTCCACTAC ATTCCACTAC ATTCCACTAC ATCCACTATAT CGGATACCATTAG GGATACCATTAG GGA	ATAATGTTA TAACGGTGTC GAGTGAGGCG CCTGGGGCGC CCTCCGGGCAC CTGTGGCCGA AAGGAGGATC CTACCATTT ATCATATGCT CTCTTCAGAA TTGAAGGAT TCAACATCTGC CAACATCTGC CAACATCTGC CAACTCGGAAC AAGGGGAGT TCAACATCGC CAACTGGAA AAGGTGGAAC AAGTGGAAC AAGTGGAAC GTGAACTTTCACAAG TCACTGAAGT TCACTGAAGT TCACTGAAGT TCACTGAAGT ACTGGCAAC GTGTTGTTTG TGGAGAATGG GAAGAAGAGA	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCGGGTCTGGG CCCCAGGT CCAGGGGCTA CGGAACAATG AAAAGAGGTG AAGGCAATTT TAGAATGTATT AGAGTGTATT TAGATGTATT TACCAAGCC CTTTAATCCA AGATAATGGG AGATAATGGG AGATAATGGG CGCACTGGGG CCCAGTTTCT TCCTAAGCTG GAGCGACTGG GAGCCACTGG	CCCACACTOS AACACTGSCA AACACTGGCA CGCTGGCTCGC CAGCCTTAGT GCCGGTCTGC CAGCCCTTGG AAGGATTGCA GTGGGGACTT CCAGGACCCCA TGGTCCTCAG CACCCTGGCT CGAGGAGTAG CCCTTGGTCAACAGCTTG AACAGCTTG ATTCGTCCTA ATTCGTCCTA AGGATGGGAG TGTCAGCAG AACATTTTC GATGGCATCA GGGAACAGAG GATATACTGT GCAAGCCGCA ACAATTGTGC CTATGTGCTACT CGTATGTACTACT CGTATGTACT CGTATGTACTACT CGTATGTGCC CTATGTGCCTACT CGAGCCCCCA ACAATTGTGC CGTATGCTACT	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1500 1500 1680 1740
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTGCCT GAATCTGCCT GATCTGCCT GATCTGCCT GTATCGGCT GTATCGGCT GTATCGGTT TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTTT ATAATAAAT TGAGGGCAAC GGAATTACGG GGCCAATCC GGAATTACGG TCTTCTTGGAT TCTTCCAGG AGGTGTCAG TGTTCTTCAGGAT TCTTCAGGAT TCTTCAGGAT TCTTCAGGAT TCTTGAGCAA TACCTGAAT GGGACAGACT	CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG GCACGTGTA GCCACTGTA CCCCCAGAG AGACCTAATA TITTGGAACT GCACTATGCA TCCACCAGT TCTCCCGCAGAG AGACCTAATA TCTAGCAC TCCACCAGT TCACGGTA TCAAGAATGG AACTGAGCCT CCCAGTGGGA CAAGTATGTA CTCATCTCTT CTATCGCAGAG AAATGAAGAT GGAATACAC GGAATACAC GTTTGGCTCT GACAATACAC ATTAACTGAT GGAAATACAC GTTGCATTTG GGAAATACAC GTTTGCATTTG GGAAATACAC GTTTGCATTTG	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGCCCC CGAGCCTCC CGAGCCTCC CGAGCCTCC CGAGCCTCC CGAGCCTCC CGAGCCTCC CGAGCTTCACCGAG GTCTTCACCGGAG CATATCAAGC CTTGACAAACC TTTGACAAACC TTTGACAAACC TTTGACAAACC TTTGCCAATAT TCTCTTGGAG CCCTTATTTT AGAGCCTGAA CGGTGCATAC ACCATGGAG GGAGAAGAAG CGGTGCATC ACCATGGAT ATTCCACTTATC ATTCTGATA	ATAATGTTA TAACGGTGTC GAGTGAGGCG GAGTGAGGGCG CCTCGGGGAC GTCCACACGG TCGTGGCCGA AAGGAGATC CTACCATTT ATCATATGCT CTATCAGAA TTGAAGGAT TCAACATCTGC TCACATGGA AAGACTCTT CAACATCTGC TCAGAAA AAGACCTCTT CAACATCTGC TCAGAAACACACG GTGAACAGAC GTGAAGAGC ACTTGAAGA GAGACAACAACA GTGAAATAGAG GAAGACAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCGGGTCTGGG CCGCGAGAGG TGCCCCAGGT CCAGGGGCTA CGGAACAATG AAAAGAGGTGA AAAGAGAAAA AACGGTGTAATT TAGAATGTAT TACCAAAGC CTTTAATCCA TGGGGACTAC TCCCACTA ACATCAGTG TCCTCCACTA ACATCAGTG AGCCATTAT TCCTAAGCT TCCTCACTA ACATCAGTG CCCAGTTTCT TCCTAAGCT GGGAACTGC GGAACACT GGGACTACT GGGCCACTG GGACCACTG GGTACCTAACT GCTACCTGTG GCTACCTGTG	CCCACACTOS AACACTGGCA CGCTGGCTCGC CAGCCTTAGT GCCGGTCTGG CAGCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCCTGGCT CGACCCTGGT CACCCTGGTC CACCCTGGTC CACCCTGGTC CACCCTGGTC CACCCTGGTC CACCCTGGTC CACCCTGGTC CACCCTGGTC CACCCTGCTG CACCCTGCTG CACCCTGCTG CATCGCTCTTTG CGTCTCTTTG CTGTCCTCTT AAGATGGGAG TGTCAGCAGG GATATTTTTC GATGGCATCA GGGAACAGAG GGAACAGAG GGAACAGAG GGAACAGAG GGAACAGAG CAATTGTGC CATAATGTAG CATGCTCTC CATAATGTAG	120 180 240 300 360 420 660 660 720 780 840 1020 1140 1200 1320 1380 1440 1500 1660 1620 1680
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTGCCT GAATCTGCCT GATCTGCCT GATCTGCCT GTATCGGCT GTATCGGCT GTATCGGTT TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTTT ATAATAAAT TGAGGGCAAC GGAATTACGG GGCCAATCC GGAATTACGG TCTTCTTGGAT TCTTCCAGG AGGTGTCAG TGTTCTTCAGGAT TCTTCAGGAT TCTTCAGGAT TCTTCAGGAT TCTTGAGCAA TACCTGAAT GGGACAGACT	CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG GCACGTGTA GCCACTGTA CCCCCAGAG AGACCTAATA TITTGGAACT GCACTATGCA TCCACCAGT TCTCCCGCAGAG AGACCTAATA TCTAGCAC TCCACCAGT TCACGGTA TCAAGAATGG AACTGAGCCT CCCAGTGGGA CAAGTATGTA CTCATCTCTT CTATCGCAGAG AAATGAAGAT GGAATACAC GGAATACAC GTTTGGCTCT GACAATACAC ATTAACTGAT GGAAATACAC GTTGCATTTG GGAAATACAC GTTTGCATTTG GGAAATACAC GTTTGCATTTG	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGCCCC CGAGCCTCC CGAGCCTCC CGAGCCTCC CGAGCCTCC CGAGCCTCC CGAGCCTCC CGAGCTTCACCGAG GTCTTCACCGGAG CATATCAAGC CTTGACAAACC TTTGACAAACC TTTGACAAACC TTTGACAAACC TTTGCCAATAT TCTCTTGGAG CCCTTATTTT AGAGCCTGAA CGGTGCATAC ACCATGGAG GGAGAAGAAG CGGTGCATC ACCATGGAT ATTCCACTATAT ATTCCACTATAT ATTCCACTATAT ATTCCACTATAT ATTCCACTATAT ATTCCACTATAT ATTCCACTATAT AATTCCACTATA	ATAATGTTA TAACGGTGTC GAGTGAGGCG GAGTGAGGGCG CCTCGGGGAC GTCCACACGG TCGTGGCCGA AAGGAGATC CTACCATTT ATCATATGCT CTATCAGAA TTGAAGGAT TCAACATCTGC TCACATGGA AAGACTCTT CAACATCTGC TCAGAAA AAGACCTCTT CAACATCTGC TCAGAAACACACG GTGAACAGAC GTGAAGAGC ACTTGAAGA GAGACAACAACA GTGAAATAGAG GAAGACAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCGGGTCTGGG CCGCGAGAGG TGCCCCAGGT CCAGGGGCTA CGGAACAATG AAAAGAGGTGA AAAGAGAAAA AACGGTGTAATT TAGAATGTAT TACCAAAGC CTTTAATCCA TGGGGACTAC TCCCACTA ACATCAGTG TCCTCCACTA ACATCAGTG AGCCATTAT TCCTAAGCT TCCTCACTA ACATCAGTG CCCAGTTTCT TCCTAAGCT GGGAACTGC GGAACACT GGGACTACT GGGCCACTG GGACCACTG GGTACCTAACT GCTACCTGTG GCTACCTGTG	CCCACACTOS AACACTGSCA AACACTGGCA CGCTGGCTCGC CAGCCTTAGT GCCGGTCTGC CAGCCCTTGG AAGGATTGCA GTGGGGACTT CCAGGACCCCA TGGTCCTCAG CACCCTGGCT CGAGGAGTAG CCCTTGGTCAACAGCTTG AACAGCTTG ATTCGTCCTA ATTCGTCCTA AGGATGGGAG TGTCAGCAG AACATTTTC GATGGCATCA GGGAACAGAG GATATACTGT GCAAGCCGCA ACAATTGTGC CTATGTGCTACT CGTATGTACTACT CGTATGTACT CGTATGTACTACT CGTATGTGCC CTATGTGCCTACT CGAGCCCCCA ACAATTGTGC CGTATGCTACT	120 180 240 300 360 420 660 660 720 780 840 1020 1140 1200 1320 1380 1440 1500 1660 1620 1680
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCT GTAACGGTAG TTAAGGCTAA ATAATCTGGT AGTTTGGAT AGTTTGGAT ATAATAAAAT TGAGGGCAAC TGAAATTGGA TACTTGGAT TATACTGGAT TTTTACTGGAT TTTTACTGGAT TCTTCAGG AGGTGTCAGA TGAGAGAGAT ACAAAGGCGA TCTTGAGCAA TATCCTGAGC TATCCTGAGC TCTTGAGCAA TTTGAGCAA TTTGTAGTAT TTTTACTGACT TTTTACTGACAA TCTTGAGCAA TTTTGAGCAA TTTGAGCAA TTTTGAGCAA TTTGAGCAA TTTTGAGCAA TTTTT	CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTAA GCTCTGGAG AGACCTAATC CTCCGCAGAG AGACCTAATC GGAGAAACCT TCTGCAGTT TCTGCCGGTA TCAAGATGG AACTGAGCT TCCACAGTGTT TCTACCAGGA ACACTGATGCA TCAATTATGAA CTCATCTCTT CTATGGAGAG AAATGAGAG AAATGAAGGT GGAAATACAC ATTAACTGAT GGAAAATACAC ATTAACTGAT GGAAAATACAC ATTAACTGAT GGAAAATACAC ATTAACTGAT CTCATTTTTC	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGACCCG CGAGCCTCCC TGTACCGGAG GTCACACCAG GTCACACCAG GTGTACAGAG CATATCAAGC CATATCAAGC CATATCATGAC CCTTCTTGGAATTAT TCTCTTGGAG TTTGCCCAAT GACCATCAGA GGAGAAGAG CGGTGCATCC ACCATGATG ACCATCAGA GGAGAAGAG CGGTGCATTC ACCATGATG ACCATCAGA AGGAGTACACC ATTCCAACTA ATCCAACTA ATCCAACTAT ATCCAACTA ATCCAACTAT CAAGAGTGAT CAAGAGTGAT	ATAAATGTTA TAACGGTGTC GAGTGAGGCGC CCTCGGGCAC CTCCGGGCAC GTCCACACGG TCGTGGCCGA AAGGAGGATC CTACCATTT ATCATATGCT CTCTCAGAA TTCAAGAGATT TCAACATCT CAACATCTC CAACATCTC CAAGTGGAAC AAGGTGGAAC AAGGTGGAAC AAGTTGGAAGT TCACTGAAGT TCACTTCTTT TGGACAATTGG GAAAATTAGAG GATTTCTTCAC TGTTTCTTCA	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCGGGTCTGGG CCCCAGGT CCACGGGCTA CCGAACAATG AAAGGACAAA AAAGGAAAA AAAGGAAAA AAAGGAATT TAGAATGTAT TAGAATGTAT TACCAAAGCC CTTTAATCCA TGGGGACTGC AGATAATGG GGGAACTATG ACATCAGTG ACATCAGTG ACATCAGTG ACATCAGTG AGCCCTGGAG ACCCTGGAG AGCCCTGGAG AGCCACTGG AGCCACTGC AGCCACTG	CCCACACTOS AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CAGCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCCTGGCT CCAGGAGTTAG CACCCTGGCT CACAGGCTCTCTCTA ATTOGTCCTA ATTOGTCCTA ATTOGTCCTT AAGATGGAG TGTTCCCTGTT CATGGCAGG AATCTTTTTC GATGGCAGG AATCTTTTTC GATGGCAGG AATCTTTTTC GATGGCAGG AATCTTTTTC GATGGCAGG AATCTTTTTC GATGGCAGG AATCTTTTTC CATGGCAGG CATTAACTTTC CATAGCTACT ACAATTGTGC CTATATGTAG AATGAATTGC AATGAATTGC AATGAATTGC	120 180 240 300 360 420 660 660 720 780 840 900 1020 1140 1200 1320 1380 1440 1500 1560 1620 1680 1740 1860
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCC CCGGGACCGC GATCTGCCT GTAACGGATG TTAAGGATG ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAACC TGAAATTGGG TACTCTTGAG GGGCAATCA GGAATTACGGT TTTCTTCAGG AGGTGTCAGA TCTCTCAGG AGGTGTCAGA TCTTGAGAATTGCTTTACTGAT TTCTTCAGG AGGTGTCAGA TCTTGAGCAA TCTTGAGCAA TCTTGAGAATTACGCTTTTCTCAGAT ACAAACGCGAA TCTTCTAGATT TTCTTAGATTAAAAT TTTGTAGTAT AATCATCAAA	CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG GCTGGAGCG GCCACGTGTA GCTCTGCAGCT CTCCGCAGAG AGACCTATGCA TTTTGGAACT TCTGCAGTT TCTGCAGTT TCTGCAGTT TCTGCAGTT TCTGCAGTT TCTAGAGATGC AACTATGAA ACTCATTCT CTATGGAGAG AAATATGTA AGTGACAAGG GAGATACCTC GACTATGCA GAGATACTCT GACAATACGAG ATTAACTGAT ATTGCATTGC	ACGTCTCCAT GATTCGGGGG ACTCACCAT CGCTAGGTCG CGCAGCCCC CGAGCCCCC CATATCAAGC CTTATCAAGC CCCATATT TCTCTTGGAG CCCTATTTT AGACCCTGGA TTCCCACTAT GACCATCAGA CGGAGAAGAG CGGTGCATTC ACCATGGATG ACCATCAGATG ACCATCAGT ATTCCACTT ATTCCACTT AGCACTATG AATTCTAATT CAAGAGTAT CAAGAGTGAT CAAGAGTGAT CAAGAGTGAT TAACTTGGTA	ATAAATGTTA TAACCGTGTTA TAACCGTGTTC GAGTGAGGCG CGAGTCTCCG GCCCACACGG TCGTGGCGAA AAGGAGGATT ATCATATGCT CTTCTCAGAA ATTGAAGGATTTCAACATGGA AAGAGCTCTT CAACATCTGC TCAAGAAGCC CAAGTGGAAC AAGTGGAAC AGGTGGAAC AGGTGGAAC TCACTGAAGT TCACTGAAGT TCACTGAAGT TCACTGAAGT TCACTGAAGT TCACTGAAGT TCACTGAAGT TCACTGAAGT AACTGGCAAC GGGAAGAAGA GGAATTCTTTG GGAAGAAGA GAAAATAGAG GATTTCTTTCA GTAGTAACTT TGTTTCTCACAG GTAGTTACTTTCACAGAC GAAGAAGAG GAAAATAGAG GAAATTCTTTCACAGAC GGATTTCTTCACAGC GTAGTTACTTCACAGC GTAGTTACTTCACACACACACACACACACACACACACACA	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CCGCGAGAGAG CCGCAGGT CCAGGGCTA CGGAACAATG AAAGAGGTG AAAGAGTG AAAGAGTT TAGAATGTATT TAGATGTATT TAGATGTATT TACCAAAGCC CTTTAATCCA TGGGGACTAT TCCTCCACTA ACATCAGTGG ACCTCTAGTGGG CCCAGTTCT TCCTAGCTGGG CCCAGTTCT TCCTAACCT GAGCCACTGGG GATACCTGTG GATACCACT TCCTGAGAA ACCTTACCT TCCTGAGAA ACCTTACCT TCCTAGACT TCCTAACCT TCCCTAGGAAA ACCTTACCT TCCCTAGGAAA ACCTTACCT TCCCTAGGAAA ACCTTACCT TCCCAGAGAA ACCTTACCT TCCGAGGAAA ACCTTACCT TCCTAGGAGAA ACCTTACCT TCCTAGCT TCCTAGGAGAA ACCTTACCT TCCTAGGAGAA ACCTTACCT TCCTAGCT TCCTA	CCCACACTOS AACACTGSCA AACACTGSCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CAGCCCTTGG AAGGATTGCA GTGGGACCTCA TGGTCCTCAG CACCCTGGCT CAGACCCCA TGGTCCTCAG CACCCTGGCT AACAGCTTG ATTCGTCCTA ATTCGTCCTA TGTCCTGT AACAGCTTG CACCAGGAACAGCAG AATCTTTTC GATTGCAGCAGG AATCTTTTTC GATAGCATCA GGGAACAGAG GATATACTGT GCAAGCCGCA ACAATTGTGC GTATGCTACT CATAATTGTGC ATTGAATTGC ACTAATTGTAC ACCTAGAATAA	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1500 1560 1680 1740 1800 1860 1920
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCT GTAACGGTG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGCAAC GGAATTACGG TACTCTTGAG GGGCCAATCC GGAATTACGG TCTTCACGAA TCTTCACGAA TCATCAGAT TCTTCACGAA ACATAGCAA CGGACAGACT TTTGTAGTAA AATCATCAAT AATCATCAAA ACATTAATGT ACATTAATGT AATCATCAAA ACATTAATGT	CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG GCTGGGAGAG GCACGTGTA GCTCTGCAGAG AGACCTAATA TITTGGAACT GCACTATCA GCACTATCA TCACAGAGT TCACAGAGT TCACAGAGT TCACAGAGT ACTAGGCA AACTATGA AACTAGGCA CAAGTATGA AATGAAGAT GGACTACTCT CTATGGAGAG AAATGAAGAT AGTGACAAGG GAGATACCTC GTTTGGCTCT GACAATTACCA ATTAACTGAT GGAAATACAC ATTAACTGAT GGAAATACAC ATTAACTGAT GGAAATAGAG GTTGCATTTG CAATGTTTA CAATGTTTA AGGCAATATAA	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGCCCC CGAGCCTCC CGAGCCCCC CGAGCTTCCC TGTACCGGAG GTCATCACACAC GTGTACCACAC GTGTACCAGA GTGTTCACAG GTGTACTAAGC CTTGACAAAC TTTGACAAAC TTTGACAAAC CTTTGACAAAC CTTTGACAAAC CCTTATTTT AGAGCCTGAA TTTCCCCAAT TTCCCCAAT GACCATCAGA GGAGAAGAAG CGGTGCATTC ACCATGGAT ATTCCAGTAA ATTCCAGTAA TCAGTAAT CAAGAGTGAT AATTGTGATA AACTTGGTA TAACTTGGTA ACATGGGATT TAACTTGGTA	ATAATGTTA TAACGGTGTC GAGTGAGGCG GAGTGAGGCG CCTCGGGGCG CCTCGGGCGA TCGTGGCCGA AGGGAGTCTCTC CTCTCAGAA TTGAAGGAT TTCAACATCTGC CAACATCTGC CAACATCTGC CAACATCTGC AAGGAGCTCTT CAACATCTGC CAACTGGAAC AGGTGGAAC AGGTGGAAC GTGAAGCAGT TCACTGAGA ACTTGCCAAC GTGTTGTTTG TGGAGAAT TGGAGAATGG GAAGAGAAG GAAATAGAG GAATTCTTTC TGTTTCTTCA TGTTTTTTTTTT	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCGGGTCTGGG CCCCAGGT CCAGGGGCTA CCGAACAATG AAAAGAGGTG AAAGAGGTG GAACAATT AGAGTGTATT TAGAATGTATT TAGATGTATT TACCAAAGC CTTTAATCCA TGGGGACTATG GGGAACTATG TCCTCACTA ACATCAGTGG AGCCCTGGG AGCCCTGGA ACCCTGCAT TCCTAAGCT GCTACCTAC TCCTAAGCT GCTACCTTACT TCCTAAGCT GCTACCTTACT TCCTAAGCT GATACCAACT GATACCAACT GCTACCTTT TCCTAAGCT GCTACCTTT TCCTAAGCT GCTACCTTACT TCCTAAGCT GCTACCTTT TCCTAAGCT GCTACCTTT TCCTAAGCT TCCTAAGCT GCTACCTT TCCTAAGCT TCCTACT TCCTAAGCT TCCTACT TCCTAAGCT TCCTACT TCCTTACCT TTTTTTAGTC TCCTCT TCCTGGGAACT TCCTTACCT TCCTTACCT TCCTTACCT TCCTTACCT TCCTTACCT TCCTTACCT TCTTACT TCTTTACT TCTTACT TCTTTACT TCTTACT TCTTTACT TCTTTACT TCTTTACT TCTTTACT TCTTTACT TCTTTTTT TCTTACT TCTTTTT TCTTACT TCTTTTT TCTTACT TCTTTT TCTTTT TCTTTT TCTTTT TCTTTT TCTTTT TCTTTT T	CCCACACTOS AACACTGGCA ACACTGGCA CGCTGGCTCGC CAGCCTTAGT GCCGGTCTGC GCAGCCTTGG AAGGATTGCA GCGACCCCA GGGCCCCA GGGCCCTAGGT CCAGACCCCA GGTCCTCAG CACCCTGGCT CGAGGAGTAG CGCTCTGCTG AACAGCTTG AACAGCTTG AACAGCTTG AACAGCTTG AAGATGGGAG TGTCCCTGTTA GGGAACAGG GATATACTGT GCAAGCCGCA ACAATTGTG CATAATGTAG AATGAATTGA CATAATGTAG AATGAATAGC CACCTGGAAAAA CTCCTTTTGT	120 180 240 300 360 420 540 660 660 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1500 1620 1680 1640 1740 1860 1860 1920
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTGCCT GAATCTGCCT GAATCTGCCT GATCTGCCCT GTATCGGCT GTACGGATCG GTTTGCCT GTAACGGTA TTAAGGCTAA ATAATCTGGT AGTTTGGAT CATCAGCTAT ATAATAAAAT TGAGGGCAACC GGAATTACGG TACTCTTGAG GGGCCAATCC GGAATTACGG TCTTGTGGT TTTACTGGAT TCTTCAGG AGGTGTCAGA ACAAAGGCGA TCTTGAGCAA TCTTGAGCAA TGGGACAGCT TTTGTAGTAT ACTTGAGTAT AATCATCAAA ACATTAATGA ACTTCACTCA	CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGT CCCCCAGAGT TCTCGCAGAG AGACCTAATA TITTTGGAACT GGAGAAACCT GCACTATGCA TCCACCTGT TCTGCCGGTA TCAAGAATGC ACTGATGCT CCCAGTGGTA CCACTGTTT CTTCTCGGGA AAATAGAAGAT AGTGACAAGG GAGATACCTC GTTTGGAGAG AAATAGAAGAT AGTGACAAGG GAGATACCTC GTTTGGCTCT GACAATACAC ATTAACTGAT GGAAAATAGA GGTTGCATTTG CAATGTTTA AGGCATTAAA	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGCCCC CGAGCCTCC CGAGCCCCC GGAGCCCG GTCTCCACCACC GTTTCACCGGAG GTCATCACACCAG GTCTTCACAGG CATATCAAGC CATATCAAGC CTTGACAAACC TTTGACAAACG TTTGACAAACG TTTGACAAACG TTTGCCCATATT TCTCTTGGAG CCTTATTTTT AGAGCCTGGA TTTGCCCAAT ATCCACTAGAA GGACAACACC ATTCCACTAGAA GGACAACCAT ACCATGGATG ATTCCACTATAT ATCCAGTATG ATTCCACTATAT ATCCAGTATG AATTCTGATA CAAGAGTGAT CAAGAGTGAT ACATGGGATT ACTAGGATT ACTAGGATT ACTTGGTAT ACTAGGATT ACTAGGATT AGTAGTTTAT	ATAAATGTTA TAACGGTGTC GAGTGAGGCT CTGGGGGCG CGAGTCTCCG CCTCCGGCCA AGGGAGTCTCCG TCGTGGCCGA AAGGAGATC CTACCATTT ATCATATGCT CTACTACAGA TTGAAGGATT TCAACATCTGC TCAAGAACATCGC TCAAGAAGCC TCAAGAAGCC TCAAGAAGCC TCAAGAAGCAGT TCACTGAAGT TGAGAAATAGAG GAATTCTTTG TGTTTCTTCA TGTTTCTTCA TTCCTCAATG TCTTTAATAT	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCCGGGTGGGGAG CGCGCAGGGT CCACGGGCTA CCGAACAATG AAAGAGGTA AAAGAGGAAAA AAGGCAATT TAGCATGTATT TAGCATGTATT TACCAAAGC CTTTAATCCA TGGGGACTGC AGATAATGGG GGGAACTATG TCCTCACTA ACATCAGTGG AGCCCTGGAG AGCCCTGCAG AGCCCTGCAG AGCCCTGCACT TCCTAAGCT ACATCAGTGA ACCTTACT TCCTAAGCT TCCTAAGCT ACATCAGTAC ACCTTACT TCCTAAGCT ACATCAGTAC ACCTTACT TCCTAAGCT ACATCAGTAC ACCTTACT TCCTAAGCT ACCTTACT TCCTAAGCT ACCTTACT TCCTAAGCT ACCTTACT TCCTAAGCT ACCTTACT TCCTAAGCT ACCTTACT ACTTTACTT ATTTTACTTC AAGTTACATT	CCCACACTOS AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CAGCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA GGTCCTCAG CACCCTGGCT CAACACGTTG CACCCTGGCT CAACACGTTG ATTCGTCCTA ATTCGTCCTA ATTCGTCCTT AAGATGCAGG AATCTTTTTC GATGCATCA GGTGAACTTTA GGGAACAGC GATTATACTTTT GCAAGCCGCA CAATTGTGC CAACACTTGACTCA ACAATTGTGC CATAGCTCAC ACAATTGTGC CATAGCTAC AATGATTGC CATAGCTAC AATGATTGC CATAGCTAC AATGATTGC CATAGCTAC AATGATTGC CATAGCTAC AATGATTGC CATAGCTAC ACCTTGTAGT CATAGCTAC CATCAGCATC ACCTTGTAGT CATCAGCTCCTCA	120 180 240 300 360 420 660 660 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1500 1660 1740 1680 1740 1800 1860 1980 2040
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTGCCT GAATCTGCCT GAATCTGCCT GATCTGCCCT GTATCGGCT GTACGGATCG GTTTGCCT GTAACGGTA TTAAGGCTAA ATAATCTGGT AGTTTGGAT CATCAGCTAT ATAATAAAAT TGAGGGCAACC GGAATTACGG TACTCTTGAG GGGCCAATCC GGAATTACGG TCTTGTGGT TTTACTGGAT TCTTCAGG AGGTGTCAGA ACAAAGGCGA TCTTGAGCAA TCTTGAGCAA TGGGACAGCT TTTGTAGTAT ACTTGAGTAT AATCATCAAA ACATTAATGA ACTTCACTCA	CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGT CCCCCAGAGT TCTCGCAGAG AGACCTAATA TITTGGAACT GGAGAAACCT GCACTATGCA TCCACCTGT TCTGCCGGTA TCAAGAATGC ACTGATGCT CCCAGTGGTA CCACTGTGT CCCAGTGGGA CAAGTATGTA CTCATCTCTT CTATGGAGAG AAATCAAGAT AGTGACCACAGGT GGAAAATACAC ATTAACTGAT AGGACTTTAA AGGCCATATA	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGCCCC CGAGCCTCC CGAGCCCCC GGAGCCCG GTCTCCACCACC GTTTCACCGGAG GTCATCACACCAG GTCTTCACAGG CATATCAAGC CATATCAAGC CTTGACAAACC TTTGACAAACG TTTGACAAACG TTTGACAAACG TTTGCCCATATT TCTCTTGGAG CCTTATTTTT AGAGCCTGGA TTTGCCCAAT ATCCACTAGAA GGACAACACC ATTCCACTAGAA GGACAACCAT ACCATGGATG ATTCCACTATAT ATCCAGTATG ATTCCACTATAT ATCCAGTATG AATTCTGATA CAAGAGTGAT CAAGAGTGAT ACATGGGATT ACTAGGATT ACTAGGATT ACTTGGTAT ACTAGGATT ACTAGGATT AGTAGTTTAT	ATAAATGTTA TAACGGTGTC GAGTGAGGCT CTGGGGGCG CGAGTCTCCG CCTCCGGCCA AGGGAGTCTCCG TCGTGGCCGA AAGGAGATC CTACCATTT ATCATATGCT CTACTACAGA TTGAAGGATT TCAACATCTGC TCAAGAACATCGC TCAAGAAGCC TCAAGAAGCC TCAAGAAGCC TCAAGAAGCAGT TCACTGAAGT TGAGAAATAGAG GAATTCTTTG TGTTTCTTCA TGTTTCTTCA TTCCTCAATG TCTTTAATAT	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCCGGGTGGGGAG CGCGCAGGGT CCACGGGCTA CCGAACAATG AAAGAGGTA AAAGAGGAAAA AAGGCAATT TAGCATGTATT TAGCATGTATT TACCAAAGC CTTTAATCCA TGGGGACTGC AGATAATGGG GGGAACTATG TCCTCACTA ACATCAGTGG AGCCCTGGAG AGCCCTGCAG AGCCCTGCAG AGCCCTGCACT TCCTAAGCT ACATCAGTGA ACCTTACT TCCTAAGCT TCCTAAGCT ACATCAGTAC ACCTTACT TCCTAAGCT ACATCAGTAC ACCTTACT TCCTAAGCT ACATCAGTAC ACCTTACT TCCTAAGCT ACCTTACT TCCTAAGCT ACCTTACT TCCTAAGCT ACCTTACT TCCTAAGCT ACCTTACT TCCTAAGCT ACCTTACT ACTTTACTT ATTTTACTTC AAGTTACATT	CCCACACTOS AACACTGGCA ACACTGGCA CGCTGGCTCGC CAGCCTTAGT GCCGGTCTGC GCAGCCTTGG AAGGATTGCA GCGACCCCA GGGCCCCA GGGCCCTAGGT CCAGACCCCA GGTCCTCAG CACCCTGGCT CGAGGAGTAG CGCTCTGCTG AACAGCTTG AACAGCTTG AACAGCTTG AACAGCTTG AAGATGGGAG TGTCCCTGTTA GGGAACAGG GATATACTGT GCAAGCCGCA ACAATTGTG CATAATGTAG AATGAATTGA CATAATGTAG AATGAATAGC CACCTGGAAAAA CTCCTTTTGT	120 180 240 300 360 420 660 660 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1500 1660 1740 1680 1740 1800 1860 1980 2040
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCC CCGGGACCGC GATCTGCCT GTAACGATA ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGCAAC TGAAATTGG TACTCATTGG TACTCATTGG TACTCATTGG TACTCATTGG TCTTTACTGAGT TTTTACTGAGT TTTTTCTCAGG AGGTGTCAGA TCTTCAGGAAT TCTTCAGGAAT TTTTTGAGCAAT TTTTTGAGCAAT TTTTTGAGCAAT TACTCAAAAGCCAA TATCCTGAAT ACAAAGCCAA ACATTAATGT ACTTCACTCAAAACCCAA ACCACATCAAAACCCAA ACATTAATGTA	CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG GCTGGGAGAG GCTCGCAGCT CCCCCAGAGC CTCCCCAGAGC TTTTTGGAACT TTTTGGAACT TCTACCGGTA TCACTATGCA TCACTATGCA TCACTATGCA TCACTATGCA CCACTAGGGA AAATGAGCCT CCAGTGGGA AAATGAGCCT CTATGGAGAG AAATAAGA ATTTTGGCTCT GTATGCACTCT GACAATACCA ATTAACTGAT CGACTATGCA ATTAACTGAT CGACTATCC GTTTTGCTCTT CTATGCAGAG GAGATACTC GTTTGGCTCT CATTGCATTCC CATTGCATTCC ATTAACTGAT CAATTGTTTA CAATTGTTTA CAATTGTTTA CAATTGTTTA AGCCATATAA	ACGTCTCCAT GATTCGGGGG ACTCACCAT CGCTAGGTCG CGCAGACCCG CGCAGACCCG CGCAGACCCG CGCAGACCCG CGCAGACCCG CGCAGACCCG CGCAGACCCG CGCAGACCCG CGCACCCG CGCACCCG CGCACCCG CATATCAAGC CTTGACAAGC CTTGACAAGC CTTATTTT ACGCCAAATT TCTCTTGGAG CCTTATTTT AGACCTGGA GACAACACA GACAACAC ATTCCACAT ACCATGATG ACTCCATATG ATTCCACAT ATCCACATAT ATCCACATAT ATCCACATAT ATTCCACATAT ATTCCACATAT ATTCCACATAT AATTCTGATA CCACGGATTC ACATGGATG TAACTTCGTA ACATGGGATT TAACTTCGTA ACATGGGATT AGTAGTTTTAA	ATAAATGTTA TAACCGTGTTC GAGTGAGGCG CGAGTGAGGCG CCTCGGGCAC GTCCACACGG TCGTGGCGAA AAGGAGGATC CTACCATTTT ATCATATGCT CTCTTCAGAG AAGGAGTCTTT CAACATGGA AAGGAGCTCTT CAACATCTGC TCAAGAACC CAAGTGGAAC AAGGTGGAAC AAGTGGAAC GTGAAGCAGT TCACTGAAGT TCACTGAACT TTCACTACAAC GTGTTTTTTTG GAAGAATAGAG GAAAATAGAG GATTTCTTCAC GTAGTAACTT TTCCTCAATG TCTTTAATAT	CAOGGGCATC ATTTGCTTGG CGGGTCTGGG CCTGGGGGAG CCGCGAGAGGG TGCCCCAGGT CCAGGGCTA CGGAACAATG AAAAGAGGTG AAAGAGGTG AAGGGAACAATG GAAGCATTTATTAGATGTAT TAGATGTATT TAGATGTATT TAGATGTATT ACATCAGAGC CTTTAATCCA TCGCGGACTGC GGGAACTATG TCCTCCACTA ACATCAGTGG AGCCTTGCT GAGCCACTTCCT GAGCCACTTGCT GAGCCACTTGCT TCCTAAGCTG GAGCCACTGGAGACCACTG GAGCCACTTCCT TCCTAAGCTG GAGCCACTGG GATACCACTG TGCCAGAGAA ACCTTACCTT	CCCACACTOS AACACTGSCA AACACTGSCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CGACCCTTGGC AAGGATTGCA GTGGGACCTCAG CACCCTGGCT CAGACCCCA TGGTCCTCAG CACCCTGGCT CAGACAGCTTG CAACAGCTTG ATTCGTCCTA ATTCGTCCTA TGTCCCTGT AAGATGGAA TGTCAGCAGG AATCTTTTC GATTGGCATCA GGGAAATCTTTC GATAGCATCA GGAAACAGAG GATATACTGT CAAAGCTGC AACAGCTTG CAATGGAACAGC AATCTTTTC CATAGCATCA ACAATTGTGC TCCTTTGC CATAATGTAC CACTAGAAAA CTCCTTTTTTT CGTGCACC AACAGTTAC CACTAGAAAAA CTCCTTTTTT CTGCTCCTCA ATAGGTTACA	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1140 1200 1320 1320 1340 1500 1660 16740 1860 1740 1860 1920 1980 2040 2100
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCT GTAACGGTG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA GGGCCAATCC GGAATTACGGT TTTCTTCAGG AGGTCAGA TCTTTACTGGAT TTTTACTGGAT TTTTGACTAT ACAAAGGCGA TCTTGAGCAAT ACAAATCCAAAA ACAATAAATA ACATTAATGA AACAAATGCA ATTCCTCACAA AACAAATGCA ATTCCTCACAA	CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG GCTGGGAGAG GCACTGCT CCCGCAGAG AGACTATC GCACTAATA TITTGGAACT GCACTAGCA TCGACTGCT TCTGCAGAG TCACTATGCA TCGACTGTTT TCTGCCGGTA TCAAGAATGG AACTATGGA ACTATGTA CTCATCTTCT CTATGGAGAG AAATAACTGT GGAATACACA GTTGGCTCT GACAATACACA ATTAACTGAT GGAAAATAGA GTTGCATTTG CAATGTTTT CAATGCTTTT ACTGTTTT CAATGCTTTT ACTGCTTTTA CTATTTTTTTTT CAATGCTTTAA AGGCTATATA AGGCTATATA AGGCTATATA AGGCTATATA ATTTTTTTTTGTG CCTATCTTTTA	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGCCCC CGAGCTTCCC CGAGCTTCCC CGAGCTTCCC CGAGCTTCACCGGAG GTGTTCACGGAG GTGTTCACAGA GTGTTCAAGG CGTGAATTAT TCAGCCAAACC TTTGACAAAG CCTTATTTT AGACCTAGA CCTTATTTT AGACCTAGA GGAGAAGAAG CGGTGCATTT ACACTAGA GGAGAAGAAG CGGTACATCA ATTCCAGTAG ACATGGAT ATTCCAGTAT ATCCAGTAT CAAGAGTGGT ATTCCAGTAT TAACTTGGTA ACATGGAT TAACTTGGTA ACATGGAT ACATGGAT TAACTTGGTA ACATGGAT ACTGGAT TGGTTTTGAA TTGCTACAGAAA TCCACCAGAAA	ATAAATGTTA TAACGGTGTC GAGTGAGGCG GAGTGAGGCG CCTCGGGGCG CCTCGGGCAC GTCCACACGG TCGTGGCCGA AAGGAGGATC CTACCATTT ATCATATGCT CTCTTCAGAA TTGAAGGAT TCAACATCGC CAACTCGG CAACTCGGC CAAGTGGAAC CAAGTGGAAC CTACAAGTGAAC AAGGGGAAT TCAACATCGC CAAGTGGAAC CTAGAAGCC CAAGTGGAAC GTGACTTGGC ACTTGAACAC GTGTTGTTTG TGGAGAATGG GAAATAGAG GATTTCTTCA GTGTTTCTTCA TTCTTCAATG TCTTTAATATT AGCTAATTTG AGTGTTTTCTT	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCGGGTCTGGG CCGCGAGAGG TGCCCCAGGT CCAGGGGCTA CGGAACAATG AAAAGAGGTG AAGGCATTT TAGAATGTATT AGAGTGTATT TAGCTGTATT TACCATAAGCC CTTTAATCCA TGCGGGACTGC AGATAATGGG GGGAACTATG TCCTCACTA ACATCAGTGG CCCGGAG CCCAGTTTCT TCCTAAGCTC TCCTAAGCTC TCCTAAGCTC GAGCCACTGC GATACCAGCT GAGCCACTGGAACT TCCTTAACCACT GAGCCACTGGAACT TCCTTAACCACT ACTTCTAAGCTC AAGTTACCTT TCCTAAGCTC AAGTTACCTT TCCTAAGCTG AAGTTACCTT ACTTTAAGTTC AAGAATTTC TTTTTAATT AGAAAATTTC TTTTTTAAATTTC TTTTTTTAAATTTC	CCCACACTOS AACACTGSCA AACACTGGCA CGCTGGCTCGC CAGCCTTAGT GCCGGTCTGC CAGCCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCCTGGCT CGAGGAGTTA CGCTCTGTC CAACAGCTTC ATTCGTCCTA ATTCGTCCTT GTGTCCCTGT AAGATGGGA TGTCAGCAG AATCTTTTC GATGGCATCA GGGAACAGAG GATATACTGT CCTATGATTTAC GCTAATGTGC CATAATGTGC CATAATGTAC ACTAGAATTG CATAATGTAC ACTAGAATTG CATGAATTTG CATGAATTTG CATGAATTTG CATGAATTGC CATAATGTAC ACTAGAATAG ACCTTTTGT CTTTTGTCCTCCA ACTAGTAAAAA CTCCTTTTGT CTGCTCCTCA ATAGGTTACA CACAGCCTTT	120 180 240 300 360 420 540 660 6720 780 840 900 960 1020 1140 1200 11500 1560 1680 1740 1800 1860 1920 1980 2040 2160
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTGCCT GAATCTGCCT GAATCTGCCT GATCTGCCCT GTATCCAGCCC CCGGGACCGC GATCTGCCT GTAACGGTTA TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA GGGCCAATCC GGAATTACGG ACGTGTCCAGA TCTTCACGAA TCATCAGCAAA TCATCAGAT GGGACAGACT TTTGTAGTAT AATCATCAAA ACATTAATGT ACTTCACTCA ACAAATGCT AACAAATGCT AAAACTGCAAT	CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG GCAGGTGT GCACCCAGGG TGATGCAATC CCCCCAGAG AGACCTAATA TITTGGAACT GCACTATGCAA TCGACTGTTT TCTGCCGGTA TCAAGAATGG AACTGAGCCT CCCAGTGGGA AACTGAGCCT CCCAGTGGGA AATGAAGATG CAAGTATGTA CTCATCTCTT CTATGGAGGA AAATGAAGAT GGAATACAC ATTAACTGAT GGAAATACAC ATTAACTGAT GGAAATACAC ATTAACTGAT CAATGTTTA CGAATTACTGAT CGAATTACTGAT CGAATTACTGAT CGAATTACTGAT CGAATTACTGAT CGAATTACTGAT CGAATTACTGAT CGAATTACTGAT CGAATTACTGAT CGAATGTTTA CGAATTTTG CAATGTTTA CGAATTTTG CAATGTTTA CGAATCTAATT CTCTCCCAT TTCCTCCCAT TTCCTCCCAT TTCCTCCCAT TTCCTCCCAT TTCCTCCCAT TCCCCCTTTACTTTCCCCCTCCCCCCCC	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGCCCC CGAGCCTCC CGAGCCTCC CGAGCCTCC CGAGCCTCC CGAGCCTCC CGAGCCTCC CGAGCTTCCC TGTACCGGAG GTCTTCACAGC CATATCAAGC CTTGACAACC TTTGACAACC TTTGACAACC TTTGACAACC TTTGACAACC TTTGCCAAT TCTCTTGGAG CCTTATTTTT AGAGCCTGAA CGGTGCATAT ATCCAGTAGA CGGTGCATC ATTCCACTAGA ACCAGGAGTCAT ATCCAGTAT AACTTGGTA ACATGGGAT ACTTGGTT AGACTTTTT AGACTTTTT AGACTTGTAT ACTTGGTT ACTTGTTTTAA ACATGGGAT ACTTGGTTTTT AGTGTTTTTAA TCCACAGAAA CCACTGTTTTT TGTGTTTTAA TCCACAGAAA CCACTGTTTTT	ATAATGTTA TAACGGTGTC GAGTGAGGCG GAGTGAGGCG CCTCGGGGCA GTCCTCACAGG TCGTGGCCGA AAGGAGGATC CTACCATTT ATCATATGCT CTCTCAGAA TTGAAGGAT TCAACATCTGC CAACTACGG AAGGAGTCTT CAACATCTGC CAACTACGGA AAGGACACTAC AGGACAGAAC AGGACAGAAC GTGTTGTTTG TGAAGAATGG GAACAGAAC GTGTTTTTG TGGAGATTGTTTG TGGAGATTGTTTG TGGAGAATGG GAATTTCTTC TGTTTCTTCA GTATTCTTC TTCCTCAATG TTCCTCAATG TCTTTAATAT AGCTAATTTTC TTCCTCAATG TCTTTTAATAT AGCTAATTTTC TTCTTCAATG TCTTTTAATAT AGCTAATTTTC TGTTTTTCTTCAATG TCTTTTAATATT TCCTCCAATG TCTTTTAATATT TGCTTCTCTCAATG TCTTTTAATATT TGCTTTTCTTCAATG TCTTTTAATATT TGCTTCAATG	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCGGGTCTGGG CCGCGAGAGG TGCCCCAGGT CCAGGGGCTA CGGAACAATG AAAAGAGGTTG AAAGAAAA AACGGTGTATT TAGAATGTAT TACCAAAGC CTTTAATCCA TGGGGACTGC AGATCATGG AGCCATTGT TCCTAAGCT TCCTCACTA ACATCAGTGG AGCCACTG GGGAACTATG TCCTCACTA ACATCAGTGG AGCCACTGGA ACCTTGCT TCCTAAGCTG TCCTAAGCTG TCCTCACTA ACATCAGTGG AGCCACTGGA ACCTTTCT TCCTAAGCTG TCCTAAGCTG AGCCACTGTG TCCTAAGCTG TCCTAAGCTG TCCTAAGCTG TCCTAAGCTG TCCTAAGCTG TTCTTTAGTTG AGAAAATTTC TTTTTTAATTGC AAGTTACATT	CCCACACTOS AACACTGGCA ACACTGGCAC CGGGGCTCGC CAGCCTTAGT GCCGGTCTGC GAGCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCCTGGTT CAACACCTTGGT ATTCGTCCTA ATTCGTCCTA ATTCGTCCTA ATTCGTCCTA AGATGGCAC ATTCGTCCTT AAGATGGCAC GGTAATTTTT GGTGAACTTTT GGAACAGAG GGAACAGAG GGAACAGAG GATATACTGT CATAATGTAC AATGATTCAC ACTGCTACT CATAATGTAC ACTCCTTTTAGCAC ACTAGAATTGTAC ACTAGAATTGTAC ACTAGATTAC CTCCTTTTTAG CTTAAGGTTACA CTCCTTTTTAG CTCCTCTTTAG CTCTCTTTAG CTCTCTTTAG CTCTCTTTTAG CTCTCTTTTAG CTCTCTTTAG CTCTCTTTAG CTCACACTTTT CTTAAGGTTACA	120 180 240 300 360 420 660 660 660 720 780 900 960 1020 1140 1200 1320 1380 1440 1500 1620 1680 1740 1800 1980 2040 2160 2220
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCC CCGGGACCGC GATCTGCCT GTAACGATA ATAACGATA ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATAAAT TGAGGGCAAC TGAAATTGGA TGAATTCATTGG TACTCTTGAG TCCTGTGGCT TTTACTGAT TTCTTCAGA TCTTTGAGAT TCTTCAGA TCTTTGAGAT ACAAAGCGAA TATCCTGAAT ACAAAGCGAA TATCCTGAAT ACAAAGCGAA TATCCTGAAT ACTCACAAA ACAAATCCA AAAACTGGAT TTCCTCCACA AAAACTGGAAT ACTTCCTCCAAAACCAAAAACCAAAAACCGAAT TTTCCTCCACAAAACCAAAAACCAAAAACCGAAAAACCGAAT ATATCTGTTT	CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG GCTGGGAGAG GCTGGGAGC CCGCTCAGCT CTCCGCAGAG AGACCTAATA TTTTGGAACT TCTGCAGT TCGACTGTT TCTGCCGGTA ACTATGCA TCAGAGATACT CCAGTGGGA AAATGAGCCT CCAGTGGGA AAATGAGCCT CTATGCAGCT CTATGCAGCT CTATGCAGCT CTATGCAGCT CTATGCAGAGAGAAACAT AGTAACAAGA GAGAATACTC GTTTGGCTCT GACAATACAC ATTAACTGAT CGACTATTCAT TGGGTCTT AGGGAAAACAG CCATTGGTTT CTGCTCTT CATGCTCTT CATGCTCTT CATGCTCTT CATGCTCTT CATGCTCTT CATGCTCTT AGCAATACAC ATTAACTGAT CCATTTTTTTTTGTG CCATTTTTTTTTT	ACGTCTCCAT GATTCGGGGG ACTCACCAT CGCTAGGTCG CGCAGACCCG CGCAGACCCG CGCAGACCCG CGCAGACCCG CGCAGACCCG CGTTACCGGG GTCACACCAG GTGTTCACGG CATATCAAGC CTTGACAAGC TTTGACAAGA CCTTATTTT AGACCTAGA GCCATATT AGACCATGAT GACCATCAGA GAGAAGAGAG CGGTGCATTC ACCATGATG ATTCCACATA ATCCACTATT ATTCCATATG AATTCTCAATA ATCCAGTATG AATTCTGATA CAAGGGTTAT TAACTTGGTA ACATGGATT ACTAGGATTAT TCACAGAAT ACCACGGATT AGTGGTTTTAA CCACGGATT AGTAGGTTTTT AGTAGGTTTTT CGTCACAGCCT	ATAATGTTA TAACCGTGTTA TAACCGTGTTC GAGTGAGGCG CGAGTCTCCG GCCCACACGG TCGTGGCGAC GTCCACACGG TCGTGGCGA AAGGAGGAT TCAACATGT ATCATATGCT TCAACATGGA AAGAGCTCTTT CAACATCGC TCAACATCTGC TCAAGAGACT TCAACATCTGC TCAAGAGACT TCAACATCTGC GTGAAGCAGAC AGGTGGAAC AGGTGGAAC GTGAAGCAGA GGACTGATTTTTG GAACATCTGC GAAGATCAGAC GTGTTTCTTCA GTAGTTTCTTCA GTAGTTCTTCA GTAGTTCTTCA GTAGTTAATTT AGCTAATTTG TCTCAATATTT AGCTAATTTG GTGTTTTCT TGAAGGTCCT GAGCATACTC GAGCATACTC GAGCATACTC GAGCATACTC GAGCATACTC	CAOGGGCATC ATTIGCTIGG CGGGTCTGGG CCGGGTCTGGG CCGCGAGAGGG TGCCCAGGT CCAGGGCTA CGGAACAATG AAAGAGGTG AAAGAGGT TAGGATGTA TAGATGTAT TAGATGTAT TAGATGTAT TACCAAAGCC CTITAATCA TGCGGACTGG GGAACTATG TCCTCACTA ACATCAGTGG ACCTTGCATG ACCTTGCATT ACATCAGTGG ACCTTGCATT TCCTAAGCT TCCTAAGCT TCCTAAGCT TCCTAAGCT TCCTAAGCT TCCTAAGCT TCCTACTT TTCTTACCT GAGCCACTTGC TTCTTACTAC ACTTACCTT TTTTTTTTTT	CCCACACTOS AACACTGSCA AACACTGSCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CGACCCTTGG AAGGATTGCA GTGGGACCTCA TGGTCCTCAG CACCCTGGT CAGACCCTAG CACCCTGGT CAGACAGCTTG ATTCGTCCTA ATTCGTCCTA ATTCGTCCTA ATTCGTCCTA ATTCGTCCTA CATTCGTCCTA CATTCGTCCTC CATTAGTTCC CATTCGTCCTC CATTCGTCCTC CATTCGTCCTC CATTCGTCCTC CATTCGTCCTC CATTCGTCCTC CATTCGTCCTC CATTCGTCCTC CATTCGTTCC CATCGTTACG CACCTTTTTGT CTGCTCCTCC CATCGTTACGTTA	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1140 1260 1320 1340 1500 1660 1740 1860 1740 1800 1920 1920 2940 2160 2220 2280
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	TGTTTATTTC GATACGCACC CCTCTGCCCT GAATCTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCCT GTAACGGTG TTAACGGTT AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAAC CATCATCATGG TACTCTTGAG GGGCCAATCC GGAATTACGGT TTTACTGGAT TCTCTCAGG AGGTGTCAGA TCTTCACGAT TCTTCACGAT TCTCTCAGG TCCTTGAGCAT TTTGACAAT ACAAAGCCGAA TCTCATGAAT GGGACAGACT TTTGTAGTAT AATCATAAA ACAATCAAAAACCCAAAAACCAAAAACCAAACCAAAAACCAAAACCAAAA	CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG GCTGGAGAG CCGCTCAGCT CTCCGCAGAG AGACCTATCA TTTTGGAACT TCTGCAGCT TCAGCAGTGC ACCAGTAGCA TCAAGAACT TCTGCAGAG AACTATGCA ACTATGCA CCAGTGGGA AACTATGCA CTCATCTT CTATGGAGAG AACTATGTA CTCATCTTT CTATGGAGAG AAATACAGA GGAGATACCTC GACAATACAC GGAAATACAC GTTGCATTT CAGCATTTC AGGAAATACAC ATTAACTGAT AGGAAATACAC CCATTGCTTC CAGTGGTTCA AGCCATTAC CCATTCATTA CTCTCTCAT CCCTATCTTTA CTCTCCCAT TCCTCCGAT CCCCATTCCTCAC CCCCATTCCTCAC CCCATTCCTCAC CCCCATTCCTCAC CCCCATTCCTCAC CCCCATTCCTCAC CCCCATTCCTCAC CCCCCATTCCTCAC CCCCCCTCTCCCCAT CCCCCCTCTCCCCAT CCCCCCTCTCCCCAT CCCCCCTCTCCCCAT CCCCCCTCTCCCCAT CCCCCCTCTCCCCAT CCCCCCTCTCCCCCAT CCCCCCCTCTCCCCCAT CCCCCCTCCCCCAT CCCCCCTCTCCCCCAT CCCCCCTCTCCCCCAT CCCCCCTCTCCCCCAT CCCCCCTCCCCCTCCCCCTCCCCCTCCCCCAT CCCCCCTCCCCCATCCCCCAT CCCCCCCC	ACGTCTCCAT GATTCGGGGG ACTCGACCAC ACTCGCGCCC CGCAGCCCC CGCAGCCCC CGCAGCCCC CGCAGCCCC CGCACCCC CGCACCCC CGCACCCC CGCACCCC CGCACCCC CGCACCCC CTTCCCACAC GTGTTCACGG GTGTCACAGC GTGCATATT CAGCCAAAC CTTTGACAAAC CTTTGACAAAC CTTATTTT AGACCTGGA TTTCCCCAAT TCCCCAAT GACCATCAGA CGGTACATC ACTTCCACAT ACTCCACTAT ACACAGCC ATTCCACTAT CAGCATGGAT CACATGGAT ACATGGAT TACTTGTA ACATGGAT TACTTGTA ACATGGAT TACTTGTA TCCACAGAA CCACTGTTTT TGTCACAGAA CCACTGTTTT TGTCACAGAA CCACTGTTTT TGTCACAGAAA CCACTGTTTT TGTCACAGAAA CCACTGTTTT TGTCACAGCCC CTTTCCACAC	ATAATGTTA TAACCGTGTC GAGTGAGGCG GAGTGAGGCG CCTCGGGCAC CTCCGGGCAC CTCCCACACGG TCGTGCCGA AAGGAGATCTCGC CTACCATTT ATCATATGCT CTCTCAGAA ATCACATGGA AAGAGCTCTT CAACATCTGC TCAAGAGAC CAAGTGGAAC AAGGTGGAAC AAGTGGAAC GTGAAGAGAGA GACTGCTTTCACAAC GTGTTGTTTG TGAGAATAGG GAATTCTTTG GAGAATAGAG GATTTCTTTAC TTCTTCAATG TTTTTTTCTTCATATG TCTTTAATGAT TTCTTCAATG TCTTTTAATGAT TTCTTCAATG TTTTTTTTTCT TGAGAGTCTTC TTTTAATGTTTTCT TGAAGGTCTTCT TTCTTAATGTTTTCT TGAAGGTCCTC TATGTTTTTAA	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CCGCGAGAGGG CCACGGGTCCAGGT CCAGGGGCTA CGGAACAATG AAAAGAGGTTG GAAGGAATAT GAAGGCATTT TAGTATGTTAT ACACTAGTATT TACCAAAGCC CTTTAATCCA TACCACAAGCC CTTTAATCCA TACCTCCACTA ACATCAGTGG AGCTACCTGGG GGCACTGC GGTACCTGGG GACCACTGC GGTACCTGT TCCTAAGCTG TCCTAAGCTG GACCACTGC GATACTGGAACTACT TCCTAAGCTG TCCTAACTTT TCTTAAGCTG TCCAGAGAA ACTTACCTT TCTTTTTTTTTT	CCCACACTOS AACACTGSCA AACACTGSCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CAGCCTTGG AAGATTGCA GTGGGACTCCA TGGTCCTCAG CACCCTGGCT CGAGGAGTAG CCCTTGGTCCAG CACCCTGGTT CAGAGAGTAG ATTCGTCCTA AGAATGGCAT TGTCCCTGT AAGATGGCAG AATCTTTTC GATGCATCA GATGCATCA GATGAATTTA GGGAACAGAG GATATACTGT CATTAGTACT ACATTGTCC CATTAGAAT CCCTTTGGATTTAG CAAGCCTGC ATTAGTACT CATTAGTACT CATTAGATTGC ACTTAGAATAG ACATTGTAC CATTAGATTAC ACAGGACTTTT TCTCCTCTCT CTTTGGATTTAG ACATTGTAG ACATTGTAG ACATTGTAG ACATTGTAG ACATTGTAG ACATTGTAG ACATTGTAG ACATTGTAG ACATTGTAG ACATGGTTAA CTCCTTTTGT CTTCTCCTCTG ATTAGGTTAA GAAGACCTGA GTCAGGCGAC	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1500 1560 1680 1740 1800 1920 1980 2040 2160 22100 2220 2230
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	TGTTTATTTC GATACGCACC CCTCTGCCCT GAATCTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCCT GTAACGGTG TTAACGGTT AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAAC CATCATCATGG TACTCTTGAG GGGCCAATCC GGAATTACGGT TTTACTGGAT TCTCTCAGG AGGTGTCAGA TCTTCACGAT TCTTCACGAT TCTCTCAGG TCCTTGAGCAT TTTGACAAT ACAAAGCCGAA TCTCATGAAT GGGACAGACT TTTGTAGTAT AATCATAAA ACAATCAAAAACCCAAAAACCAAAAACCAAACCAAAAACCAAAACCAAAA	CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG GCTGGAGAG CCGCTCAGCT CTCCGCAGAG AGACCTATCA TTTTGGAACT TCTGCAGCT TCAGCAGTGC ACCAGTAGCA TCAAGAACT TCTGCAGAG AACTATGCA ACTATGCA CCAGTGGGA AACTATGCA CTCATCTT CTATGGAGAG AACTATGTA CTCATCTTT CTATGGAGAG AAATACAGA GGAGATACCTC GACAATACAC GGAAATACAC GTTGCATTT CAGCATTTC AGGAAATACAC ATTAACTGAT AGGAAATACAC CCATTGCTTC CAGTGGTTCA AGCCATTAC CCATTCATTA CTCTCTCAT CCCTATCTTTA CTCTCCCAT TCCTCCGAT CCCCATTCCTCAC CCCCATTCCTCAC CCCATTCCTCAC CCCCATTCCTCAC CCCCATTCCTCAC CCCCATTCCTCAC CCCCATTCCTCAC CCCCCATTCCTCAC CCCCCCTCTCCCCAT CCCCCCTCTCCCCAT CCCCCCTCTCCCCAT CCCCCCTCTCCCCAT CCCCCCTCTCCCCAT CCCCCCTCTCCCCAT CCCCCCTCTCCCCCAT CCCCCCCTCTCCCCCAT CCCCCCTCCCCCAT CCCCCCTCTCCCCCAT CCCCCCTCTCCCCCAT CCCCCCTCTCCCCCAT CCCCCCTCCCCCTCCCCCTCCCCCTCCCCCAT CCCCCCTCCCCCATCCCCCAT CCCCCCCC	ACGTCTCCAT GATTCGGGGG ACTCGACCAC ACTCGCGCCC CGCAGCCCC CGCAGCCCC CGCAGCCCC CGCAGCCCC CGCACCCC CGCACCCC CGCACCCC CGCACCCC CGCACCCC CGCACCCC CTTCCCACAC GTGTTCACGG CATATCAAGC CTTGCACAAC CTTTGACAAAC CTTTGACAAAC CTTTATTTT AGACCTGGA TTTCCCCAAT TCCCCAAT TCCCCAAT GACCATCAGA CGGTACATC ACTTCCACTAT AGACATGAT CACCATCAGT AGACATCACT ATTCCACATA ATCCACTATG AATTCCACTAT TAACTTGGTA ACATGGGAT ACATGGAT TAACTTGTA ACATGGTAT TGTCTTTTAA TCCACAGAAA CACTGTTTTT TGTCACAGAA CACTGTTTTT GTCACAGCCC CTTTCCACAC	ATAATGTTA TAACCGTGTC GAGTGAGGCG GAGTGAGGCG CCTCGGGCAC CTCCGGGCAC CTCCCACACGG TCGTGCCGA AAGGAGATCTCGC CTACCATTT ATCATATGCT CTCTCAGAA ATCACATGGA AAGAGCTCTT CAACATCTGC TCAAGAGAC CAAGTGGAAC AAGGTGGAAC AAGTGGAAC GTGAAGAGAGA GACTGCTTTCACAAC GTGTTGTTTG TGAGAATAGG GAATTCTTTG GAGAATAGAG GATTTCTTTAC TTCTTCAATG TTTTTTTCTTCATATG TCTTTAATGAT TTCTTCAATG TCTTTTAATGAT TTCTTCAATG TTTTTTTTTCT TGAGAGTCTTC TTTTAATGTTTTCT TGAAGGTCTTCT TTCTTAATGTTTTCT TGAAGGTCCTC TATGTTTTTAA	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CCGCGAGAGGG CCACGGGTCCAGGT CCAGGGGCTA CGGAACAATG AAAAGAGGTTG GAAGGAATAT GAAGGCATTT TAGTATGTTAT ACACTAGTATT TACCAAAGCC CTTTAATCCA TACCACAAGCC CTTTAATCCA TACCTCCACTA ACATCAGTGG AGCTACCTGGG GGCACTGC GGTACCTGGG GACCACTGC GGTACCTGT TCCTAAGCTG TCCTAAGCTG GACCACTGC GATACTGGAACTACT TCCTAAGCTG TCCTAACTTT TCTTAAGCTG TCCAGAGAA ACTTACCTT TCTTTTTTTTTT	CCCACACTOS AACACTGSCA AACACTGSCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CAGCCTTGG AAGATTGCA GCGGCCTCA GCGCCCCA GGTCCCCA GGTCCCCA CGCCTCGCT CAGAGACCCCA CGCCCTGCT CAACAGCTTG ATTCGTCCTA AGAATGGCA ATTCGTCCTT GATGCATCT CATGGCATC AACAGCTTC GATGCATCA ACAATTGTCC CATGAATTTC GATGCATCA GCAAGCCCCA CCTATATTGTC CATGAATTGCA CATGATTTC CATGAATTGCA CATGATTGC ATTGATTCC CATTAGAAAA CCCCTTTGG AACAGCTCC ATTGATTCC CATTAGAAAA CTCCCTTTTG CTCCCTCC ATTAGAATAC CACAGACTTTT GTTAAGGTAA CAAGACCTGA CAAGACCTTTC CATTAGGCAAA CTCCCTTTTGT CTCCCCCCCC ATTAGGCAAAA CTCCCTTTTGT CTCCCCCCCC CATGAAAAA CTCCCTTTTGT CTCCCCCCC CATGAAAAA CTCCCTTTTGT CTCCCCCCCC CATGAAAAA CTCCCTTTTGT CTCCCCCCC CATGAACACCGC CAGGACCTTT GTTAAGGTAA GAAGACCTGA GTCAGGCGAC	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1500 1560 1680 1740 1800 1920 1980 2040 2160 22100 2220 2230
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTCGG GTCTTCCTGC AATCCAGCCT CCGGGACCGC GATCTGCCT GTAACGGTG TTAAGGCTAA ATAATCTGGT AGTTTGGATG AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGCAAC CGAAATTACGG TACTCTTGAG GGGCCAATCC GGAATTCCTGAG TCTTCATCGGA TCTTCATCGGA TCTTCACGAT TTTTACTGAT TTTGTACTAAT ACATACATAAA ACATTAATA ACTTCATCA AACAATGCA AACAATGCA AAACTGCAI ATTCCTGCAG AAACTGGAT ATTCCTGCAG AAACTGGAT ATTCCTGCAG AAAACTGGAT ATTCCTGCAG AAAACTGGAT ATTCCTGCAG AAAACTGGAT TTTCCTGCAG AAAACTGGAT ATTCCTGCAG AAAACTGGAT ATTCCTGCAG AAAACTGGAT TTTCCTGCAG AAAACTGGAT TTTCCTGCAG AAAACTGGAT TTTCCTGCAG AAAACTGGAT TTTCCTGCAG AAAACTGGAT TTTCCTGCAG AAAACTGGAT TTTCCTGCAG ATTTCCTTCCAGC TTTCCTGCAG AAAACTGGAT TTTCCTGCAG AAAACTGGAT TTTCCTGCAG ATTTCCTTCCAGC AAAACTGCAT TTTCCTGCAG ATTTCCTTCCTACAGACCTC TTCCAAGAGACTC TTCAAAGACTCC TTCAAAAGACTCC TTCAAAAGACTCC TTCAAAAGACTCC TTCAAAAAACTCCATTTCC TTCAAAAGACTCC TTCAAAAGACTCC TTCAAAAAACTCCATTCC TTCAAAAAACTCCATTTCC TTCAAAAAACTCCATTCC TTCAAAAAACTCCATTCC TTCAAAAAACTCCATTCC TTCAAAAAACTCCATTCC TTCAAAAAACTCCATTCC TTCAAAAAACTCCATTCC TTCAAAAACTCCATTCC TTCAAAAAACTCCATTCC TTCAAAAAACTCCATTCC TTCAAAAAACTCCATTCC TTCAAAAAACTCCATTCC TTCAAAAAACTCCATTCC TTCAAAAAACTCCATTCC TTCAAAAAACTCCATTCC TTCAAAAACTCCATTCC TTCAAAAAACTCCATTCC TTCAAAAAACTCCATTCC TTCAAAAAAAA	CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG GCTGGGAGAG GCACGTGT CCCGCAGAG AGACCTAATA TITTGGAACT GCACTAGTG TCTCCGCAGAG AGACCTAATA TCTTGCAGT TCAGCAGTT TCTGCCGGTA TCAAGAATGG AACTATGCA CCCATTGGGA CAAGTATGTA CTCATCTCT CTATGGAGAG AAATGAAGAT AGTGACAAGG GAGTAACCT GACAATACACA ATTAACTGAT GGAAAATAGA GTTGCATTTG CAATGTTTA AGGCTTTCAT AGGCTTTCAT AGGCTTTCAT CACATTTTTT CCCTATTTT CCTTCCCAT TCTTCCCCAT TCTTCCCCAT CCCCATTTTT CCCCATTTTTT CCCCATTTTT CCCCATTTT CCCCATTT CCCCATT CCCCATTT CCCCATT CCCCATTT CCCCATTT CCCCATT	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGCCCC CGAGCTTCCC CGAGCTTCCC CGAGCTTCCC CGAGCTTCACCGGAG GTGTTCACGGAG GTGTTCACAGA GTGTTCACAGA GTCCCATATT TCAGCCAAACC TTTGACAAAG CCTTATTTT AGAGCCTGGA TTTCCCAAT GACCATCAGA GGAGAAGAAG CGGTGCATTC ATTCCACAT ATCCAGTAT GGATACAGC TTTCAACTA ATCCAGTAT ACATGGAT AATCCAGTAT TAACTTGGAT TAACTTGGAT TAACTTGGAT TAACTTGGAT TACTCGATT TACTCGATT TACTCGATT TACTCGATT CGTACAGCAT TCCACAGAAA CCCTGTTTTT CGTCACAGAA CCCTGTTTTT CTTTCCACAT CCTTCCACAT CCTTTCCACAT CCTTTCCACAT CCTTTCCACAT CCTTTTCACAT CCTTTTTAGACCT CCTTTTCACAT CCTTTTTAGACCT CCTTTTCACAT CCTTTTTAGACCT CCTTTTTCACAT CCTTTTTTAGACCT CCTTTTTCACAT CCTTTTTTAGACT CCTTTTTAGACT CCTTTTTAGACT CCTTTTTTAGACT CCTTTTTAGACT CCTTTTTTAGACT CCTTTTTTAGACT CCTTTTTTAGACT CCTTTTTTAGACT CCTTTTTTAGACT CCTTTTTTAGACT CCTTTTTAGACT CCTTTTTTAGACT CCTTTTTTAGACT CCTTTTTTAGACT CCTTTTTTAGACT CCTTTTTTAGACT CCTTTTTTAGACT CCTTTTTTAGACT CCTTTTTTTTAGACT CCTTTTTTAGACT CCTTTTTTTTTT	ATAATGTTA TAACGGTGTC GAGTGAGGCG GAGTGAGGCG CCTCGGGGCG CCTCGGGCGA AGGGAGTCTCCG TCGTGGCCGA AAGGAGGATC CTTCTCAGAA TTGAAGGAT TTGAAGGAT TCAACATCTGC CAAGTGGAAC AAGGTGGAAC GTGAAGCAGT TCATCAGAA AGAGTTGTT CAACATCTGC CAAGTGGAAC GTGAAGCAGT TCACTGAAGA GTGAAGCAGT TGACATGGC ACTTGACAAC GTGTTGTTTG TGGAGAATGG GAAGAGAAGA	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCGGGTCTGGG CCGGGGCGAGGG TGCCCAGGT CCAGGGGCTA CGGAACAATG AAAAGAGGTG AAGGCATTT TAGAATGTAT AGAGTGTATT TAGCTGTAT TAGCATAGCC CTTTAATCCA TGGGGACTGG GGGAACTATG GCGCTGGAG CCCGGGGCACTGC GCTACCTGG AGCCATGGA ACCTTCATTG TCCTAAGCTG GGAACTATG TCCTCACTA ACATCAGTGG AGCCATGGAGCAACT TCCTAAGCTG GATACCAACT GCTACCTGG AAGTTACATT TGCTAAGCTG TTCTTAAGCTG CTACCTGGAGAAA TCTTTACGTG AAGTTACATT AGAAAATTCC TTTTTTAATT CCAAGTCCGT CCCAGGCGCTGCG CCCCCTGGCTGCCCCCCCCTGCCTCCCCCCCC	CCCACACTOS AACACTGSCA AACACTGGCA CGCTGGCTCGC CAGCCTTAGT GCCGGTCTGC GCAGCCTTGG AAGGATTGCA GCGCCCAG GCGCCCCAG GCGCCCCAG CACCCTGGCT CGAGGAGTAG CACCCTGGCT CAACAGCTTG ATTCGTCCTA ACTCGTCCTT GTGTCCTGT GTGTCCTTTG GTGTCCTTTT GTGTCCTTTT GTGTCCTTTT GATGGCATCA ACAATTTTC GATGGAATTTT GCAACAGAG GATATACTGT CATAATGTAG ACTATTTTGTCCTCT CATAATGTAG ACTATTTTC CATAATGTAC ACTCCTTTTGT CCTCTCTCAACAGAGAG CCTCTTTTGT CCTCTCTCAACAGAGAGAG ACAATTTTC CATAATGTAG ACTCCTCTTTTGT CTCCTCCTCAACAGAGAGAGAGAGAGAGTTTT GTTAAGGTTAA GAAGACTTTT GTTAAGGTTAA GAAGACCTGA GTCAGGGGAC GCCAGGGGAC GCCAGGGGAC GACATATAGT GGCACAGGACCTGA GGACACTTGA GTCAGGGGAC GCCAGGGGAC GACATATAGT	120 180 240 360 420 540 660 660 6720 780 840 900 960 1020 1140 1200 11500 1560 1620 1680 1740 1800 1920 2040 2160 2220 2280 2240 2400
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCC CCGGGACCGC GATCTGCCT GTAACGATG TTAACGATG ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATAAAT TGAGGGCAAC TGAAATTGGA CATCAGTGG TCCTGTGGCT TTTACTGAGT TCCTCTGGAG AGGTGTCAGA TGAGAGGAA TCTTGAGCAA TATCCTGAGAA TATCCTGAGAA TATCCTGAGAA TATCATTAGAC ACAAATCCAAT ACAAAATCCAAT ACTTAACTCAAAA ACCAAATCCGAT ATAACTGGAT TTTCTTCGCAG AAAACTGGAT TTTCTTCGCAG AAAACTGGAT TTTCCTGCAG AAAACTGGAT TTTCCTGCAG AAAACTGGAT TTTCCTGCAG AAAACTGGAT TTTCCTGCAG AAAACTGGAT TTCCTGCAG AAAACTGGAT TTCCTGCAG AAAACTGGAT TTCCTGCAG AAAACTGGAT TTCCTGCAG AAAACTGGAT TTCCTGCAG AAAACTGGAT TTCCTCAAAGACTCAAAACTCAAT TTCCTCAAAAACTGGAT TTCCAAGAACTCAAAAACTCAACAAACTCAACAAACTCAACAAACTCAACAA	CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG GCTGGGAGC GCTGGGAGC CCGCTCAGCT CTCCGCAGAG AGACCTAATA TTTTGGAACT TCTGCAGT TCGACTGTT TCTGCCGGTA ACTGTTT CTTGCAGGC CACAGTAGGA AAATGAGCCT CCCAGTGGGA AAATGAGCCT CTATGGAGAG GAGAAACCT CTATGGAGAG AAATGAGCCT CTATGGAGAG GAGAATACTC GTTTGGCTCTT GACAATACAC ATTAACTGAT CGACAATACAC ATTAACTGAT CGACAATACAC ATTAACTGAT CGACAATACAC ATTAACTGAT CCATTGTT CACTGTTTC CATTGCATTTC CATTGCATTTC CATTGCATTTC CATTGCTCTT CACATTGTT CATTGCTCTT CACATTGTT CACATTGTT CACATTGTT CACATTGTT CACATTGTT CACATTGTT CACATTGTT CACACATTGTT CACCATTGTT CACCATTGT	ACGTCTCCAT GATTCGGGGG ACTCACCAT CGCTAGGTCG CGCAGCCCC CGCAGACCCG CGCAGCCCG CGCAGCCCG CGCAGCCCG CGCAGCCCG CGCAGCCCG CGCAGCCCG CGCAGCCCG CGCAGCCCG CGCAGCCCG CATACCAGG GTGTACAGG GTCTCACAGG GTCTCACAGG GTCTATTTT AGACCTGGA TTCCCATATT AGACCATGGAT GCCATACGAT ACCATCAGA GGGTACAGCCT ATTCCACATA ATCCAGTATG AATCCAGTATG AATCCAGTATG AATTGTGATA CCAGGGTGAT CCACAGAAA CCATCGGTT TCCACAGAAA TCCACAGAAA TCCACAGAAA CCCTGTTTTT CGTCACAGCCT CTTTCCACAT CGCCTTATAGG CCTTTTCCACAT CGCCTTATAGG CCCTTTTCCACAT CGCCTTATAGG CCCTTTTCCACAT CGCCTTTTCCACAT CGCCTTATAGAT CGCCTTATAGAT CGCCTTATAGAT TCCCCACAGAAA TCCACAGCCT CTTTCCACAT TCCACAGCCT CTTTCCACAT TTTTCACAT TCCCCTTATAGAT TCCCCTTATAGAT TCCCCTTATAGAT TCCCCTTATAGAT TCCCCTTATAGAT TTTTTCACAT TTTTTCACAT TTTTTCACAT TTTTTCACAT TTTTTCACAT TTTTTCACAT TTTTTTTT	ATAATGTTA TAACCGTGTTA TAACCGTGTTC GAGTGAGGCG CGAGTGACGG CCTCGGGCAC GTCCACACGG TCGTGGCGA AAGGAGGATC TCTACCATTTT ATCATATGCT TCAACATGGA AAGAGCTCTTT CAACATGGA AAGAGCTCTT TCAACATGGA AAGTGGAAC AAGTGGAAC AAGTGGAAC GTGAAGCAGTTTTTTG GTAGTTTTTG GAACATCTGC TCAAGAGAGA ACTGGCAAC TCATCTTCTTTG GTAGTTTTTTG TGTTTTTG GTAGTTTCTTCA GTAGTTTCTTCA GTAGTTAATTT TCTCAAGT TCTCTCAATG TCTTTAATAT AGCTAATTTG GTGTTTTTTTC TTTCTCAAGT TCTTTAATAT TGAAGGTCCT TAAGTTTCTTCC TATGTTTTTC TGAAGGTCT TTGAAGGTCT TTTTTTTTT	CAOGGGCATC ATTIGCTTGC CGGGTCTGGG CCGGGTCTGGG CCGGGGCGAG CCGCAGGT CCAGGGCTA CGGAACAATG AAAAGAGGT AAGGGAAAAA GACGTGGAG GAAGCATT TAGAATGTAT TAGAATGTAT TAGAATGTAT TACCAAAGCC CTITAATCCA TGGGGACTGC AGATAATGGG GGAACTATG TCCTACATG ACATCAGTGG ACCCTGGAG ACCTTGCTTCT TTCTAAGCTG GAGCGACTGC GATACCTGT TGCCAGAGAA ACCTTACCTT	CCCACACTOS AACACTGSCA ACACTGSCA CGCTGGCTCC CGGCCTTAGT GCCGGTCTGC CGACCCTTGGT AAGGATTGCA GTGGGACCTCA TGGTCCTCAG CACCCTGGCT CGAGCCTCAG TGGTCCTCAG CACCTGGCT CAGAGAGTTG CAACAGCTTG ATTCGTCCTTT AGATGGAT TGTCCTCTTT AGATGGATC ATTCGTCCTAT GGGAACAGAG ATCTTTTTC GATTGCATCA GGGAACAGAG GATATATCTGC TCATATGTAG AACAGTTGC ACAGACTTCA TGCAAGCGGA ACAATTGTC CATAGTAGCA ACAATTGTC CATAGTAGAAAA CCCTAGAAAA CCCTAGAAAA CCCTAGAAAA CCTTAGAACTGTC CATAGGTTAC AACACTTTT TGTTAAGGTAA GAAGACTTGC GTCAGGCGCA CGACATATGTGC GGCACCGCA CGACATTTGT TGTTAGGTAA GAAGACCTGA GAAGACCTGA GGAACACTGA GAAGACCTGA GACACTATAGT TAGAAGTGTA TAGAAGTGTA	120 180 240 300 360 420 660 660 660 720 780 840 900 1020 1140 1200 1320 1380 1440 1500 1680 1740 1860 1980 2040 2100 2220 2280 2340 2460
50 55 60 65 70 75	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC CAATCCAGCC CCGGGACCGC GATCTGCCT GTAACGATG TTAAGGATG ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA TACTCATTGG TACTCTTGAG GGGCAATCC GGAATTCGGT TTTCTCAGG AGGTGTCAGA TCTTCAGGAAT TCTTCAGGAAT TTCTTCAGGAAT TTCTTGAGCAAT TTCTTGAGCAAT TTTCTTGAGCAAT TTTCTGAGCAAT TTTCTGAGCAAT TTTCTTGAGCAAT TTTCTTGAGCAAT TTTCTTGAGCAAT ACAAAGCCGA TTTCCTGAGAT ACATAATTTA ACTTCAACT AACAAATCCAAT ACTTCACTCAAC TTTCCTGCAG AAAACTCGAT TTTCTTGAGTAT ACTTCACTCAAC TTTCCTGCAG AAAACTCGAT TTTCTTGAGTAT ACTTCACTCAAC ACAAATCCAAT TTTCTTGAGTAT ACTTCACTCAAC TTTCCTGCAG AAAACTCGAT TTTCTTGAGCAAT CCTTCTTTCAAGGACTCAC CCTTCTTTTCACCCAC AGGTACTCAC CCTTCTTTTTTCCTCCAC CAGGTACTCAC CCTTCTTTTTTCCTCCAC CAGGTACTCAC CCTTCTTTTTTTTTCCTCCAC CCTTCTTTTTTTT	CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG GCTGGGAGAG GCTGGGAGC CCGCTCAGCT CTCCGCAGAG TGATCCATAGC TTTTGGAACT TCTGCAGT TCTGCAGT TCAGCAGT TCAGCAGT TCAGCAGT TCAGCAGT TCAGCAGT CCAGTGGA AACTATGCA AACTATGTA CTCATCTCTT CTATGGAGAG AAATAAGAG AATAACTAGT GGACAATACAG GGAAAATAGA GGTTGCATTGC CATTAGCTT CATTGCTCTT CTATGGAGAG AAATAAGAG TGATACTAGT AGGCATACAG GAAAATAGA TGAATACTAT AGGCATACAG CAATGATTAC CACATTCTT CCAGCTTTCAGGCTT CAGCATTCTCAGGCTT CAGCATTCTCAGGCTT CACAGTGTT CACAGTGTT CACAGTGTT CCTCCTCGAT CCACATTCT CCCCATTGT CCACATTCT CACCATTGT CACCATTGT TCTCCCTCGAT TCATCTCTTAG TTCTCCTGAT TTCTTCCTGAT TTCTTCCTGAT TTCTTCCTGAT TTCTTCTTATTIT TTTTTTTTTT TTTTCTTCCTGAT TTCTTCTATTTT TTTTTTTTTT	ACGTCTCCAT GATTCGGGGG ACTCGCGCG CGCAGACCCG CGCAGACCCG CGCAGCCTCTCCACCAT CGCTAGGTCG CGCAGCCCG CGCAGCCCG CGCAGCCCG CGCAGCCCG CGCACCCG CGCACCCG CGTTACCAGG GTCTCACCG CATATCAAGC CTTTCACAAG GTCCCATATT TCTCTTGGAG CCTTATTTT AGACCTAGA GGAGAAGAG CCGTACTCTCACAC ATTCCAACTA ATTCCACTAT GGATACACC ATTCCACTAT AGTCCATATT CACCTGTAT TATCCACTAT AGTCCATATT CCACTGTTT AGTACTATA CCACGGATT CCACCGCT TTTCCACAT CCACTGTTTT TGTCACACCC CTTTCCACAT CCCTTTTTTT TGTCACACCC CTTTCCACAT CCCTTTTTTTT TGTCACACCC CTTTCCACAT TGTACACCC CTTTCCACAT TTTCACACT TTTTCACACT TTTTCACACT TTTTTTTT	ATAATGTTA TAACCGTGTTA TAACCGTGTTC GAGTGAGGCG CGAGTGAGGCG CCTCGGGCAC GTCCACACGG TCGTGGCGAC CTACCATTT ATCATATGCT CTCTTCAGAA ATGAAGAGTCTTT ATCATATGCT TCAACATGGA AAGAGCTCTT TCAACATGGA AAGAGCTCTT TCAACATGGA AAGAGCTCTT TCAACATCTGC TCAAGAGCAC GTGAAGCAGT GGACTGGAAC GTGAAGCAGT GGACATCTTTACACAC GTGTTTTTTACACAC GTGTTTTTTTACACAC GTAGTAACTT TTCTTCAATAT AGCTAATTT AGCTAATTT AGCTAATTT CGAGGATACT TTATTTACACAC TTATTTTACACAC TTATTTTACACAC TTATTTTACACAC TTATTTTACACAC TTATTTTACACAC TTATTTTACACACAC	CAOGGGCATC ATTTGCTTGGC CGGGTCTGGG CCTGGGGGAG CCGCGAGAGAGG TGCCCAGGT CCAGGGCTA CGGAACAATG AAAGAGGTG AAGGGAATAT GAAGTGTATT TAGATGTAT TAGATGTAT TAGATGTAT TACCAAAGCC CTTTAATCCA TGGGGACTATG GGGACCTTGCACTA ACATCAGTGGA ACCTTCACTA ACATCAGTGGA ACCTTACTTG GAGCCACTTGCAGA ACCTTACCTT	CCCACACTOS AACACTGSCA AACACTGSCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CAGCCTTGG AAGGATTGCA GGGACCCCA TGGTCCTCAG CACCCTGGCT CAGACACCTTG ATTCGTCCTAG ATTCGTCCTAG ATTCGTCCTAG ATTCGTCCTAG ATTCGTCCTTTG GTGTCCTGTTTG GTGTCCTGTTTG GTGTCCTGTTTG GTGTCCTGTTTG GTGTCCTGTTTG GTGTCCTGT AAGATGGCAG AATCTTTTTC GATTGGCATCA GGGAACAGAG GATATACTGT CATAATGTAG CACTAGAAAA CTCCTTTTGTC ATTAGGTAC ATTAGGTAC ATTAGGTAC ATTAGGTAC ATTAGGTAC CATTAGGTAC CACAGACTTTT GTTAAGGTAC GACAGACTTTA TGTTAAGGTAC TTCTGACAGT TTCTGACAGT	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1140 1260 1320 1380 1440 1500 1560 1680 1740 1880 2040 2160 2220 2340 2460 2460 2520
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC CAATCCAGCC CCGGGACCGC GATCTGCCT GTAACGATG TTAAGGATG ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA TACTCATTGG TACTCTTGAG GGGCAATCC GGAATTCGGT TTTCTCAGG AGGTGTCAGA TCTTCAGGAAT TCTTCAGGAAT TTCTTCAGGAAT TTCTTGAGCAAT TTCTTGAGCAAT TTTCTTGAGCAAT TTTCTGAGCAAT TTTCTGAGCAAT TTTCTTGAGCAAT TTTCTTGAGCAAT TTTCTTGAGCAAT ACAAAGCCGA TTTCCTGAGAT ACATAATTTA ACTTCAACT AACAAATCCAAT ACTTCACTCAAC TTTCCTGCAG AAAACTCGAT TTTCTTGAGTAT ACTTCACTCAAC TTTCCTGCAG AAAACTCGAT TTTCTTGAGTAT ACTTCACTCAAC ACAAATCCAAT TTTCTTGAGTAT ACTTCACTCAAC TTTCCTGCAG AAAACTCGAT TTTCTTGAGCAAT CCTTCTTTCAAGGACTCAC CCTTCTTTTCACCCAC AGGTACTCAC CCTTCTTTTTTCCTCCAC CAGGTACTCAC CCTTCTTTTTTCCTCCAC CAGGTACTCAC CCTTCTTTTTTTTTCCTCCAC CCTTCTTTTTTTT	CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG GCTGGGAGAG GCTGGGAGC CCGCTCAGCT CTCCGCAGAG TGATCCATAGC TTTTGGAACT TCTGCAGT TCTGCAGT TCAGCAGT TCAGCAGT TCAGCAGT TCAGCAGT TCAGCAGT CCAGTGGA AACTATGCA AACTATGTA CTCATCTCTT CTATGGAGAG AAATAAGAG AATAACTAGT GGACAATACAG GGAAAATAGA GGTTGCATTGC CATTAGCTT CATTGCTCTT CTATGGAGAG AAATAAGAG TGATACTAGT AGGCATACAG GAAAATAGA TGAATACTAT AGGCATACAG CAATGATTAC CACATTCTT CCAGCTTTCAGGCTT CAGCATTCTCAGGCTT CAGCATTCTCAGGCTT CACAGTGTT CACAGTGTT CACAGTGTT CCTCCTCGAT CCACATTCT CCCCATTGT CCACATTCT CACCATTGT CACCATTGT TCTCCCTCGAT TCATCTCTTAG TTCTCCTGAT TTCTTCCTGAT TTCTTCCTGAT TTCTTCCTGAT TTCTTCTTATTIT TTTTTTTTTT TTTTCTTCCTGAT TTCTTCTATTTT TTTTTTTTTT	ACGTCTCCAT GATTCGGGGG ACTCGCGCG CGCAGACCCG CGCAGACCCG CGCAGCCTCTCCACCAT CGCTAGGTCG CGCAGCCCG CGCAGCCCG CGCAGCCCG CGCAGCCCG CGCACCCG CGCACCCG CGTTACCAGG GTCTCACCG CATATCAAGC CTTTCACAAG GTCCCATATT TCTCTTGGAG CCTTATTTT AGACCTAGA GGAGAAGAG CCGTACTCTCACAC ATTCCAACTA ATTCCACTAT GGATACACC ATTCCACTAT AGTCCATATT CACCTGTAT TATCCACTAT AGTCCATATT CCACTGTTT AGTACTATA CCACGGATT CCACCGCT TTTCCACAT CCACTGTTTT TGTCACACCC CTTTCCACAT CCCTTTTTTT TGTCACACCC CTTTCCACAT CCCTTTTTTTT TGTCACACCC CTTTCCACAT TGTACACCC CTTTCCACAT TTTCACACT TTTTCACACT TTTTCACACT TTTTTTTT	ATAATGTTA TAACCGTGTTA TAACCGTGTTC GAGTGAGGCG CGAGTGAGGCG CCTCGGGCAC GTCCACACGG TCGTGGCGAC CTACCATTT ATCATATGCT CTCTTCAGAA ATGAAGAGTCTTT ATCATATGCT TCAACATGGA AAGAGCTCTT TCAACATGGA AAGAGCTCTT TCAACATGGA AAGAGCTCTT TCAACATCTGC TCAAGAGCAC GTGAAGCAGT GGACTGGAAC GTGAAGCAGT GGACATCTTTACACAC GTGTTTTTTACACAC GTGTTTTTTTACACAC GTAGTAACTT TTCTTCAATAT AGCTAATTT AGCTAATTT AGCTAATTT CGAGGATACT TTATTTACACAC TTATTTTACACAC TTATTTTACACAC TTATTTTACACAC TTATTTTACACAC TTATTTTACACAC TTATTTTACACACAC	CAOGGGCATC ATTTGCTTGGC CGGGTCTGGG CCTGGGGGAG CCGCGAGAGAGG TGCCCAGGT CCAGGGCTA CGGAACAATG AAAGAGGTG AAGGGAATAT GAAGTGTATT TAGATGTAT TAGATGTAT TAGATGTAT TACCAAAGCC CTTTAATCCA TGGGGACTATG GGGACCTTGCACTA ACATCAGTGGA ACCTTCACTA ACATCAGTGGA ACCTTACTTG GAGCCACTTGCAGA ACCTTACCTT	CCCACACTOS AACACTGSCA ACACTGSCA CGCTGGCTCC CGGCCTTAGT GCCGGTCTGC CGACCCTTGGT AAGGATTGCA GTGGGACCTCA TGGTCCTCAG CACCCTGGCT CGAGCCTCAG TGGTCCTCAG CACCTGGCT CAGAGAGTTG CAACAGCTTG ATTCGTCCTTT AGATGGAT TGTCCTCTTT AGATGGATC ATTCGTCCTAT GGGAACAGAG ATCTTTTTC GATTGCATCA GGGAACAGAG GATATATCTGC TCATATGTAG AACAGTTGC ACAGACTTCA TGCAAGCGGA ACAATTGTC CATAGTAGCA ACAATTGTC CATAGTAGAAAA CCCTAGAAAA CCCTAGAAAA CCCTAGAAAA CCTTAGAACTGTC CATAGGTTAC AACACTTTT TGTTAAGGTAA GAAGACTTGC GTCAGGCGCA CGACATATGTGC GGCACCGCA CGACATTTGT TGTTAGGTAA GAAGACCTGA GAAGACCTGA GGAACACTGA GAAGACCTGA GACACTATAGT TAGAAGTGTA TAGAAGTGTA	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1140 1260 1320 1380 1440 1500 1560 1680 1740 1880 2040 2160 2220 2340 2460 2460 2520

	CTGAAGCATA	GTTAGTTTAG	GAAATCACTT	CATATTGATT	GTATTAGAAT	TATCTTGGAA	2640
	TTGAAGATAT	ATCCCTAGAG	CAGGGGACCC	CAACCCCCAG	GCCATGGGCC	ACACAGCAGG	2700
				TCATCTGTAT			2760
-				CAGCTCAGTG			2820
5	GAGCACAAAT	CCTATTGTGA	ACTCTGCATG	CAAGGGATCT	AGGCTATGCG	CTCCTTATGA	2880
	CAATYTAATC	CTTGATGACC	TO A CONTOUR A	CAGTTTCATC	CTCAAACCAC	Contract of Colored	2940
				ACTGGTCCCT			3000
	CCACTGCTCT	AGAGAGAGGT	CATGATATCA	TACCAACCAA	ATGGAAATGA	CAAATGTTTT	3060
	ATGTCAAGTG	TTAATTCCAG	TOTAGETAGE	TTTTTTTTT	TTTTTGGTAG	ADARCDARCA	3120
10 .							
10.				GCAGGTGCTC			3180
	GATGAGCAAG	TGGTTAGGAT	GCAGGGAGAG	CTACTATGGG	TGATATTTTC	CTTGTTTAGG	3240
	AGCTGTGAGT	ATENTAAAAT	TOTTTGGG	TTTATCTAAG	GAAAGTCAAA	TCTTGACAGA	3300
				GACATTGTAT			3360
	ATAACTTCCT	TCTTGCTGAA	CATATTTTAT	TCTCTTTTCA	GAGAAGGAAA	ataaaaagga	3420
15	TTCTAAAAGT	TTGATGCATT	GGAAAAATTT	CCTTGAGGCA	TTTAGCAACA	CATAGAAAAT	3480
				CATAGGGTCT			
							3540
	aatgaaaatt	GAGAAATATA	AGATGAAAAG	GAATGATAAA	AATATCTTTT	AGGGGGCTTT	3600
	TAATTGGTGA	TCTGAAATCT	TGGGAGAAGC	TGTTCTTTTC	AGGCCTGAGG	TGCTCTTGAC	3660
				CATTCTAAGG			3720
20							
20	ACTCCTTTGA	CCTCATTCTT	CATATAGTAG	TCTAGGAAAA	AGTTGCAGGT	AATTTAAACT	3780
	GTCTAGTGGT	ACATAGTAAC	TAAATTTCTA	TTCCTATGAG	AAATGAGAAT	TATTTATTTG	3840
				AAATTTATTG			3900
	GAAAGTTAGA	GAACATTATG	TTTGTATCAT	TTCTTTCATA	AAACCTCAAG	AGCATTTTTA	3960
	AGCCCTTTTC	ATCAGACCCA	GTGAAAACTA	AGGATAGATG	TTTAAAAAACT	GGAGGTCTCC	4020
25				TTTAAGTAAT			4080
23							
	ACCCTTTCTT	GTTAAATAGA	TTTAACAGGA	ACATCTGCAC	ATCTTTTTTC	CTTGTGCACT	4140
	ATTTGTTTAA	TTGCAGTGGA	TTAATACAGC	AAGAGTGCCA	CATTATAACT	AGGCAATTAT	4200
				TAATTGATCG			
							4260
~ ^	AGCATTAGGA	ACATGTGAAG	CTAATCTGCT	CAAAAAGATC	AACAAATTAA	TATTGTTGCT	4320
30	GATATTTGCA	TAATTGGCTG	CAATTATTTA	ATGTTTAATT	GGGTTGATCA	AATGAGATTC	4380
				AACTGGTGGC			4440
				TTTTTCAGTT			4500
	TGTCAGCTTT	TTTGAAAACA	CATCAGTAGA	AACCAAGATT	TTAAAATGAA	GTGTCAAGAC	4560
				ATTTGCTGTT			4620
35							
22				CCAAAAGAAG			4680
	TCCATGCTCT	CTAGCACAGG	AATGAATAAA	TTTATAACAC	CTGCTTTAGC	CTTTGTTTTC	4740
	DADDGCDCDA	ACCAMAGEC	DAAGGGAAAG	AGAAACAAGT	GACTGAGAAG	TCTTGTTAAG	4800
				CTCTATTCTT			4860
			GGIAAACAII	CICIMITCII	TICICAMANG	MIIGCIGIAM	4000
4.0	GAAAAAATGT	AAGAC					
40							
	Com TD 170.	119 Protein					
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	1		21	31	41	51	
	1	11		31	41	51 	
15	l	11 	2 <u>1</u> 	1	1	l	
45	   MKDCSNGCSA	11   ECTGEGGSKE	21       VVGTFKAKDL	   IVTPATILKE	 KPDPNNLVFG	 TVFTDHMLTV	60
45	   MKDCSNGCSA	11   ECTGEGGSKE	21       VVGTFKAKDL	1	 KPDPNNLVFG	 TVFTDHMLTV	60 120
45	 MKDCSNGCSA EWSSEFGWEK	11   ECTGEGGSKE PHIKPLQNLS	21   VVGTFKAKDL LHPGSSALHY	   IVTPATILKE   AVELFEGLKA	KPDPNNLVFG FRGVDNKIRL	TVFTDHMLTV FQPNLNMDRM	120
45	 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP	11   ECTGEGGSKE PHIKPLQNLS VFDKEELLEC	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE	   IVTPATILKE   AVELFEGLKA   WVPYSTSASL	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE	TVFTDHMLTV PQPNLNMDRM PSLGVKKPTK	120 180
45	 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV	11   ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY	 IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS	TVFTDHMLTV PQPNLNMDRM PSLGVKKPTK LFAQCEAVDN	120 180 240
	 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV	11   ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY	   IVTPATILKE   AVELFEGLKA   WVPYSTSASL	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS	TVFTDHMLTV PQPNLNMDRM PSLGVKKPTK LFAQCEAVDN	120 180
	 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG	11   ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE	 IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ	120 180 240 300
45 50	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY	11   ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG	 IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ	120 180 240
	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY	11   ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG	 IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ	120 180 240 300
	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY	11   ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG	 IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ	120 180 240 300
	MKDCSNGCSA EWSSEFGWEK YRSAVRATLEP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT	11   ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS	 IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ	120 180 240 300
	MKDCSNGCSA EWSSEFGWBK YRSAVRATLP ALLFVILSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO:	11   ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ	120 180 240 300
50	MKDCSNGCSA EWSSEFGWBK YRSAVRATLP ALLFVILSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO:	11   ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ	120 180 240 300
	MKDCSNGCSA EMSSEFGWBK YRSAVRATLP ALLFVILSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac	11     ECTGEGGSKE   PHIKPLQNLS   VPDKEELLEC   GPYFSSGTFN   EDHQITEVGT   LTMDDLTTAL   DIQYGREESD   120 DNA secild Accession	21 VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence n #: NM_005:	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ	120 180 240 300
50	 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQOVLWLYG GWGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac Coding seq	11     ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA sec id Accession uence: 121.	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence 1 #: NM_005:	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV	KPDPNNLVFG KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LPAQCEAVDN RRCILDLAHQ HIPTMENGPK	120 180 240 300
50	MKDCSNGCSA EMSSEFGWBK YRSAVRATLP ALLFVILSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac	11     ECTGEGGSKE   PHIKPLQNLS   VPDKEELLEC   GPYFSSGTFN   EDHQITEVGT   LTMDDLTTAL   DIQYGREESD   120 DNA secild Accession	21 VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence n #: NM_005:	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ	120 180 240 300
50	 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding sequil	11   ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA secid Accession uence: 121. 11	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence 1 #: NM_005: .1194 21	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI	TVFTDHMLTV PQPNLNMDRM PSLGVKKPTK LPAQCEAVDN RRCILDLAHQ HIPTMENGPK	120 180 240 300 360
50	 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding sequil	11   ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA secid Accession uence: 121. 11	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence 1 #: NM_005: .1194 21	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI	TVFTDHMLTV PQPNLNMDRM PSLGVKKPTK LPAQCEAVDN RRCILDLAHQ HIPTMENGPK	120 180 240 300
50 55	 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQOVLWLYD GWGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding seq 1   ACAGAGGGCG	11   ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD  120 DNA sec id Accession uence: 121. 11   GGTCGCGGGG	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence 1 #: NM_005: 1194 21   TCGGTGGCCG	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV  377 31 I TTGTGCGCGT	KPDPNNLVFG KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI  41	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC	120 180 240 300 360
50 55	 MKDCSNGCSA EWSSEFGMEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEPKVSERY LASRILSKLT Seq ID NO: Nucleic Ac. Coding seq 1   ACAGAGGGCG CCCAGCTGGA	11     ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA secial Accession uence: 121. 11   GGTCGCGCGC GGGGAACTAG	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence 1 #: NM_005: 11194 21   TCGGTGGCCG TCTGCTCCAG	IVTPATILKE AVELFEGLKA WYPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI  41   GTGTGGAGTG GCGTGAGCAA	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LPAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAAGCCAAC	120 180 240 300 360
50	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Accoding seq 1   ACAGAGGGCG CCCAGCTGGA ATGGACCGCG	11   ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD  120 DNA secid Accession uence: 121. 11   GGTCGCGGGC GGGGAACTAG ACTGGTACCA	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence a #: NM_005: .1194 21   TCGGTGGCCG TCTGCTCCAG TCACTACTTC	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV  377 31   TTGTGCGCGT TACGACTATG	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI  41   GTGTGGAGTG GCGTGAGCAA ACGGCGGGA	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAAGCCAAC GGATTTCTAC	120 180 240 300 360 60 120 180
50 55	 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCOQVLWLYD GCGQVLWLYD GWGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding seq 1   ACAGAGGGCG CCCAGCTGGA ATGGACCGCG CGCTCCACGA	11   ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD  120 DNA see id Accession uence: 121. 11   GGTCGCGGGG GGGGAACTAG ACTGGTACCA CGCCCAGCGA	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence 1 #: NM_005: .1194 21   TCGGTGGCCG TCTGCTCCAG TCACTATTC GGACATCTGG	IVTPATILKE AVELFEGLKA WYPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV 377 31   TTGTGCGCGT GTGCAAGCT TACGACTATG ARGAAATTCG	KPDPNNLVFG KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI  41  GTGTGGAGTG GCGTGAGCAA ACGGCGGGGA ACTTGGTGCC	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCCTGG	120 180 240 300 360 60 120 180 240
50 55	 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCOQVLWLYD GCGQVLWLYD GWGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding seq 1   ACAGAGGGCG CCCAGCTGGA ATGGACCGCG CGCTCCACGA	11   ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD  120 DNA see id Accession uence: 121. 11   GGTCGCGGGG GGGGAACTAG ACTGGTACCA CGCCCAGCGA	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence 1 #: NM_005: .1194 21   TCGGTGGCCG TCTGCTCCAG TCACTATTC GGACATCTGG	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV  377 31   TTGTGCGCGT TACGACTATG	KPDPNNLVFG KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI  41  GTGTGGAGTG GCGTGAGCAA ACGGCGGGGA ACTTGGTGCC	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCCTGG	120 180 240 300 360 60 120 180
50 55	MKDCSNGCSA   MKDCSNGCSA   MKDCSNGCSA   EWSSEFGWEK   YRSAVRATLP   ALLFVLLSPV   GCQOVLWLYG   GGFTUSEN   LASRILSKLT   Seq ID NO: Nucleic Accoding seq 1   ACAGAGGGCG   ACTGGACCGCG   ATGGACCGCG   ACTTGGGTCC   ACTTGGTCC   ACTTGGGTCC   ACTTGGTCC   ACTTGGGTCC   ACTTGGGTCC   ACTTGGGTCC   ACTTGGGTCC   ACTTGGGTCC   ACTTGGTCC	11   ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD  120 DNA sec id Accession Lence: 121. 11   GGTCGCGGGG GGGAACTAG ACTGGTACCA ACTGGTACCA GCCCAGGGA GCAGCCGGGA GCAGCCGGGA	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS  Quence 1 #: NM_005: .1194 21   TCGGTGGCCG TCTGGTCCAG TCACTATTG GGACATCTGG ACCCAGCCCT	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV   377   31   TTGTGCGCGT GTGGCAAGCT TACGACTATG AAGAAATTCG CAGCTTTGGT CAGCTTTGGT	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI  41   GTGTGGAGTG GCGTGAGCAA ACGGGGGGGC CTCCTGGAAC	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LPAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCCTGG GCGCCCCTGG GCGGCCCTGG	120 180 240 300 360 60 120 180 240 300
50 55	MKDCSNGCSA EWSSEFGMEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac. Coding sequ 1 ACAGAGGGCG CCCAGCTGGA ATGGACCGCG CGCTCCACGA ACTTGGGTCC CGGTTGCCCTG	11   ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD  120 DNA secid Accession Lence: 121. 11   GGTCGCGGGC GGGGAACTAG ACTCGTACCA CGCCCAGCGA GCAGCCGGGGA GCGGCGGGGA GCGGCGGGGA GGGACGAGACA	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence 1 #: NM_005: .1194 21   TCGGTGGCCG TCTGCTCCAG TCACTATTTC GGACATCTGG ACCCAGCCCT GGAATCCCAG	IVTPATILKE AVELFEGLKA WYPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV   377   31   TTGTGGGGGT TACGACTATG AAGAATTCG CAGCTTTGGT GACTACTGGA	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI  41   GTGTGGAGTG GCGTGAGCAA ACGGCGGGGA ACTTGGTGCC CTCCTGGAAC AAGCTTGGGAAC AAGCTTGGGAA	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LPAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCTGG GTGGCCGGTA CGCGAACTAC	120 180 240 300 360 120 180 240 300 360
50 55 60	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFRVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding seq 1 ACAGAGGGCG CCCAGCTGGA ATGGACCGGG CGCTCCACGA ACTTGGGTCG GGCTGCCCTCA	11   ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD  120 DNA see id Accession uence: 121. 11   GGTGGGGGG GGGACTAG ACTGGTACCA CGCCAGCGA CGCAGCAGCA GCAGCAGACA TCCGCGGGA TCCGCGGGA TCCGCGGGA	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence 1 #: NM_005: .1194 21   TCGGTGGCCG TCTGCTCCAG TCACTATTTC GGACATCTGG ACCCAGCCT GGAATCCCAG	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV  377  31 I TTGTGCGCGT GTGGCAAGCT TACGACTATG AAGAAATTCG CAGCTTTGGT GACTACTGGA AGCGGCTTCT	KPDPNNLVFG KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI  41   GTGTGGAGTG GCGTGAGCAA ACGGTGGGGA AGTTGGTGCC CTCCTGGAAC AAGCTTGGAGCA AGCTTGGAGCA CCCACCAGGA	TVFTDHMLTV FQPNLINDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCCTGG GTGGCCGGTAC GCGAACTAC GCCGACTAC GCCGCTGAG	120 180 240 300 360 120 180 240 300 360 420
50 55	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFRVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding seq 1 ACAGAGGGCG CCCAGCTGGA ATGGACCGGG CGCTCCACGA ACTTGGGTCG GGCTGCCCTCA	11   ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD  120 DNA see id Accession uence: 121. 11   GGTGGGGGG GGGACTAG ACTGGTACCA CGCCAGCGA CGCAGCAGCA GCAGCAGACA TCCGCGGGA TCCGCGGGA TCCGCGGGA	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence 1 #: NM_005: .1194 21   TCGGTGGCCG TCTGCTCCAG TCACTATTTC GGACATCTGG ACCCAGCCT GGAATCCCAG	IVTPATILKE AVELFEGLKA WYPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV   377   31   TTGTGGGGGT TACGACTATG AAGAATTCG CAGCTTTGGT GACTACTGGA	KPDPNNLVFG KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI  41   GTGTGGAGTG GCGTGAGCAA ACGGTGGGGA AGTTGGTGCC CTCCTGGAAC AAGCTTGGAGCA AGCTTGGAGCA CCCACCAGGA	TVFTDHMLTV FQPNLINDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCCTGG GTGGCCGGTAC GCGAACTAC GCCGACTAC GCCGCTGAG	120 180 240 300 360 120 180 240 300 360
50 55 60	MKDCSNGCSA MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQOVLWLYG GWGFFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding seq 1	11   ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFM EDHQITEVGT LTMDDLTTAL DIQYGREESD  120 DNA see id Accession Lence: 121. 11   GGTCGCGGGG GGGGAACTAG ACTCGTACCA CGCCCAGCGA GCAGCGGGA GCAGCAGGA GCAGCCGGGA GCAGCAGGA GCAGCCGGGA GTCACCTGCT TCCGCCGTGA GTGACCTGCT	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS  Quence n #: NM_005: .1194 21   TCGGTGGCCG TCTGCTCCAG TCACTATTC GGACATCTGG ACCCAGCCCT GGAATCCCAG CTGCATGTGG TGCCATGTGG TGCCATGTGG TGCCATGTGG TGCCATGTGG TGCCATGTGG	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV  377 31 ITTGTGCGCGT GTGGCAAGCT TACGACTATG AAGAAATTCG CAGCTTTGGT GACTACTGGA AGCGGCTTCT GCGCCCTCGG	KPDPNNLVFG KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI  41  GTGTGGAGTG GCGTGAGCAA ACGTGGGGGA ACGTGGGGA AAGTTGGTGCC CTCCTGGAAC AAGCTTGGGA CCACCCAGGA GATACTCGCC	TVFTDHMLTV FQPNLIMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAGCCAAC GGATTTCTAC GCCGCCCTGG GTGGCCGGTA CGCGAACTAC GCCGCTGGAG CAAGGAGTTC CAAGGAGTTC	120 180 240 300 360 60 120 240 300 360 420 480
50 55 60	MKDCSNGCSA   MKDCSNGCSA   MKDCSNGCSA   EWSSEFGMEK   YRSAVRATLP   ALLFVLLSPV   GCQQVLWLYG   WGEPKVSERY   LASRILSKLT   Seq ID NO: Nucleic Ac: Coding seq 1   ACAGAGGGCG   ACGAGCTGGA   ATGGACCGCG   ACGCTCCACGA   ACTTGGGTCC   GCCTCCCTCA   AGAGCGGTGA   AGAGCGGTGA   AGAGCGGTGA   AGAGCGGTGA   AGAGCGGTGA   AGAGCGGTGA   AGAGCGGTGA   GCCACCCCG	11   ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD  120 DNA secid Accession Lence: 121. 11   GGTCGCGGGG GGGGAACTAG ACTGTACCA CGCCAGGGA GCAGCGGGGA GCAGCGGGGA GCGACGGGGA GCGACGGGGA GCGACGGGA GCGACGGGA GCGACGGGA GCGACGGGA GCGACGCGTGA ACTACACTCC	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS  Quence 1 #: NM_005: 1194 21   TCGGTGGCCG TCTGCTCCAG TCACTATTTC GGACATCTGG ACCCAGCCT GGAATCCCAG TGCGTTGGC CTGCATGTGG TGCGTTGGC CGAGCTTGGC CGAGCTCGAA	IVTPATILKE AVELFEGLKA WYPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV   377   31   TTGTGCGCGT GTGGCAAGCT TACGACTATG AAGAATTCG CAGCTTTGGT GACTACTGGA AGCGGCTTCT GGCGCCCTCGG GCCGCCACC	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI  41  GTGTGGAGTG GCGTGAGCAA ACGGCGGGAA ACGTTGGTGCC CTCCTGGAAC AAGCTTGGGA CCACCACGGA GATACTCGCC TAGCGCCCAT	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LPAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCCTGG GTGGCCGGTAC GCGGACTAC GCCGCTGGAG CCAGGCATAC GCCGCTGGAG CCAGGCTTCCCCTGT CTTCCCCTGT	120 180 240 360 120 180 240 360 420 540
50 55 60	MKDCSNGCSA   MKDCSNGCSA   EWSSEFGWEK   YRSAVRATLP   ALLFVLLSPV   GCQQVLWLYG   WGEPKVSERY   LASRILSKLT   Seq ID NO: Nucleic Ac: Coding sequit   ACAGAGGGCG   CCCAGCTGGA   ATGGACCGCG   CGCTCCACGA   ACTTGGGTCC   GGGTGCCTCA   GGAGCGGTTGA   GCCACCCCG   TTGTTGGGCG   TTGTTGGGCG   TTGTTGGGCG   TTGTTGGGCG   TTGTTGGGCG   TTGTTGGGCG   TTGTTGGGCG   TTGTTGGGCG   TTGTTGGGCG   ACACCCCCG   TTGTTGGGCG   TTGTTGGCG   TTGTTGGCG   TTGTTGGGCG   TTGTTG	11   ECTGEGGSKE PHIKPLQNLS VFDKELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD  120 DNA sec id Accession uence: 121. 11   GGTCGCGGGC GGGGAACTAG ACTCGTACCA GCCCAGGGA GCAGCGGG GCAGCGGG GCAGCGGA GCAGCGGGG GCAGCGGGG GCAGCGGGG GCAGCGGGG GCAGCGGGA TCCGCCGTGA TCCGCCGTGA TCCGCCGTGA ACTCGCCTGCA ACCCCAAGAT	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS  Quence n #: NM_005: .1194 21   TCGGTGGCCG TCTGCTCCAG TCACTACTTC GGACATCTGG ACCAGCCCT GGAATCCCAG CTGCATGTGG CTGCATGTGG CTGCATGTGG CTGCATGTGG CTGCATGTGG CCAGGCCTGCAGGCCTGCAGGCCTGCACTGGACACCTGCAGGCCTGCAGGCCTGCAGGCCTGCACGCCTGCAGGCCTGCACGCCTGCACGCCTGCACGCCTGCACGCCTGCACGCCTGCACGCCTGCACCTTGCACCTGCACCTGCACCTGCACCTGCACCTGCACCTGCACCTGCACCTGCACCTGCACCTGCACCTGCACCTGCACCTGCACCTACCT	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV   377   31   TTGTGCGCGT GTGCAAGCT TACGACTATG AAGAAATTCG CAGCTTTGGT GACTACTGGA AGCGCCTCGG GCCGCCACC TCCAGGTCTG TCCAGGTCTG	KPDPNNLVFG KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI  41   GTGTGGAGTG GCGTGAGCAA ACGGCGGGA AGTTGGTGCC CTCCTGGAAC CTCCTGGAAC CCACCAGGA GATACTCGCC TAGCGCCCAT AGAGCCCCAAG	TVFTDHMLTV FQPNLINDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCCTGG GTGGCCCTGG GTGGCCGTAC GCCGCTGGAG CCAAGACTAC GCCGCTGGAG CCAAGGAGTTC CTTCCCCTGT CGACTCCGAG	120 180 240 300 360 60 120 180 240 300 420 480 540 600
50 55 60	MKDCSNGCSA   MKDCSNGCSA   EWSSEFGWEK   YRSAVRATLP   ALLFVLLSPV   GCQQVLWLYG   WGEPKVSERY   LASRILSKLT   Seq ID NO: Nucleic Ac: Coding sequit   ACAGAGGGCG   CCCAGCTGGA   ATGGACCGCG   CGCTCCACGA   ACTTGGGTCC   GGGTGCCTCA   GGAGCGGTTGA   GCCACCCCG   TTGTTGGGCG   TTGTTGGGCG   TTGTTGGGCG   TTGTTGGGCG   TTGTTGGGCG   TTGTTGGGCG   TTGTTGGGCG   TTGTTGGGCG   TTGTTGGGCG   ACACCCCCG   TTGTTGGGCG   TTGTTGGCG   TTGTTGGCG   TTGTTGGGCG   TTGTTG	11   ECTGEGGSKE PHIKPLQNLS VFDKELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD  120 DNA sec id Accession uence: 121. 11   GGTCGCGGGC GGGGAACTAG ACTCGTACCA GCCCAGGGA GCAGCGGG GCAGCGGG GCAGCGGA GCAGCGGGG GCAGCGGGG GCAGCGGGG GCAGCGGGG GCAGCGGGA TCCGCCGTGA TCCGCCGTGA TCCGCCGTGA ACTCGCCTGCA ACCCCAAGAT	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS  Quence n #: NM_005: .1194 21   TCGGTGGCCG TCTGCTCCAG TCACTACTTC GGACATCTGG ACCAGCCCT GGAATCCCAG CTGCATGTGG CTGCATGTGG CTGCATGTGG CTGCATGTGG CTGCATGTGG CCAGGCCTGCAGGCCTGCAGGCCTGCACTGGACACCTGCAGGCCTGCAGGCCTGCAGGCCTGCACGCCTGCAGGCCTGCACGCCTGCACGCCTGCACGCCTGCACGCCTGCACGCCTGCACGCCTGCACCTTGCACCTGCACCTGCACCTGCACCTGCACCTGCACCTGCACCTGCACCTGCACCTGCACCTGCACCTGCACCTGCACCTGCACCTACCT	IVTPATILKE AVELFEGLKA WYPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV   377   31   TTGTGCGCGT GTGGCAAGCT TACGACTATG AAGAATTCG CAGCTTTGGT GACTACTGGA AGCGGCTTCT GGCGCCCTCGG GCCGCCACC	KPDPNNLVFG KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI  41   GTGTGGAGTG GCGTGAGCAA ACGGCGGGA AGTTGGTGCC CTCCTGGAAC CTCCTGGAAC CCACCAGGA GATACTCGCC TAGCGCCCAT AGAGCCCCAAG	TVFTDHMLTV FQPNLINDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCCTGG GTGGCCCTGG GTGGCCGTAC GCCGCTGGAG CCAAGACTAC GCCGCTGGAG CCAAGGAGTTC CTTCCCCTGT CGACTCCGAG	120 180 240 360 120 180 240 360 420 540
50 55 60	MKDCSNGCSA MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCOQVLWLYG MGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding seq I   ACAGAGGGGG CCCAGCTGGA ATGGACCGG GGCTCCACGA ACTTGGGTC GGGTTCCTCA AGAGCGGTGAAGAAATGGGGGGGTGAAGAAAAGGGGTAAGAAAA	11   ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD  120 DNA see id Accession LENCE: 121. 11   GGTGGGGGG GGGGAACTAG ACTGGTACCA GGCCAGCGGA TCGGCGGGG GCAGCGGGA TCCGCCGTGA GTGACCTGCT ACTACACTCC AGCCCAAGAT TCGACGTGAC	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS  Quence 1 #: NM_005: 1194 21   TCGGTGGCCG TCTGGTCCAG TCACTATTC GGACATCTGG ACCAGCCTT GGAATCCCAG CTGCATGTGG CGAGCTCGAA CCAGGCCTGC AGTAAAGAAGAAG	IVTPATILKE AVELFEGLKA WYPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV   377   31   TTGTGCGCGT TACGACTATG AAGAAATTCG CAGCTTTGGT AAGCAGCTTTG GCCCCTCGG GCCGGCAACC TCCAGGTCTG AGGCAGTCTT	KPDPNNLVFG KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI  41  GTGTGGAGTG GCGTGAGCAA ACGGCGGGA ACGTTGGGGC CTCCTGGAAC CCACCTAGGA GATACTCGCC TAGGGCCCAT AGAGCCCAAG TGAGTACGCC TGAGTACGCC	TVFTDHMLTV FQPNLIMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCCTGG GTGGCCGGTA CGCGACTAC GCCGCTGGAG CAAGGAGTTC CTTCCCCTGT CGAACTCCAG GAAGCCACC	120 180 240 300 360 60 120 180 240 300 480 540 660
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	MKDCSNGCSA   MKDCSNGCSA   MKDCSNGCSA   EWSSEFGWEK   YRSAVRATLP   ALLFVLLSPV   GCQOVLWLYG   GWEFREVSERY   LASRILSKLT   Seq ID NO: Nucleic Ac: Coding seq	11	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS  Quence 1 #: NM_005: 1194 21   TCGGTGGCCG TCTGCTCCAG TCACTATTC GGACATCTGG ACCCAGCCCT GGAATCCCAG CTGCATGGG CGAGCTTGGC CGAGCTTGGC CGAGCTTGGA CCAGGCCTGGA CCAGGCCTGGA CCAGGCCTGGA CCAGGCCTGGA CCAGGCCTGGA CCAGGCCTGGA CCAGGCCTGGA CCTTCTGGAT CCTTCTGGAT	IVTPATILKE AVELFEGLKA WYPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV   377   31   TTGTGCGCGT GTGGCAAGCT TACGACTATG GACTATTGGT GACTATTGGT GACTATTGGT GCGCCCTCGG GCCGCAACC TCCAGGTCTG AGGAGTCTT CCCCGCATGA	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI  41    GTGTGGAGTG GCGTGAGCAA ACGTGGGGCCCAT ACACCTAGGA CCACCAGGA GATACTCGCC TAGCGCCCAT ACAGCCCCAG ATGACCCCAG ATGACTACGCC ATGTCCTCCCA	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LPAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCCTGG GCGCCCTGG GCGCCCTGG CAGGAGTTC CCCTGTTCCCCTGT CGACTCCCAGC CAAGCCAAC CAAGCCAGC CAAGCCAGC CAAGCCAGC CAAGCCAGC CAAGCCAGC CAAGCCAGC CAACTCCCATC CATCTCCATC	120 180 240 300 360 120 180 240 360 420 540 660 720
50 55 60	MKDCSNGCSA   MKDCSNGCSA   MKDCSNGCSA   EWSSEFGMEK   YRSAVRATLP   ALLFVLLSPV   GCQQVLWLYG   WGEPKVSERY   LASRILSKLT   Seq ID NO: Nucleic Ac. Coding seq 1   ACAGAGGGCG   ATGGACCGCG   ATGGACCGCG   AGAGCGTGA   AGAGCGTGA   AGAGCGTGA   AGAGCGTGA   AGAGCGTGA   AGAGCGTGA   ACATCGCGC   ACACCCCCG   ACACCCCCCG   ACACCCCCCG   ACACCCCCCG   ACACCCCCCG   ACACCCCCCCCCC	11   ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD  120 DNA secid Accession Lence: 121. 11   GGTCGCGGGC GGGGAACTAG ACTCGTACCA GCCCAGGGA GCGACGAGGA GCGACGAGGA GCGACGGGA GCGACGGGA GCGACGGGA TCCGCCGTGA GTGACCTGCT ACTACACTCC AGCCCAAGAT TCGACGTGAC AGCCCAAGAT TCGACGTGAC AGCCCAAGAT ACGACAACTA	21   VVGTFKAKDL LHPGSSALHY IQQIVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS  Quence 1 #: NM_005: .1194 21   TCGGTGGCCG TCACTATTTC GGACATCTGG ACCCAGCCT GGAATCCCAG CCGAGCTCGAA CCAGGCTGC AGTAAAGAAG CCTGGATAAAGAAG CCTTCTGGAT TGCTGCCCT TGCGTTCTGGAT TGCTGCCCCT TGCTTCTGGAT TGCTGCCCCT TGCTTCTGGAT TGCTGCCCCT	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV  377  31   TTGTGCGCGT TACGACTATG AAGAAATTCG CAGCTTTGGT GACTATGGT AGCGCTCGG GCCCCTCGG GCCCCTCGG GCCCCTCGG TCCAGGTCTT CCCCGCATCA AGGAATTCT CCCCGCATGA TTTCCTCCAG	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI  41  GTGTGGAGTG GCGTGAGCAA ACGGCGGGA AGTTGGTGCC CTCCTGGAAC AAGCTTGGGA CCACCCAGGA AGATACTCGCC TAGCGCCCAT AGAGCCCAAG TGAGTACCCCA ATGATACTCGCA ATGATACTCGCA ATGATACTCCTCA AAAGCTGCTT	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LPAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCGCCCTGG GTGGCCGCTGCAG GCGGCCTGGAG CCAGCTGCAG GCAGCCATC CCCTGCTGCAG GCAGCCATC CCCAGCACTCC CCAAGAAGGG CCATCCCATC	120 180 240 300 360 120 180 240 300 360 420 480 660 660 780
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	MKDCSNGCSA   MKDCSNGCSA   MKDCSNGCSA   EWSSEFGMEK   YRSAVRATLP   ALLFVLLSPV   GCQQVLWLYG   WGEPKVSERY   LASRILSKLT   Seq ID NO: Nucleic Ac. Coding seq 1   ACAGAGGGCG   ATGGACCGCG   ATGGACCGCG   AGAGCGTGA   AGAGCGTGA   AGAGCGTGA   AGAGCGTGA   AGAGCGTGA   AGAGCGTGA   ACATCGCGC   ACACCCCCG   ACACCCCCCG   ACACCCCCCG   ACACCCCCCG   ACACCCCCCG   ACACCCCCCCCCC	11   ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD  120 DNA secid Accession Lence: 121. 11   GGTCGCGGGC GGGGAACTAG ACTCGTACCA GCCCAGGGA GCGACGAGGA GCGACGAGGA GCGACGGGA GCGACGGGA GCGACGGGA TCCGCCGTGA GTGACCTGCT ACTACACTCC AGCCCAAGAT TCGACGTGAC AGCCCAAGAT TCGACGTGAC AGCCCAAGAT ACGACAACTA	21   VVGTFKAKDL LHPGSSALHY IQQIVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS  Quence 1 #: NM_005: .1194 21   TCGGTGGCCG TCACTATTTC GGACATCTGG ACCCAGCCT GGAATCCCAG CCGAGCTCGAA CCAGGCTGC AGTAAAGAAG CCTGGATAAAGAAG CCTTCTGGAT TGCTGCCCT TGCGTTCTGGAT TGCTGCCCCT TGCTTCTGGAT TGCTGCCCCT TGCTTCTGGAT TGCTGCCCCT	IVTPATILKE AVELFEGLKA WYPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV   377   31   TTGTGCGCGT GTGGCAAGCT TACGACTATG GACTATTGGT GACTATTGGT GACTATTGGT GCGCCCTCGG GCCGCAACC TCCAGGTCTG AGGAGTCTT CCCCGCATGA	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI  41  GTGTGGAGTG GCGTGAGCAA ACGGCGGGA AGTTGGTGCC CTCCTGGAAC AAGCTTGGGA CCACCCAGGA AGATACTCGCC TAGCGCCCAT AGAGCCCAAG TGAGTACCCCA ATGATACTCGCA ATGATACTCGCA ATGATACTCCTCA AAAGCTGCTT	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LPAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCGCCCTGG GTGGCCGCTGCAG GCGGCCTGGAG CCAGCTGCAG GCAGCCATC CCCTGCTGCAG GCAGCCATC CCCAGCACTCC CCAAGAAGGG CCATCCCATC	120 180 240 300 360 120 180 240 360 420 540 660 720
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	MKDCSNGCSA   MKDCSNGCSA   MKDCSNGCSA   EWSSEFGWEK   YRSAVRATLP   ALLFVLLSPV   GCOQVLWLYG   GCOQVLWLYG   GCOQVLWLYG   GCOTCAGCTGA   ACAGAGGGGC   GCTCCACCAGA   ACTGGGTCC   GGOTGCGGTG   GCTCCCTCA   AGAGCGGTGAGACACCCCG   GGTGAAGAAA   ATCATCGCGG   GCTCCACAGAACACCACCAGCAACGCTCCAAGAGACGCTCCAAGAGACGCTCCAAGAGACGCTCCAAGAGACAGCAACCGCTCCAAGAGACACCCCCCAGCAACGCTCCAAGAGACACCCCCCAGCAACGCTCCAAGAACACCTCCAAGAACACCTCCAAAGAACACCTCCAAACAACACCTCCAAAACACCCTCCAAAGAACACCTCCAAAACACCCTCCAAAGAACACCTCCAAACAACACCTCCAAAACACCCTCCAAAACAAC	11   ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD  120 DNA see id Accession uence: 121. 11   GGTCGCGGGC GGGAACTAG ACTCGTACCA CGCCAGCGA TCCGCCGTGA TCCGCCGTGA TCCGCCGTGA TCGCCGTGA TCGACGTGAC TCGCCTGCAGAT TCGACGTGAC TGGCTGCAGGA AGCACAACTA GGATGCCCCC GGAGACTAG AGCACAACTA GGATGCCCCC	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS  Quence 1 #: NM_005: .1194 21   TCGGTGGCCG TCTGCTCCAG TCACTATTTC GGACATCTGG ACCAGCCTT GGAATCCAG CTGCATGGG CGGAGTCGAA CCAGCCTGCA CCAGCCTGCA CTGCATTGGC CTGCATTGGC TGCCTTTGGAT CCAGCCTGCA CCAGCCTGCA CCAGCCTGCA CCAGCCTGCA CCAGCCTGCA CCAGCCTGCA CCAGCCTGCA ACAAGAAGA CCAGCCCTGCA ACAAGAGAGCCTA AAAAGAGGCCT	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV  377  31 ITGTGGGCGT GTGGCAAGCT TACGACTATG AAGAAATTCG CAGCTTTGGT GACTACTGGA GCCCCTCGG GCCCCTCGG TCCAGGCTTCT CCCGCAAGC TTCCAGGCATCA TTCCTCCAG CTAGAGAGAG	KPDPNNLVFG KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVTI SDILYKGETI  41  GTGTGGAGTG GCGTGAGCAA ACGTGGGGA AGTTGGTGCC CTCCTGGAAC AAGCTTGGGA CCACCAGGA GATACTCGCC TAGGCCCCAGGA TGAGTACGCC ATCTCTTCCA AAGCTCCTTCCA AAAGCTCCAGGA AAAGCTCCAGGA AAAGCTCCAGGA AAAGCTCCAGGA	TVFTDHMLTV FQPNLIMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAAGCCAAC GGAATTCTAC GCCGCCTGG GTGGCCGGTA GCGGACTAC GCCGCTGGAG CAAGGAGTTC CTTCCCCTGT GACTCCCAGG GAAGCCAGTC CATCTCCATC CCCAGAAGGAGT CCCAAGAAGGAGT CCCAAGAAGGAGG GGGAAAGGAT	120 180 240 300 360 60 120 180 240 306 480 540 660 720 780 840
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>		11   ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD  120 DNA see id Accession LENCE: 121. 11   GGTCGCGGGG GGGGAACTAG ACTCGTACAC CGCCAGCGG GGGAACTAG GTGACCTGCT ACTACACTCC AGCCCAGGAT TCGAGGTGAC TCGGTGAGA TGGGTGCAG AGGACAGAGT TCGAGGTGAC AGGACAGACT AGGATGCCCC AGGACACACTA AGGATGCCCCC ATGAAGAGAT	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS  Quence 1 #: NM_005: 1194 21   TCGGTGGCCG TCTGCTCCAG GCATTCCAG GCATCTCG GCATTGG TCGCATGTGG TCGCATGTGG TGCATGTGG TGCATGCCTGC AGTAAAGAAG CCTTCTGGAT TGCTGCCCT TGTGAGCCTC	IVTPATILKE AVELFEGLKA WYPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV  377  31 ITGTGCGCGT TACGACTATG AAGAAATTCG CAGCTTTGGT GCGCCTCGG GCCGCAACC TCCAGGTCTT CCCCGCATGA TTTCCTCCAG TTTCCTCCAG CTAGAGAGAG CCACCTGTAG	KPDPNNLVFG KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI  41  GTGTGGAGTG GCGTGAGCAA ACGTGGGA ACTTGGTGC CTCCTGGAAC CCACCAGGA GATACTCGCC TAGGGCCCAGG GATACTCGCA TGAGTACGGC ATGTTCTCCA AAAGCTCCAGG AAAGTTACGGG AAAGTTACGGG AAAGTTACGGG AAAGTCCAGG	TVFTDHMLTV FQPNLIMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCGCCCTGG GTGGCCGGTA CGCGACTAC GCGGACTAC GCGGACTAC GCGACTGGAG CAAGGAGTTC CTTCCCCTGT CGACTCCGAG GAAGCCAGTC CATCTCCATC CCAAGAAGGGT TGCCCAGTCC	120 180 240 300 360 120 180 240 360 420 540 600 720 780 840 900
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>		11	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS  Quence n #: NM_005: .1194 21   TCGGTGGCCG TCTGCTCCAG TCACTATTTC GGACATCTGG ACCAGCCT GGAATCCCAG CCGCTTGGC CCAGCCTTGGCAGTTGGC CCAGCCTTGGAGCCT AAAAGAAG TGCTGCCCCT TGTGAGCCT TGTGAGCCT TGTGAGCCT TTATGATACT TTATGATACT	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV  377 31 ITTGTGCGCGT GTGGCAAGCT TACGACTATG AAGAAATTCG GACTATTGGT GACTACTGGT GCGCCCTCGG GCCGCAACC TCCAGGTCTT ACGCAGTCTT CCCCGCATGA TTTCCTCCAG CTAGAGAAGAG CTAGAGAGAGG CCACCTGTAG GAGAATTGGA	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI  41  GTGTGGAGTG GCGTGAGCAA ACGGCGGGAA CCACCAGGA CCACCAGGA GATACTCGCC TAGCGCCCAT AGAGCCCAGG TGAGTACGCG AAAGCTCCTC AAAGCTCCAGA AAGCTCCTC AAAGCTCCAGA AAGCTCCTT AAGCTCCAGA AAAGCTGCTT AAAGCTCCAGA AAAGCTGCTT AAAGCTCCAGA AAAGCTAGGAC CCAAGAAGAA	TVFTDHMLTV TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LPAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAGCCAAC GGATTTCTAC GCCGCCCTGG GCAGCCAGC GCAGCCAGC GCAGCCTGGA CCGGCCTGGA CAGGAGTTC CTTCCCCTGT CGACTCCGAG GAAGCCAGT CCATCTCCATC CCAAGAAGGG GGGAAAGGGT TGCCCAGTC CCAAGAAGGG GGGAAAGGGT TGCCCAGTCC GTACCACGC	120 180 240 300 360 120 180 240 420 480 600 600 780 840 960
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>		11	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS  Quence n #: NM_005: .1194 21   TCGGTGGCCG TCTGCTCCAG TCACTATTTC GGACATCTGG ACCAGCCT GGAATCCCAG CCGCTTGGC CCAGCCTTGGCAGTTGGC CCAGCCTTGGAGCCT AAAAGAAG TGCTGCCCCT TGTGAGCCT TGTGAGCCT TGTGAGCCT TTATGATACT TTATGATACT	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV  377 31 ITTGTGCGCGT GTGGCAAGCT TACGACTATG AAGAAATTCG GACTATTGGT GACTACTGGT GCGCCCTCGG GCCGCAACC TCCAGGTCTT ACGCAGTCTT CCCCGCATGA TTTCCTCCAG CTAGAGAAGAG CTAGAGAGAGG CCACCTGTAG GAGAATTGGA	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI  41  GTGTGGAGTG GCGTGAGCAA ACGGCGGGAA CCACCAGGA CCACCAGGA GATACTCGCC TAGCGCCCAT AGAGCCCAGG TGAGTACGCG AAAGCTCCTC AAAGCTCCAGA AAGCTCCTC AAAGCTCCAGA AAGCTCCTT AAGCTCCAGA AAAGCTGCTT AAAGCTCCAGA AAAGCTGCTT AAAGCTCCAGA AAAGCTAGGAC CCAAGAAGAA	TVFTDHMLTV TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LPAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAGCCAAC GGATTTCTAC GCCGCCCTGG GCAGCCAGC GCAGCCAGC GCAGCCTGGA CCGGCCTGGA CAGGAGTTC CTTCCCCTGT CGACTCCGAG GAAGCCAGT CCATCTCCATC CCAAGAAGGG GGGAAAGGGT TGCCCAGTC CCAAGAAGGG GGGAAAGGGT TGCCCAGTCC GTACCACGC	120 180 240 300 360 120 180 240 420 480 600 600 780 840 960
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	MKDCSNGCSA MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding seq I	11   ECTGEGGSKE PHIKPLQNLS VFDKELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD  120 DNA sec id Accession Lence: 121. 11   GGTCGCGGGC GGGAACTAG ACTCGTACCA GCCCAGGGA GCAGCAGGA TCCGCCGTGA GTACCTGCC AGCCAAGGAT TCGACGTGAC AGCACAACTA AGCACAACTA AGCACCATCA ACCCATCCA ACCCATCCA ACCCATCCA ACCACCATCA ACCCATCCA GCAAGAGACCG ACGAAGAGACGAC GCAAGAGACCG	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS  Quence 1 #: NM_005: .1194 21   TCGGTGGCCG TCTGCTCCAG TCACTACTTC GGACATCTGG ACCCAGCCCT GGATCCCAG CTGCATGGG CTTCTGGAT TGGTGCCCT AAAAGAGGCT TGTGACCTC TATGATACT GAATGATCA	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV   377   31   TOTGGCAGGT GTGGCAAGGT TACGACTATGA AAGAATTCG CAGCTTGGT GCCCCCCATG GCCCCCCCATG AGGCAGCTTCCCCGCATGA TTTCCTCCAG CTAGAGAGAG CCACCTGTAG GAGAATTGGA CGAGTATGA CGTTCGCGGT	KPDPNNLVFG KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGSTI SDILYKGETI  41   GTGTGGAGTG GCGTGAGCAA ACGTGGGGGA AGTTGGTGCC TCCTGGAAC CTACCAGGA GATACTCGCC TAGAGCCCAT AGAGCCCAAG TGAGTACGC ATCTCTTCCA AAAGCTGCTT AAGCTCCAGG AAAGCTGCTT AAGCTCCAGG AAAGTGAGGC CCCAAGAAGAA TCTTGGCCCT	TVFTDHMLTV FQPNLINDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCTGG GTAGCGAGTAC CCTCCCTGT CGACTCCCAG GAAGCAGTC CATCCCAGG GAAGCAGTC CCATCCCAGG GAAGCAGTC CCAGGAAGGAGTT CCCAGGAAGGAGTT CCCAGGAGAAGGAT TGCCCAGTC CGACTCCCAG GAAGCCAGTC CCAAGAAGGAT TGCCCAGTCC GTACCACAGC GTACCACAG	120 180 240 300 360 120 180 240 300 420 480 540 660 720 840 900 900 1020
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>		11   CONTROL OF CONTRO	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS  Quence 1 #: NM_005: .1194 21   TCGGTGGCCG TCTGCTCCAG TCACTATTTC GGACATCTGG ACCAGCCTT GGAATCCCAG CTGCATGGC CGAGCTCGAA CCAGCCTGCA ACTACATGG TGCCTTTGGCT TGCATTTGGCTTCAGGCTCT AAAAGAGGCT TGAATAACAT CTCTAGGGTT GAATGATCAAC CTCTAGGGTT GAATGATCAAC CTCTAGGGTT CAATGATCAAC CTCTAGGGTT CAATGATCAAC CTCTAGGGTT CAATGATCAAC CTCTAGGGTT CAATGATCAAC CTCTAGGGTT CAATGATCAAC CTCTAGGGTT	IVTPATILKE AVELFEGLKA WYPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV  377  31 ITGTGCGCGT TACGACTATG AAGAAATTCG CAGCTTTGGT GCCCCTCGG GCCGCAACC TCCAGGTCT AGGCAGTCT AGGCAGTCT AGGCAGTCT AGGCAGTCT AGGCAGTCTT CCCCGCATGA TTTCCTCCAG CTACAGAGAG CCACCTGTAG GAGAATTGGA CGTTCGCGGT TCCAGGTTCGCGGT TCCAGGAGAGAGC CTACAGAGAGAG CCACCTGTAG GAGAATTGGA CGTTCGCGGT TCCAAGTAA	KPDPNNLVFG KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI  41  GTGTGGAGTG GCGTGAGCAA ACGGCGGGA ACGTTGGGCC CTCCTGGAAC CCACCAGGA GATACTCGCC TAGGCCCAGGA TGAGTACGCC ATCTTTCCA AAAGCTGCTT AAGCTCCTGGA CCAAGAAGAA ACTTCAGC CCAAGAAGACA TCTAGAGCC TAGGCCCAGG AAAGTGAGGC CCAAGAAGACA TCTGAGCCCT TGATCCTAGT	TVFTDHMLTV TVFTDHMLTV TVFTDHMLTV PSQPKLPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCTGG GTGGCCGTGA CCCGGACTAC CCCTGCTGCC CAAGCAGCA GAAGCCAGT CAAGCAGT CAAGAAGGA GAAGCAGT CCCAAGAAGGA GAAGCAGT CCCAAGAAGGG GGAAAAGGAT TGCCCAGTC CTACCACC CCAAGAAGGG CAAGAACGAC CAAGAACGAC CAAGGACCAGC CAAGGACCAGC CAAGGACCAGC CAAGGACCAGC CAAGGACCAGC CAAGGACCAGC CAAGGACCAC CAAGGACCACC	120 180 240 300 360 120 180 240 306 420 480 540 660 720 840 900 960 1020 1080
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	MKDCSNGCSA   MKDCSNGCSA   CWSSEFGWEK   YRSAVRATLP   ALLFVLLSPV   GCQOVLWLYG   GCGTLSKLT   GGGTGAGAGGGGG   CCCAGCTGGA   ACTGGGGGGGCGCCCCCGGGGTGAGAGAGAGAGAGAGAGA	11	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS  Quence 1 #: NM_005: 1194 21   TCGGTGGCCG TCTGCTCCAG TCACTATTC GGACATCTGG ACCCAGCCT GGAATCCCAG CTGCATTGGC AGTAAAGAGG CCTTCTGGAT TGCTGGCC TTGTGAT TGTGAGCCT TTGTGAGCCT TTGTGAGCCT TTGTGAGCCT TTGTGAGCCT TGTAGGCCT GGAATCATAGG CTTATGATACT GGAAGCCGAG CTCTAGGGTT GGAAGCCGAG	IVTPATILKE AVELFEGLKA WYPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV  377  31 ITTGTGCGCGT TACGACTATGA AAGAAATTCG CAGCTTTGGT GACTACTGGA AGCGGCTTCT CCCGCATGA TTTCCTCCAG TTCAGAGAGC CTAGAGAGA CCTACGAGTCT CCCGCATGA CTAGAGAGA CCACCTGTAG GAGAATTGGA CGACCTGTAG GAGAATTGGA CGACCTGTAG GAGAATTGGA CGACCTGTAG GAGAATTGGA CGACCTGTAG GAGAATTGGA CGACCTGTAG GAGAATTGGA CGACGATGA TTCCAAAGTAA GAGAGGATGG	KPDPNNLVFG KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI  41    GTGTGGAGTG GCGTGAGCAA ACGTGGGAA ACGTGGGGGA AAGTTGGTGCC TAGCGCCCAT AGAGCCCAAG ATCATCCAG ATCATTCCA AAAGTTACTGC TAGGGCCCAT AAAGTTACGG CCAAGAACAA CCTTGGCC TAGCTCAGG TGATCAGGC CCAAGAAGAA TCTTGGCCT TGATCCTAGT CTACGGAGAA	TVFTDHMLTV TVFTDHMLTV TVFTDHMLTV PSPLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAGCCAAC GGATTTCTAC GCCGCCTGG GTGGCCGTA GCGGACTAC GCGGACTAC GCAGTCCAGT CCAGTCCAGT	120 180 240 360 360 120 180 240 360 420 780 840 960 960 1020 1140
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	MKDCSNGCSA   MKDCSNGCSA   CWSSEFGWEK   YRSAVRATLP   ALLFVLLSPV   GCQOVLWLYG   GCGTLSKLT   GGGTGAGAGGGGG   CCCAGCTGGA   ACTGGGGGGGCGCCCCCGGGGTGAGAGAGAGAGAGAGAGA	11	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS  Quence 1 #: NM_005: 1194 21   TCGGTGGCCG TCTGCTCCAG TCACTATTC GGACATCTGG ACCCAGCCT GGAATCCCAG CTGCATTGGC AGTAAAGAGG CCTTCTGGAT TGCTGGCC TTGTGAT TGTGAGCCT TTGTGAGCCT TTGTGAGCCT TTGTGAGCCT TTGTGAGCCT TGTAGGCCT GGAATCATAGG CTTATGATACT GGAAGCCGAG CTCTAGGGTT GGAAGCCGAG	IVTPATILKE AVELFEGLKA WYPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV  377  31 ITTGTGCGCGT TACGACTATGA AAGAAATTCG CAGCTTTGGT GACTACTGGA AGCGGCTTCT CCCGCATGA TTTCCTCCAG TTCAGAGAGC CTAGAGAGA CCTACGAGTCT CCCGCATGA CTAGAGAGA CCACCTGTAG GAGAATTGGA CGACCTGTAG GAGAATTGGA CGACCTGTAG GAGAATTGGA CGACCTGTAG GAGAATTGGA CGACCTGTAG GAGAATTGGA CGACCTGTAG GAGAATTGGA CGACGATGA TTCCAAAGTAA GAGAGGATGG	KPDPNNLVFG KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI  41    GTGTGGAGTG GCGTGAGCAA ACGTGGGAA ACGTGGGGGA AAGTTGGTGCC TAGCGCCCAT AGAGCCCAAG ATCATCCAG ATCATTCCA AAAGTTACTGC TAGGGCCCAT AAAGTTACGG CCAAGAACAA CCTTGGCC TAGCTCAGG TGATCAGGC CCAAGAAGAA TCTTGGCCT TGATCCTAGT CTACGGAGAA	TVFTDHMLTV TVFTDHMLTV TVFTDHMLTV PSQPKLPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCTGG GTGGCCGTGA CCCGGACTAC CCCTGCTGCC CAAGCAGCA GAAGCCAGT CAAGCAGT CAAGAAGGA GAAGCAGT CCCAAGAAGGA GAAGCAGT CCCAAGAAGGG GGAAAAGGAT TGCCCAGTC CTACCACC CCAAGAAGGG CAAGAACGAC CAAGAACGAC CAAGGACCAGC CAAGGACCAGC CAAGGACCAGC CAAGGACCAGC CAAGGACCAGC CAAGGACCAGC CAAGGACCAC CAAGGACCACC	120 180 240 360 360 120 180 240 360 420 780 840 960 960 1020 1140
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	MKDCSNGCSA EWSSEPGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEPKVSERY LASRILSKLT  Seq ID NO: Nucleic Ac: Coding sequity ACAGAGGGCG CCCAGCTGGA ACTTGGACCGCG GGGTGCCCTCA AGAGCGCTG GCTCCCTCA AGAGCGTTGA ACTTGGGCG GGTTGAAGAAA ATCATCGCGG CACCAGCAAC GCTCCAAAGA GTTCAAAGA GTTCCAAGA TACCTGGAGC GTACCCCCG GATACTCAC GAATACTCAC GAATGCCAC GAATACTCAC GAATGCCAGC GAATACTCAC GAATGCCAGC	11   ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD  120 DNA sec id Accession Lence: 121. 11   GGTCGCGGGC GGGGAACTAG ACTCGTACCA ACTCGTACCA GCGCAGGGA GGGACGGGA GGGACGGGA GGGACGGGA TCGGCGGGA TCGCCGGGA TCGACGTGAC TCGACGTGAC TGCGTGAGA AGCACACTA GGATGCCCC ATGAAGAGAT AACCCATCCA ATGAAGAGAT AACCATCCA GCAAGAGACG TGGCGGGCGGC TGGCGGCGGCTGA GCAAGAGACG TGGCAGCTGC ATGAAGAGAT AACCCATCCA GCAAGAGACG GCAGGCGGC ATGAACTGCC ATGAAGAGAT AACCCATCCA GCAAGAGACG GCAGGCGGC ATGAACTGCC GCAGGCGGCTG TGGCCAGCTG TGGCCAGCTG TGGCCAGCTG TGGCCAGCTG ATGAACTGGC GACGCCAATT	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS  Quence 1 #: NM_005: .1194 21   TCGGTGGCCG TCACTATTC GGACATCTGG ACCAGCCTT GGAATCCCAG CCGAGCTCGAA CCAGCCTGC AGTAAAGAAGA CCTTCTGGAT TGCTTGGCC TTGTGACCTT TGTGAGCCT TGTAACTACT GAATGATCAA CTTTAGGGTT GGAAGCCGAG GGAAGCCGAG GGAAGCCGAG GGAAGCCGAG GGAAGCGGAG GGAAGAAGAG	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV  377  31   TTGTGCGCGT GTGGCAAGCT TACGACTATGG AAGAAATTCG CAGCTCTGG GCCCCTCGG GCCCCTCGG GCCGCAACC TCCAGGTCTT CCCCGCATGA TTTCCTCCAG CTAGAGAGAG CCACCTGTAG GAGAATTGG AGGAGATTGG AGGAGATGG AGGAGATTGAGAGAGA	KPDPNNLVFG KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI  41  GTGTGGAGTG GCGTGAGCAA ACGGGGGGA AGTTGGTGCC CTCCTGGAAC CTACCCAGGA GATACTCGCC ATACTCGCA AGAGCCCAAG TGAGTACGCG ATCTCTTCA AAAGCTGCTT AAGCTCCAG AAAGTAGGCC CCAAGAAGAA TCTTGGCCCT TGATCCTAGT TGATCCTAGT TGATCCTAGT	TVFTDHMLTV FQPNLINDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCTGG GTAGCCCATAC GCCGCTGAG CAAGAAGTAC GCCGTGAG CAAGAAGTTC CATCTCCATC CCAAGAAGGG GGAAAGGAT TGCCCAGTC GTACCCAGG GAAGCCAAC GTACCCAGG GAAGCCAAC GAGGACTAC GAAGCCAAC GAAGCCAAC GAAGCCAAC GAAGCCAAC GAAGGCCAC GAAGGCAC GAAGGCAAC CAAGGCCACAC GAAGGCCACAC GAAGGCCACAC GAAGGCCACAC CAAGGCCACAC CTGACCCAAAA	120 180 240 360 360 120 180 240 360 420 480 660 720 780 840 900 1020 1080 1080
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	MKDCSNGCSA MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCOQVLWLYG WGEPKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding seq I   ACAGAGGGGC CCCAGCTGGA ACTGGGACCGCC GGGTGCGGTG GCTCCCTCA AGAGCGGTGCGGT	11   ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD  120 DNA sec id Accession Lence: 121. 11   GGTCGCGGGC GGGGAACTAG ACTCGTACCA CGCCAGGAA TCGCCGGGA TCGCCGTGA TCGACTGCT ACTACACTCC AGCCCAAGAT TCGACTGCC ATGAGAGAC GGATGCCCCC ATGAGAGAC TGCGTGCAGA ACCCATCCA TGGAGTGAC TGCGTGCAGA TGGAGTGAC TGGGTGCAGA TGGAGTGAC TGGTGCAGA AGCACAACTA GGATGCCCCC ATGAAGAGAC TGCGTGCAG TGGAGTGAC TGCGTGCAG TGGAGTGAC TGGAGTGAC TGCGTGCAGAT TCTGACTTCA TTGATTCTTA	21   VVGTFKAKDL LHPGSSALHY IQQLVKLIQQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS  Quence 1 #: NM_005: .1194 21   TCGGTGGCCG TCTGCTCCAG TCACTATTTC GGACATCTGG ACCAGCCTT GGAATCCAG CTGCATGGC CGAGCTCGA CCAGCCTGC AGTAAAGAAG CCTGCACTGC AGTAAAGAAG CTTGTGGCCCT TGTGGCCCT TGTGGCCCT TGTGGCCCT TGTGGCCCT TGATGATACT GAATCATCAA CTCTAGGGTT GAATCATCAA CTCTAGGGTT GGAAGCCGAG AAAAGAAAAA AAAAGACAAA	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV  377  31 ITGTGCGCGT GTGGCAAGT TACGACTATGA AAGAAATTCG CAGCTTTGGT GACTACTGGA GCCCTCGG GCCCCTCGG GCCCCTCGG GCCCATGA TTTCCTCCAG CTACAGAGAGA CCTACAGAGAG CCACCTGTAG GAGAATTGG CAACTTGGT TCCAAAGTAA GAGAGATGAA CGTTCGCGGT TCCAAAGTAA GAGAGATGAA CAGTTTCCTCA CGTTCGCGT TCCAAAGTAA CAAGTAAC CAATTACTACAAGTAA CAAGAGATAAC CATTTCCTCT AGGAGATTACC AGTTTTCTTT	KPDPNNLVFG KPDPNNLVFG KPDPNNLVFG KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPKGETI  SDILYKGETI  GCGTGGGAGTG GCGTGAGGGA AGGTGGGGGA AGGTTGGTGCC CTCCTGGAAC CCACCAGGA GATACTCGCC TAGGCCCAAG TGAGTACGCC AAAGCTACGTA AAAGCTCCTT AAAGCTCCAGG AAAGTGAGGC CCAAGAAGAA TCTTGGCCCT TGATCCTAGT TGATCTCCCC	TVFTDHMLTV TVFTDHMLTV TVFTDHMLTV FQPNLIMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCTGG GGATTTCTAC GCCGCCTGG GGAGCTAC GCCGCTGGG GAGGCAGTC CATCCCATC CCAAGAAGGG GGAAAGGAT TGCCCAGTC GTACCACAG GAGGACAGC GTACCACAG GAGGACAGA TGCCCAGGC CAAGGAGGAC CAAGGACAGC CAAGGACAGC CTACCACAC CAAGGACAGC CAAGGCACC CTACCAAAA TCTCCCCTTT	60 120 180 360 360 120 180 240 300 420 480 540 660 720 900 900 900 1020 1080 1140 1260
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	MKDCSNGCSA   MKDCSNGCSA   EWSSEFGWEK   YRSAVRATLP   ALLFVLLSPV   GCQOVLWLYG   GGGTLSKLT   GAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	11	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS  Quence 1 \$: NM_005: 1194 21   TCGGTGGCCG TCTGCTCCAG TCACTATTC GGACATCTGG ACCCAGCCCT GGAATCCCAG CTGCATGGG CGACTTGGC CGAGCTTGGC CGAGCTTGGC CGAGCTTGGC TGCATTGGG TGCCTTTGGAT TGCAGGCTTGGC TGTGAGAGAG AGAAGAGAG ACTCTGGAT TGTGAGCCT TTATGATACT GGAATCATACT GGAATCATACT GGAATCACAG ACTCTGGGT TGTGAGCCTC TTATGATACT TGTAGGCTC TTATGATACT GGAAGCCGAG ACACACA ACACACACA ACACGCAGGAAAAGA AAAAGACACA	IVTPATILKE AVELFEGLKA WYPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV  377  31 ITGTGCGCGT TACGACTATG AAGAAATTCG GACTTTGGT GACTTTGGT GCGCCTCGG GCCGCAACC TCCAGGTCTT CCCCGCATGA TTTCCTCCAG GTAGAATTGAT CCACTGTAG GAGAATTGGA CCTTCGCGGT TCCAGGTCTT CCACGGTT CCACGGTT CCACGGTT CCACGGTT CCACGGTT CCACGGTT CCACGGTT CCACGGTT CCACGGTT CCACTGTAG GAGAATTGAA CGTTCGCGGT TCCAAAGTAA GAGAGGATGG ATTGATACC AGTTTTCTTT CACTCTGGAC	KPDPNNLVFG KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI  41  GTGTGGAGTG GCGTGAGCAA ACGTGGGAA ACGTGGGGA CCACCAGGA GATACTCGCC TAGGGCCCAGGA GATACTCGCC TAGGCCCAAG AAGCTGCTGA AAGCTGCTT AAGCTCCAGG AAAGTAGGC CCAAGAAGAAA TCTTGGCCCT TGATCCTAGT CTACGGAGAA TCTAGGGAGAA TCTACGGAGAA TCTACGGAGAA TCTACGCCCT TGATCTCCC AGTAGATTGC AGTAGATTGC AGTAGATTGC AGTAGATTGC AGTAGATTGC	TVFTDHMLTV FQPNLIMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCGGCCCTGG GTGGCCGGTA CGCGACTAC GCGGACTAC GCAGTTCCTTC CCTTCCCTGT CGACCAAG GAAGCCAGT CCAAGAAGGA TTCCCCAGT CCATCCCAGC CAAGAAGGA TGCCCAGTC CATCTCCATC CAACAACGA GGAAAGCAT TGCCCAGTC CTACCACAC GAGGGACGAC CAAGAAGGA TGCCCAGTC CTACCACAC AAGGCACCT AAGACCACT AAG	120 180 240 360 360 120 180 240 360 420 780 840 960 1020 1080 1140 1200 1200 1320
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	MKDCSNGCSA   MKDCSNGCSA   EWSSEFGWEK   YRSAVRATLP   ALLFVLLSPV   GCQOVLWLYG   GGGTLSKLT   GAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	11	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS  Quence 1 \$: NM_005: 1194 21   TCGGTGGCCG TCTGCTCCAG TCACTATTC GGACATCTGG ACCCAGCCCT GGAATCCCAG CTGCATGGG CGACTTGGC CGAGCTTGGC CGAGCTTGGC CGAGCTTGGC TGCATTGGG TGCCTTTGGAT TGCAGGCTTGGC TGTGAGAGAG AGAAGAGAG ACTCTGGAT TGTGAGCCT TTATGATACT GGAATCATACT GGAATCATACT GGAATCACAG ACTCTGGGT TGTGAGCCTC TTATGATACT TGTAGGCTC TTATGATACT GGAAGCCGAG ACACACA ACACACACA ACACGCAGGAAAAGA AAAAGACACA	IVTPATILKE AVELFEGLKA WYPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV  377  31 ITGTGCGCGT TACGACTATG AAGAAATTCG GACTTTGGT GACTTTGGT GCGCCTCGG GCCGCAACC TCCAGGTCTT CCCCGCATGA TTTCCTCCAG GTAGAATTGAT CCACTGTAG GAGAATTGGA CCTTCGCGGT TCCAGGTCTT CCACGGTT CCACGGTT CCACGGTT CCACGGTT CCACGGTT CCACGGTT CCACGGTT CCACGGTT CCACGGTT CCACTGTAG GAGAATTGAA CGTTCGCGGT TCCAAAGTAA GAGAGGATGG ATTGATACC AGTTTTCTTT CACTCTGGAC	KPDPNNLVFG KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI  41  GTGTGGAGTG GCGTGAGCAA ACGTGGGAA ACGTGGGGA ACGTTGGGAC CCACCAGGA GATACTCGCC TAGGGCCCAGG ATCTCTTCCA AAAGCTGCTT AAGCTCCAGG ATCTCTTCCA AAAGTGAGTC TAGGCCCAT TGATCAGGC CCAAGAAGAAA TCTTGGCCCT TGATCCTAGT CTACGGAGAA TCAGTAGGTA TCAGTAGGTA TCAGTAGTACTC AGTAGATTGC AGTAGATTGC AGTAGATTGC AGTAGATTGC AGTAGATTGC	TVFTDHMLTV TVFTDHMLTV TVFTDHMLTV FQPNLIMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCTGG GGATTTCTAC GCCGCCTGG GGAGCTAC GCCGCTGGG GAGGCAGTC CATCCCATC CCAAGAAGGG GGAAAGGAT TGCCCAGTC GTACCACAG GAGGACAGC GTACCACAG GAGGACAGA TGCCCAGGC CAAGGAGGAC CAAGGACAGC CAAGGACAGC CTACCACAC CAAGGACAGC CAAGGCACC CTACCAAAA TCTCCCCTTT	120 180 240 360 360 120 180 240 360 420 780 840 960 1020 1080 1140 1200 1200 1320
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVILSPV GCQQVLWLYG WGEPKVSERY LASRILSKLT  Seq ID NO: Nucleic Ac: Coding sequity ACAGAGGGCG CCCAGCTGGA ACTGGACCGCG GGCTCCACGA ACTTGGGCCGGTCCCTCA AGAGCGGTGGCTCCCTCA AGAGCGGTGAAGAAA ATCATCGCGG CACCAGCAAC GCTCCAAGAA GGTAACGAAC GCTCCAAGAA GGTACCAGCAAC GGATAACGAGA GGAACTCCCCAAGAAC GAACTCCCCAAGAAC GAACTCCCCAAGAAC GAACTCCCCAAAC GAACTCCCCAAAC GAACTCCCCAAAC AGTAACTTGT	11   ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD  120 DNA sec id Accession Lence: 121. 11   GGTCGCGGGC GGGGAACTAG ACTCGTACCA GCCCAGGGA ACTCGTACCA TCGACGTGAC ACTCACCTGCA AGCACAGGA AGCACAGCA AGCACACCA AGCACAACTA GGATGCCCC ATGAAGAGAT TCGCAGGGA GCAAGACTA GCAAGAGAC TGCGCGCGC ATGAAGAGAT TCTCTCTCTA ACCATCCCA GCACGCTGC ATGAAGAGAT TTCTGTTCTTA ACCATTCTTTA ACACTTCTTTA ACACTTCTTTA ACACTTCTTTA ACACTTCTTTTA ACACTTCTTTA ACACTTTTTTTT	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS  Quence n #: NM_005: .1194 21   TCGGTGGCCG TCTGCTCCAG TCACTATTTC GGACATCTGG ACCAGCCT GGAATCCCAG CCTCTGGAT TGCGTTGGC CGAGTTGGC CTTATGGACCTC TGTAAAGAAGA CCTTCTGGAT TGTGACCCT TGTGAGCCT TGTGAGCCT TGTGAGCCT TGTAACT GAATGATCAA CTCTAGGGT TGTAACT GAATGATCAA CTCTAGGGT GGAGCCGAG AAAAAGACACA AAAAGACCAGA AAAAGACCAGA ATACAGCAGGA ATACAGCAGA ATAC	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV  377  31   TTGTGCGCGT GTGGCAAGCT TACGACTATG AAGAAATTCG CAGCTCTGG GCCCCTCGG GCCCCTCGG CCCCCGCATGA TTTCCTCCAG CTACAGAGAGA CCACCTGTAG CTACAGAGAGA CCACCTGTAG CTACAGAGAGA CCACCTGTAG AGGAGAATTGACTAAGTAA AGGAGGAGATGAG CAGTTTCTTTT CACTCTGGAC GCATTCTTGGGAC AGTTTCTTTT CACTCTGGAC GCATTCTTGGAC GCATTCTTGAC GCATTCTTGGAC GCATTCTTGGAC GCATTCTTGGAC GCATTCTTGGAC GCATTCTTGGAC GCATTCTTGGAC GCATTCTTGAC GCATTTGTTTTTTTTTT	KPDPNNLVFG KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI  41    GTGTGGAGTG GCGTGAGCAA ACGGCGGGGA AGTTGGTGCC TCCTGGAAC CAACCCAGGA CAACCCAAG TGAGTACGCG TAGGCCCAT AAAGCTCCAG AAAGCTGCTT AAGCTCCAGG AAAGTAGGG CCAAGAAGAA TCTTGGCCT TGATCCTCT TTGATCTCCC AGTAGATTGCC AGTAGATTGCC AGTAGATTGCC AGTAGATTGCC AGTAGATTGCAAACTTTGATCTCCC AGTAGATTGCAAACTTTGAACTCCCC AGTAGATTGCAAACTTTGAACTTCCAC AGTAGATTGCAAACTTTGAACTTGAACTTGAACTTGAACTTGAACTTGAACTTGAACTTGAACTTGAACTTGAACTTGAACTTTGAACTTGAACTTTGAACTTGAACTTTGAACTTTGAACTTGAACTTGAACTTGAACTTGAACTTTGAACTTGAACTTGAACTTGAACTTTGAACTTGAACTTTGAACTTGAACTTTGAACTTGAACTTGAACTTTTTTTT	TVFTDHMLTV FQPNLINDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAGGCCAAC GGATTTCTAC GCGCCCTGG GTAGCCAAC GCAGGATTC CCTCCCCTGT CGACTCCGAG GAAGCCATC CCAGGAGCCAC GCAGGAGTTC CCAGGAGCCAC GCAGGAGCCAC GCAGGACTAC CCAGCAC GAGGACTAC CCAGCAC GAGGCCAC GAGGAACGAT TGCCCAGTC CTACCCAGC GAGGGACGAG CAAGGCCAC GAGGGACAC GAGGCCAC GAGGCCAC CTGACCAAAA TCTCCCCTTT AGAATCGATT AGAATCGATT	120 180 240 360 360 120 180 240 420 480 660 660 6720 780 840 960 1020 1020 1140 1200 1250 1380
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEPKVSERY LASRILSKLT  Seq ID NO: Nucleic Ac: Coding seq 1 ACAGAGGGCG CCCAGCTGGA ACTTGGGTCC GGGTGCGCTG GCCTCCCCCA AGAGCGGTGAGAAA ATCATCGCGG GTACAGCAAC GCTCCAAGAA GTACAGCAGA GTACCAGCAAC GATGCCAGC GAATACTTAG GAATGCCAGC AGATACTTGG CGATCCCAGC AGATACTTGG GATACCTGGC CGATACCTGACCA AGCAGCAGC CGATACCTGACCA AGCAGCAGC CGATACCTGACCA AGTACCTGACCA AGTACTTGCC CGATGCCAGCA CGATGCCAGCC CGATGCCAGCC CGATGCCAGCC CGATGCCAGCC CGATGCCAGCC CGATGCCAGCC CGATGCCAGCC CGATGCCAGCC CGATGCCAGCC CCTCTCTCCC CTCTCTCCCC CCCTCTCCCC CCCTCTCCCCC CCCTCTCCCC CCCTCTCCCCC CCCTCTCCCCCC	11   ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD  120 DNA sec id Accession Lence: 121. 11   GGTCGCGGGC GGGGAACTAG ACTGTACCA CGCCAGGGA GCAGCAGGA TCGGCGGGC GTGACTGCT ACTACACTCC AGCCCAAGAT TCGACGTGAC TGCGTGAGA AGCACAACTA GGATGCCCCC ATGAGAGGAC TGCGCAGCTGA TGCGCAGCTGA TGCGCAGCTGA TGCGCAGCTGA TGCGCAGCTGA TCGACGTGAC TCGCCTAGACTAC CGCCAAGAT TCGACTTACACTC ATGAGAGACT ACCATTCCA GCACAGCTGA TTCTGTCTTA ACATTTTTGT CACAAACAAT TCACTTATAGG TGCACTTATAGG TGCACAACAAT	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS  Quence 1 #: NM_005: .1194 21   TCGGTGGCCG TCTGCTCCAG TCACTACTTC GGACATCTGG ACCCAGCCT GGATCCAG CTGCATGTGG CTTCTGGAT TGGTAGCCTGC TAAAGAGCAGC TATGATACT GAATGACCAGA AAAAGCACA ATAAAGGCTT GGATGCTTTG GGATGCTTTTG GGATGCTTTG GGATGTTTG GGATGCTTTG GATGCTTTG GGATGCTTTG GATGCTTTG GGATGCTTTG GGATGCTTTG GGATGCTTTG GATGCTTTG GATG	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV  377  31  ITGTGCGCGT GTGGCAAGCT TACGACTATG AAGAAATTCG CAGCTTGGT GACTACTGGA GCCCCTCGG GCCCCTCGG GCCCCTCGG GCCCCTCGG GCCCCTCGG GCCCCTCGG TTCCAGAGAGAG CTACAGGAGAG CTACAGGAGAGAG CTACAGGAGAGAG CTACAGGAGAGAG GAGAATTCGAAAGTAA GAGAGATGGA CGTTTCGCGGT TCCAAAGTAA GAGAGATGGA CGATTCTTTC CACTCTGGAC AGTTTTCTTT CACTCTGGAC GCATTCTTGG GCATTCTTGG	KPDPNNLVFG KPDPNNLVFG KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPKGTI SDILYKGETI  41  GTGTGGAGTG GCGTGAGGAA ACGTGGGACAA ACGTTGGGACAA ACGTTGGGAC CCACCAGGA CCACCAGGA GATACTCGCC TAGGCCCAGGA AAGCTTGGCC TAGGCCCAAG TGAGTACGCG AAAGTGAGGC CCAAGAAGAA TCTTTGCC TGATCCTAGT TGATCTAGT TTGATCTCC AGTAGATAG TCAGGAGAA TCAGTAGGTA TCAGTAGGAT TCAGTAGGTA TTGATCTCCC AGTAGATTGC AAACTTTGAC AAACTTTGAC AAACTTTGGC AAACTTTTGGC AAACTTTTGAC AAACTTTGAC AAACTTTTGAC AAACTTT	TVFTDHMLTV FQPNLIMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAAGCCAAC GGAATTCTAC GCCGCCTGG GGAGTTCTAC GCCGCCTGG GGAGTTC CTTCCCCTGT CACTCCCAG GAAGCCAAC CAAGAAGGA GAAGCAGTC CCAAGAAGGA GGGAAAGGAT TGCCCAGTC GTACCACAG GAGGCACTC GTACCAAGA TCTCCCTT AGAATCGAT TCTCCCTTT AGAATCGATT ACCCAGCTTT ACCCAGCTT ACCAGCTCT TTCTCAGCAG	60 120 180 360 360 120 180 240 360 420 480 540 660 720 1080 1140 1260 1320 1380 1440
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	MKDCSNGCSA MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCOQVLWLYG MGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding seq ID No: ACAGAGGGGG CCCAGCTGGA ATGGACGGG GCTCCACGA AGGCGGTGCACTG GGTTGATGGGG CACCAGCAA ATCATCGGG CACCAGCAA TACCTGGAGC GTACCTGGAGA GATACTTAC GAATGCCAGCAA AGGCAGCACA AGTAACTTGT GCAGCCCAA GGCTCCCTGAAGAACTTGT GCAGCCACAA GTAACTTGT GCAGCCACACACACACACACACACACACACACACACACA	11	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS  Quence 1 #: NM_005: 11194 21   TCGGTGGCCG TCTGCTCCAG TCACTATTC GGACATCTGG ACCAGCCCT GGAATCCCAG CTGCATGTGG CTGCAGCCCT AAAAGAGGCT TATGAAACACA AAAAGACACA AAAAGACACA TACAGCAGGA ATAAAGGCTTTG GGGGTCTTCC GGGGTCTTCC GGGGTCTTCC	IVTPATILKE AVELFEGLKA WYPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV  377  31  ITGTGCGCGT TACGACTATG AAGAAATTCG CAGCTTTGGT GCGCCTCGG GCCGCAACC TCCAGGTCT CCCGCATGA TTTCCTCCAG CTAGAGAGTT CCCGCATGA CGAGATTGGT AGGAGATTGGA CGAGTTCGCGGT TCCAAGTAG CACCTGTAG GAGAATTGGA CACCTGTAG GAGAATTGGA CGATCTTCCCGGT TCCAAGTAA GAGAGATTGGT AGTTAGTAC GAGATTTCTTC CACTCTGGAC GCATTCTTGG GTGTTTTCTTGG TGCTCACTA	KPDPNNLVFG   KPDPNNLVFG   KPDPNNLVFG   KPDPNNLVFG   KPDPNNKIRL   YIRPTFIGTE   CKMGGNYGSS   LDGIILPGVT   SDILYKGETI   SDILYKGETI   STGTGGAGTG   GCTGAGGAGAA   ACGTGGGGA   ACTTGGGCCAT   AGAGCTGGTA   AGAGCTGGTA   AAGCTGGTA   AAGCTGGTA   AAGCTGGTA   AAGCTGCTA   AAGCTGCTA   AAGCTGCTA   AAGCTGCTA   AAGCTGCTA   AAGCTGCTA   CTACGAGAAA   TCTGGCCCT   TGATCCTAGT   CTACGAGAAA   TCAGTAGCTA   TTGATCCCC   AGTAGATTGC   AAACTTTGAC   AAACTTTGAC   AAACTTTGAC   ATTGATCTCCC   AGTAGATTGC   AAACTTTGGCC   ATTGATTGGCC   CTCCCAAAGAACA   CACCTTTGGC   CTCCCAAAGAACA   CACCTTTGGC   CTCCCAAAGAACA   CACCTTTGGC   CTCCCAAAGAACA   CACCTTTGGC   CTCCCAAAGAACA   CACCTTTGGC   CTCCCAAAGAACA   CTCTCAAAGAACA   CTCTCAAAGAACA   CTCTCCAAAGAACA   CTCTCCAAAGAACA   CTCTCCAAAGAACA   CTCTCCAAAGAACA   CTCTCCAAAGAA   CTCTTTGGC   CTCTCCAAAGAACA   CTCTTTGGC   CTCTCCAAAGAACTTGACA   CTCTTTGGC   CTCTCCAAAGAACA   CTCTTTGGC   CTCTCCAAAGA   CTCTTTGGC   CTCTCCAAAGA   CTCTTTGGC   CTCTCCAAAGA   CTCTTTGC   CTCTCCAAACA   CTCTTTGC   CTCTCCAAAGA   CTCTTTGC   CTCTCCAAACA   CTCTTTGC   CTCTCCAAACA   CTCTTTTCAAACA   CTCTTTTCAAACA   CTCTTTTTCAAACA   CTCTTTTCAAACA   CTCTTTTCAAACA   CTCTTTTCAAACA   CTCTTTTCAAACA   CTCTTTTCAAACA   CTCTTTTCA	TVFTDHMLTV TVFTDHMLTV TVFTDHMLTV FQPNLIMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCGCCCTGG GTGGCCGTGAC GCGGCTGAG CAAGGCAAT CGCGAACTAC CATCTCCATC CATCTCCATC CATCTCCATC CATCTCCATC CAAGAAGGG GGGAACGAC GAAGACGAG GGAACGAC CAAGAAGGG CAAGACGAC CAAGAAGGAT TGCCCAGTC CTACCACAC CAAGAAGGT TGCCCAGTC TTCCCCTTT AGAATCGATT ACCCAGCTCT TTCTCACCAAA TCTCCCCTTT TAGAATCGATT TTCTCAGCAG AAAGGCTGAC	120 180 240 300 360 120 180 240 360 420 780 960 1020 1080 1140 1260 1320 1380 1440 1500
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	MKDCSNGCSA MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCOQVLWLYG MGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding seq ID No: ACAGAGGGGG CCCAGCTGGA ATGGACGGG GCTCCACGA AGGCGGTGCACTG GGTTGATGGGG CACCAGCAA ATCATCGGG CACCAGCAA TACCTGGAGC GTACCTGGAGA GATACTTAC GAATGCCAGCAA AGGCAGCACA AGTAACTTGT GCAGCCCAA GGCTCCCTGAAGAACTTGT GCAGCCACAA GTAACTTGT GCAGCCACACACACACACACACACACACACACACACACA	11	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS  Quence 1 #: NM_005: 11194 21   TCGGTGGCCG TCTGCTCCAG TCACTATTC GGACATCTGG ACCAGCCCT GGAATCCCAG CTGCATGTGG CTGCAGCCCT AAAAGAGGCT TATGAAACACA AAAAGACACA AAAAGACACA TACAGCAGGA ATAAAGGCTTTG GGGGTCTTCC GGGGTCTTCC GGGGTCTTCC	IVTPATILKE AVELFEGLKA WYPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV  377  31  ITGTGCGCGT TACGACTATG AAGAAATTCG CAGCTTTGGT GCGCCTCGG GCCGCAACC TCCAGGTCT CCCGCATGA TTTCCTCCAG CTAGAGAGTT CCCGCATGA CGAGATTGGT AGGAGATTGGA CGAGTTCGCGGT TCCAAGTAG CACCTGTAG GAGAATTGGA CACCTGTAG GAGAATTGGA CGATCTTCCCGGT TCCAAGTAA GAGAGATTGGT AGTTAGTAC GAGATTTCTTC CACTCTGGAC GCATTCTTGG GTGTTTTCTTGG TGCTCACTA	KPDPNNLVFG   KPDPNNLVFG   KPDPNNLVFG   KPDPNNLVFG   KPDPNNKIRL   YIRPTFIGTE   CKMGGNYGSS   LDGIILPGVT   SDILYKGETI   SDILYKGETI   STGTGGAGTG   GCTGAGGAGAA   ACGTGGGGA   ACTTGGGCCAT   AGAGCTGGTA   AGAGCTGGTA   AAGCTGGTA   AAGCTGGTA   AAGCTGGTA   AAGCTGCTA   AAGCTGCTA   AAGCTGCTA   AAGCTGCTA   AAGCTGCTA   AAGCTGCTA   CTACGAGAAA   TCTGGCCCT   TGATCCTAGT   CTACGAGAAA   TCAGTAGCTA   TTGATCCCC   AGTAGATTGC   AAACTTTGAC   AAACTTTGAC   AAACTTTGAC   ATTGATCTCCC   AGTAGATTGC   AAACTTTGGCC   ATTGATTGGCC   CTCCCAAAGAACA   CACCTTTGGC   CTCCCAAAGAACA   CACCTTTGGC   CTCCCAAAGAACA   CACCTTTGGC   CTCCCAAAGAACA   CACCTTTGGC   CTCCCAAAGAACA   CACCTTTGGC   CTCCCAAAGAACA   CTCTCAAAGAACA   CTCTCAAAGAACA   CTCTCCAAAGAACA   CTCTCCAAAGAACA   CTCTCCAAAGAACA   CTCTCCAAAGAACA   CTCTCCAAAGAA   CTCTTGGC   CTCTCCAAAGAA   CTCTTTGGC   CTCTCCAAAGAACA   CTCTTTGGC   CTCTCCAAAGAA   CTCTTTGGC   CTCTCCAAAGAACATTTGACA   CTCTTTGGC   CTCTCCAAAGAACATTGACATA   CTCTTTGGC   CTCTCCAAAGAACATTGCAAAGAACTTTGACATA   CTCTTTGGC   CTCTCCAAAGAACATTGCAAAGAACATTGGC   CTCTCCAAAGAACATTGCAAAGAACATTGCAAAGAACATTGCAAAGAACATTGGC   CTCTCCAAAGAACATTGCAAAGAACATTGGC   CTCTCCAAAGAACATTGCAAAGAACATTGGC   CTCTCCAAAGAACATTGCAAAGAACATTGGC   CTCTCCAAAGAACATTGCAAAGAACATTGGC   CTCTCCAAAGAACATTGCAAAGAACATTGCAAAGAACATTGCAAAGAACATTGCAAAGAACATTGCAAAGAACATTGCAAAGAACATTGCAAAGAACATTGCAAAGAACATTGCAAAGAACATTGCAAAGAACATTGCAAAGAACATTGCAAAGAACATTGCAAAGAACTTGCAAAGAACATTGCAAAGAACATTGCAAAGAACATTGCAAAGAACATTGCAAAGAAACATTGCAAAGAACATTGCAAAGAAACATTGCAAAGAAACATTGCAAAGAAACATTGCAAAAGAAAAACATTGCAAAAAATTGCAAAAAAAA	TVFTDHMLTV FQPNLIMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAAGCCAAC GGAATTCTAC GCCGCCTGG GGAGTTCTAC GCCGCCTGG GGAGTTC CTTCCCCTGT CACTCCCAG GAAGCCAAC CAAGAAGGA GAAGCAGTC CCAAGAAGGA GGGAAAGGAT TGCCCAGTC GTACCACAG GAGGCACTC GTACCAAGA TCTCCCTT AGAATCGAT TCTCCCTTT AGAATCGATT ACCCAGCTTT ACCCAGCTT ACCAGCTCT TTCTCAGCAG	120 180 240 300 360 120 180 240 360 420 780 960 1020 1080 1140 1200 1320 1380 1440 1500
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<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	MKDCSNGCSA MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEPKVSERY LASRILSKLT  Seq ID NO: Nucleic Ac: Coding seq 1 ACAGAGGGCG CCCAGCTGGA ACTTGGGTCC GGGTGCGCTG GGCTCCCCCA AGAGCGGTGA ACTTGGGTCC TTGTTCGGCG GGTGAAGAAA ATCATCGCGG GTCCAAAGA GCTCCAAAGA GCTCCAAAGA GCTCCAAAGA GCTCCAGCAC CGATACTAGC GAATACTTAG GAATGCAGCCA GGATACTTGG GAATACTTGGGC GAATACTTGGC GAATACTTAC GCAGCCAGC AGTAACTAGT AGATGCCAGCA AGTAACTTGT AGATGCTAGCA AGTAACTTGT AGATGCTAGCA AGTAACTTGT AGATGCTAGCA AGTAACTTGT AGATGCTAGCA AGTAACTTGT AGATGCTAGCA AGTAACTTGT AGATGCTAGCA AGTACTTGT AGATGCTAGCA AGTACTAGCA AGTACTTGT AGATGCT AGAT	11   ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD  120 DNA sec id Accession Lence: 121. 11   GGTCGCGGGC GGGGAACTAG ACTGGTACCA ACTGATACCA CGCCCAGGGA GGAACTAG GGACGGGA TCGACGTGA TCGACGTGA TCGACGTGA TCGACGTGA GGATGCCCC AGCAACAT AGCACAACAT AGCACAACAT GGATGCCCC ATGAAGAGAC TGGCGGGA GGAAGACAT TCACTCC AGCACAACAT TCACATCCA GCAAGAGAC TGGCCAGCTG ATGAACAGT TCACATCCA GCAAGAGAC TTCGCTCTA ACTCATCACA GCAAGAGAC TTCGCTTAAGGGCA TTCACTCTA ACACTTTTTG CACAAACAAT TCACTTATGG GAGGGACACTT TCACAACAGT TGACTTATGG GACGGTGG ACTTTATGG GACACAGTGG ACTTTATGG GACACAGTGG ACTTTATGG GACACAGTGG ACTTTATGG ACACAGTGG ACTTTATGG ACACAGTGG ACTTTAGGC ACTTTATGG ACACAGTGG ACTTTAGGC ACTTTTAGGC ACTTTAGGC A	21   VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS  Quence 1 #: NM 005: .1194 21   TCGGTGGCCG TCACTACTTC GGACATCTGG ACCAGCCTT GGACATCTGG CCGAGCTGCAGT CCAGGCCTGC AGTAAAGAGA CCAGCCTT TGTGACCCT TATGATCTCAG TTCTGGAT TGCTGCCCT AAAAGAGACA CCTTAGGCTT GGAATCACAG AGTAAAGAG CCTTTAGGCTT GGAAGCCAG CTTATGATACT GAATGATCAA CTTTAGGTTT GGAAGCCAG GCAGAAAAGA AAAAGACACA TACAGCAGGA AAAAGACCT TGGAGTGTTTG GGGGTCTTCC GGGGTCTTCC GGGGTCTTCC TGGATGTTGT AGGAAAGGAT ACAGCAGGA AAAAGACCAC TTCTGGGTTTTG GGGGTCTTCC TGGATGTTGT AGGAAAAGGAT	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV  377  31  ITGTGCGCGT GTGGCAAGCT TACGACTTGGT AAGAAATTCG CAGCTTTGGT GCCCCTCGG GCCCTCGG GCCCTCGG CTACAGGAAC TTCCAGGTCTG AGGCAGTCTT CCCCGCATGA GAGAATTGA CTACAGGAAAC CTACAGGAAAC CTACAGGAAATTGA CTACAGAGAGAG GAGAATTGA GAGAGATGG ATTGATACC AGTTTTCTTT CACTCTGGAC GCATTTCTTG GCTTTTTCTGGTTCTCTCGGGT TCCAAAGTAA GAGAGATGG ATTGATTCTTTT CACTCTGGAC GCATTTCTTGG TGGTTCTTTGG TGGTTCTTTGG TGGTTCTTTGGGGGCTCC GCTTCTTGGGGGCTCC	KPDPNNLVFG   KPDPNNLVFG   KPDPNNLVFG   KPDPNNLVFG   KPDFNKIRL   YIRPTFIGTE   CKMGGNYGSS   LDGIILPKGETI   SDILYKGETI   SDILYKGETI   STGTGGAGTG   GCTGGGGGA   AGGTGGGGGA   AGGTGGGGGA   AGGTGGGGCCTCGGGAC   CTACCGCCAT   AAGGTCCAAGAAGATAGGGC   CCAAGAAGAA   TCTTGTCCA   AAGTTAGCTC   TGATCCTAGT   TTGATCTCCAGT   TTGATCTCCC   AGGTAGATAGT   TTGATCTCCC   AGTTAGATGCT   CTACGAGGA   TCAGTAGATAGCT   CTACGAGGA   ACCTTTGGC   ATGATTGCC   AGTTAGATTGC   AAACTTTGAC   AACTTTGAC   AACTTTGAC   AACTTTGAC   AACTTTGAC   CTCCCAAGAA   AGCCTGGAGG   TGATGCAAGG	TVFTDHMLTV TVFTDHMLTV TVFTDHMLTV FQPNLIMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK  51   CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCGCCCTGG GTGGCCGTGAC GCGGCTGAG CAAGGCAAT CGCGAACTAC CATCTCCATC CATCTCCATC CATCTCCATC CATCTCCATC CAAGAAGGG GGGAACGAC GAAGACGAG GGAACGAC CAAGAAGGG CAAGACGAC CAAGAAGGAT TGCCCAGTC CTACCACAC CAAGAAGGT TGCCCAGTC TTCCCCTTT AGAATCGATT ACCCAGCTCT TTCTCACCAAA TCTCCCCTTT TAGAATCGATT TTCTCAGCAG AAAGGCTGAC	120 180 240 300 360 120 180 240 360 420 480 560 720 780 840 900 1020 1080 11200 1260 1320 1440 1500 1500 1620

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				TATATATATG			1800
	TATATATATA	TGTATGTATA	TATGTATATA	TGTATATATA	TATGTATGTA	TATATGTATA	1860
				TATATTATGA			
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5	CCCACTCTCA	ATGCTGTGAC	TCAGAACATT	TAAGAGAACT	TCGTCTGTAA	GTAATTTGTC	1980
				GAGGGAACTT			
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	TGTCTCATTC	TGCCTCTGTT	ATGCAATGGG	TTCTACAGCA	CCCTTTCCCG	CAGGTTAGAA	2100
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	CCTGCCTCTC	ATCTCAATCC	TTGACTGATG	AATTTGAAGT	TCTACTAGAA	CCATGAAAAC	2340
	المناسلين كالمالئ للمالي	CONCOMPONE	CARGGAGCTT	GCTGGCTCTG	CAGCCACCT	TECCOCCTCC	2400
	CACCAGCCTG	CAATGAATCA	GATGTCTGTC	ACAGAATCTG	GCCCTCTCTG	AAGTTTTCTG	2460
	CAGACCTCTT	GGGA CTCATC	CACTGCTCCA	CAACGTGGAC	THECOTOME	CTCTCTTTTA	2520
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	CACACCCACT	ביורט ע נייורדי	CTCCCCACC	CTGGAGGTTA	TATEMATERA	CTCCCCTCAC	2640
	TGCAACCTCT	GCCTCCCGGG	TTCAAGCGAT	TCTCCTGCCT	GAGCCTTCCG	AGTAGCTGGG	2700
	ATCICACICC	CCTCCCACCA	CCCCTACCTA	ATTTCTGTAT	TTTTACTACA	CATCCCCTTT	2760
~~	CACCACATTG	GCCAGGCTGG	TCTTGACCTC	CTGACCTAGG	TGATCCACTG	CCTCCATGAT	2820
20	AGATTTTGCC	CCAGCTGGAC	TCTGCAGCTC	CACGTGGAAT	CCAGGTGCCT	GCCTCCAGTC	2880
	TGGGAAAGTC	ACCAACCCGC	AGCTTGTCAT	GTGGGTAACT	TCTGAACCCT	AAGCC	
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	MUDDOALISTA	ADADGGGGGGA	DOMEDONE		WEEKE CHERCH	OT WODOWNING	60
				KKPELVPPPW			60
	GCAGDETESO	DYWKAWDANY	ASLIRRDOMW	SGFSTQEPLE	RAVSDLLAVG	APSGYSPKEF	120
20				SRSESPEDSE			180
30	IIAVRADLLD	PRMNLPHISI	HOOOHNYAAP	FPPESCFQEG	APKRMPPKRA	LEREAPGGKD	240
	DKEDEELASP	PPVESEARQS	CONKRIBIDI	ENWTKKKYHS	TURKICKKNIQ	RSKFLALKUE	300
	VPALASCSRV	SKVMILVKAT	EYLHELAEAE	ERMATEKROL	ECORROLOKR	IEYLSSY	
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55	MUCIEIC WC	d vccession	TH: WRODOO	25.2			
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	CACCITITICCC	ACCOCCCCCA	CATCTCCACC	CTGGGCTGGT	decements.	GGCGCCGGGC	60
40							
40	GCCATGAGGG	TGCGCTAGGC	GGCTGTTCGT	GCCCGAGGCT	GCGCAGCACT	GAGGTGAGCT	120
	TTCCCTTCTT	CATCTTCCCT	CCTTCTTCCA	GACGACTGGC	GRENGENNEN	GGGACTAGGT	180
	CCAAACGCTA	GGTGGCTGGG	TCCAGCCGGA	GACCCGCACC	AAGGAGGAGA	TCATCGAGCT	240
	CTTGGTCCTT	GAGCAGTACC	TGACCATCAT	CCCTGAAAAG	CTCAAGCCTT	GGGTGCGAGC	300
4 ~	AAAAAAGCCG	GAGAACTGTG	AGAAGCTCGT	CACTCTGCTG	GAGAATTACA	AGGAGATGTA	360
45	CCDACCAGAA	GACCACAACA	ACACTYCA CCT	GACCAGCGAC	CACCACATCA	CCCCCAACAG	420
	AAGAGAGTCC	TCACCACCTC	ACTCAGTCCA	TTCTTTCAGT	GGTGACCGGG	ACTGGGACCG	480
	GAGGGGCAGA	AGCAGAGACA	TECACCCACC	AGACCGCTGG	TCCCACACCA	GGAACCCAAG	540
	AAGCAGGATG	CCTCCGCGGG	ATCTTTCCCT	TCCTGTGGTG	GCGAAAACAA	GCTTTGAAAT	600
	GGACAGAGAG	GACCACAGGG	ACTOCAGGGC	TTATGAGTCC	CCATCTCAGG	ATGCTGAATC	660
50							
20	ATACCAAAAT	GTGGTGGACC	TCGCTGAGGA	CAGGAAACCT	CACAACACAA	TCCAGGACAA	720
	CATGGAAAAC	TACAGGAAGC	TGCTCTCCCT	CGGAGTGCAG	CTTGCTGAAG	ACGATGGCCA	780
	CICCCACATG	ACGCAGGGCC	ACTCATCAAG	ATCCAAGAGA	AGTGCCTACC	CAAGCACCAG	840
	TCGAGGTCTA	AAAACTATGC	CTGAAGCCAA	AAAATCAACC	CACCGGCGGG	GGATTTGTGA	900
							000
	AGATGAATCT	TCCCACGGAG	TGATAATGGA	AAAATTCATC	AAGGATGTGT	CACGCAGTTC	960
55	CAAATCGGGA	AGAGCAAGGG	AGTCAAGCGA	CCGGTCACAG	AGATTCCCCA	GAATGTCAGA	1020
				GAGGGAGTCA			1080
	TGAAGGGAAT	GCATTTAGGG	GAGGCTTTAG	GTTTAATTCA	ACCCTTGTTT	CCAGAAAGAG ·	1140
				TGACACAGAT			1200
	TCAAAAAGGC	TGTCCCAGGA	AGAAGCCCTT	TGAATGTGGT	AGTGAGATGA	GAAAAGCCAT	1260
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	TTTTGGGGCA	ATGCCATATG	TATGTGATGA	GTGTGGGAGG	TOGTTCAGTG	TCATCTCAGA	1380
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65	TCATGCTAGA	CCUMP TO TOTAL	ጥሃጋር፤ እስጥሃጋጥ እ	CARMCACCAR		CCTTCATGCC	1620
				GWYTCWGGWW	TGTGAGGAAG		
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		TTTAGTGAGC	TTCAGAAAAT	ATATGGCAAA	GACAAATTCT	ACGAGTGCAG	
		TTTAGTGAGC	TTCAGAAAAT	ATATGGCAAA	GACAAATTCT		
	GGTGTGTAAG	TTTAGTGAGC GAAACCTTCC	TTCAGAAAAT TTCATAGTTC	ATATGGCAAA TGCCCTGATT	GACAAATTCT GAGCACCAGA	ACGAGTGCAG AAATCCACTT	1740
	GGTGTGTAAG TGGGGATGAC	TTTAGTGAGC GAAACCTTCC AAAGATAATG	TTCAGAAAAT TTCATAGTTC AGOGTGAACA	ATATGGCAAA TGCCCTGATT TGAACGTGAA	GACAAATTCT GAGCACCAGA CGTGAACGTG	ACGAGTGCAG AAATCCACTT AGCGCGGGGA	1740 1800
	GGTGTGTAAG TGGGGATGAC	TTTAGTGAGC GAAACCTTCC AAAGATAATG	TTCAGAAAAT TTCATAGTTC AGOGTGAACA	ATATGGCAAA TGCCCTGATT TGAACGTGAA	GACAAATTCT GAGCACCAGA CGTGAACGTG	ACGAGTGCAG AAATCCACTT	1740 1800
70	GGTGTGTAAG TGGGGATGAC AACCTTTAGG	TTTAGTGAGC GAAACCTTCC AAAGATAATG CCCAGCCCAG	TTCAGAAAAT TTCATAGTTC AGOGTGAACA CCCTTAATGA	ATATGGCAAA TGCCCTGATT TGAACGTGAA GTTTCAGAAA	GACAAATTCT GAGCACCAGA CGTGAACGTG ATGTATGGTA	ACGAGTGCAG AAATCCACTT AGCGCGGGA AAGAGAAAAT	1740 1800 1860
70	GGTGTGTAAG TGGGGATGAC AACCTTTAGG GTACGAATGT	TTTAGTGAGC GAAACCTTCC AAAGATAATG CCCAGCCCAG	TTCAGAAAAT TTCATAGTTC AGCGTGAACA CCCTTAATGA GGGAGACTTT	ATATGGCAAA TGCCCTGATT TGAACGTGAA GTTTCAGAAA CCTTCATAGC	GACAAATTCT GAGCACCAGA CGTGAACGTG ATGTATGGTA TCATCCCTGA	ACGAGTGCAG AAATCCACTT AGCGCGGGGA AAGAGAAAAT AAGAACATCA	1740 1800 1860 1920
70	GGTGTGTAAG TGGGGATGAC AACCTTTAGG GTACGAATGT	TTTAGTGAGC GAAACCTTCC AAAGATAATG CCCAGCCCAG	TTCAGAAAAT TTCATAGTTC AGCGTGAACA CCCTTAATGA GGGAGACTTT	ATATGGCAAA TGCCCTGATT TGAACGTGAA GTTTCAGAAA CCTTCATAGC	GACAAATTCT GAGCACCAGA CGTGAACGTG ATGTATGGTA TCATCCCTGA	ACGAGTGCAG AAATCCACTT AGCGCGGGA AAGAGAAAAT	1740 1800 1860
70	GGTGTGTAAG TGGGGATGAC AACCTTTAGG GTACGAATGT GAAAATCCAT	TTTAGTGAGC GAAACCTTCC AAAGATAATG CCCAGCCCAG	TTCAGAAAAT TTCATAGTTC AGCGTGAACA CCCTTAATGA GGGAGACTTT ACCCATTTGA	ATATGGCAAA TGCCCTGATT TGAACGTGAA GTTTCAGAAA CCTTCATAGC AAACAAGGGT	GACAAATTCT GAGCACCAGA CGTGAACGTG ATGTATGGTA TCATCCCTGA AAAGTGTGTG	ACGAGTGCAG AAATCCACTT AGCGCGGGGA AAGAGAAAAT AAGAACATCA AGGAAACCTT	1740 1800 1860 1920 1980
70	GGTGTGTAAG TGGGGATGAC AACCTTTAGG GTACGAATGT GAAAATCCAT TATTCCTGGT	TITAGTGAGC GAAACCTTCC AAAGATAATG CCCAGCCCAG	TTCAGAAAAT TTCATAGTTC AGCGTGAACA CCCTTAATGA GGGAGACTTT ACCCATTTGA AAAGGCGTCA	ATATGGCAAA TGCCCTGATT TGAACGTGAA GTTTCAGAAA CCTTCATAGC AAACAAGGGT GAAAACTTAC	GACAAATTCT GAGCACCAGA CGTGAACGTG ATGTATGGTA TCATCCCTGA AAAGTGTGTG AATAAGGAGA	ACGAGTGCAG AAATCCACTT AGCGCGGGGA AAGAGAAAAT AAGAACATCA AGGAAACCTT AGCTCTGTGA	1740 1800 1860 1920 1980 2040
70	GGTGTGTAAG TGGGGATGAC AACCTTTAGG GTACGAATGT GAAAATCCAT TATTCCTGGT	TITAGTGAGC GAAACCTTCC AAAGATAATG CCCAGCCCAG	TTCAGAAAAT TTCATAGTTC AGCGTGAACA CCCTTAATGA GGGAGACTTT ACCCATTTGA AAAGGCGTCA	ATATGGCAAA TGCCCTGATT TGAACGTGAA GTTTCAGAAA CCTTCATAGC AAACAAGGGT GAAAACTTAC	GACAAATTCT GAGCACCAGA CGTGAACGTG ATGTATGGTA TCATCCCTGA AAAGTGTGTG AATAAGGAGA	ACGAGTGCAG AAATCCACTT AGCGCGGGGA AAGAGAAAAT AAGAACATCA AGGAAACCTT	1740 1800 1860 1920 1980 2040
70	GGTGTGTAAG TGGGGATGAC AACCTTTAGG GTACGAATGT GAAAATCCAT TATTCCTGGT CTTTACAGAT	TITAGTGAGC GAAACCTTCC AAAGATAATG CCCAGCCCAG	TTCAGAAAAT TTCATAGTTC AGCGTGAACA CCCTTAATGA GGGAGACTTT ACCCATTTGA AAAGGCGTCA CCTTCATGCA	ATATGGCAAA TGCCTGATT TGAACGTGAA GTTTCAGAAA CCTTCATAGC AAACAAGGGT GAAAACTTAC AAGCTCAGAG	GACAAATTCT GAGCACCAGA CGTGAACGTG ATGTATGGTA TCATCCCTGA AAAGTGTGTG AATAAGGAGA CTCAGTGAGC	ACGAGTGCAG AAATCCACTT AGCGCGGGA AAGAGAAAAT AAGAACATCA AGGAAACCTT AGCTCTGTGA ATCAGAAAAT	1740 1800 1860 1920 1980 2040 2100
	GGTGTGTAAG TGGGGATGAC AACCTTTAGG GTACGAATGT GAAAATCCAT TATTCCTGGT CTTTACAGAT TCATTCTCGA	TTTAGTGAGC GAAACCTTCC AAAGATAATG CCCAGCCCAG	TTCAGAAAAT TTCATAGTTC AGCSTGAACA CCCTTAATGA GGGAGACTTT ACCCATTTGA AAAGGCGTCA CCTTCATGCA TTGAAGGCAG	ATATGGCAAA TGCCCTGATT TGAACGTGAA GTTTCAGAAA CCTTCATAGC AAACAAGGGT GAAAACTTAC AAGCTCAGAG AGGGTATGAG	GACAAATTCT GAGCACCAGA COTGAACGTG ATGTATGGTA TCATCCCTGA AAAGTGTGTG AATAAGGAGA CTCAGTGAGC AAATCTGTCA	ACGAGTGCAG AAATCCACTT AGCGCGGGA AAGAGAAAAT AAGAACATCA AGGAAACCTT AGCTCTGTGA ATCAGAAAAT TTCATAGTGG	1740 1800 1860 1920 1980 2040 2100 2160
70 75	GGTGTGTAAG TGGGGATGAC AACCTTTAGG GTACGAATGT GAAAATCCAT TATTCCTGGT CTTTACAGAT TCATTCTCGA	TTTAGTGAGC GAAACCTTCC AAAGATAATG CCCAGCCCAG	TTCAGAAAAT TTCATAGTTC AGCSTGAACA CCCTTAATGA GGGAGACTTT ACCCATTTGA AAAGGCGTCA CCTTCATGCA TTGAAGGCAG	ATATGGCAAA TGCCCTGATT TGAACGTGAA GTTTCAGAAA CCTTCATAGC AAACAAGGGT GAAAACTTAC AAGCTCAGAG AGGGTATGAG	GACAAATTCT GAGCACCAGA COTGAACGTG ATGTATGGTA TCATCCCTGA AAAGTGTGTG AATAAGGAGA CTCAGTGAGC AAATCTGTCA	ACGAGTGCAG AAATCCACTT AGCGCGGGA AAGAGAAAAT AAGAACATCA AGGAAACCTT AGCTCTGTGA ATCAGAAAAT	1740 1800 1860 1920 1980 2040 2100 2160
	GGTGTGTAAG TGGGGATGAC AACCTTTAGG GTACGAATGT GAAAATCCAT TATTCCTGGT CCTTTACAGAT TCATTCTCGA GCCATTCACT	TTTAGTGAGC GAAACCTTCC AAAGATAATG CCCAGCCCAG	TTCAGAAAAT TTCATAGTTC AGCGTGAAC CCCTTAATGA GGGAGACTTT ACCCATTTGA AAAGGCGTCA CCTTCATGCA TTGAAGGCAG AGAGTCATAC	ATATGGCAAA TGCCCTGATT TGAACGTGAA GTTTCAGAAA CCTTCATAGC AAACAAGGGT GAAAACTTAC AAGCTCAGAG AGGCTATGAG TATAACAAGA	GACAAATTCT GAGCACCAGA CGTGAACGTG ATGTATGGTA TCATCCCTGA AAAGTGTGTG AATAAGGAGA CTCAGTGAGC AAATCTGTCA CCTCTTGAAA	ACGAGTGCAG AAATCCACTT AGCGCGGGGA AAGAGAAAAT AAGAACATCA AGGAAACCTT AGCTCTGTGA ATCAGAAAAT TTCATAGTGG GTGATGAGGA	1740 1800 1860 1920 1980 2040 2100 2160 2220
	GGTGTGTAAG TGGGGATGAC AACCTTTAGG GTACGAATGT GAAAATCCAT TATTCCTGGT CTTTACAGAT TCATTCTCGGA GCCATTCACT CGAAAAGGCG	TTTAGTGAGC GAAACCTTCC AAAGATAATC CCCAGCCCAG	TTCAGAAAAT TTCATAGTTC AGCGTGAACA CCCTTAATGA GGGAGACTTT ACCCATTTGA AAAGGCGTCA CCTTCATGCA TTGAAGGCAG AGAGTCATACC GCTCTAACCC	ATATGGCAAA TGCCCTGATT TGAACGTGAAA GTTTCAGAAA CCTTCATAGC AAACAAGGGT GAAAACTTAC AAGCTCAGAG AGGGTATGAG TATAACAAGA CTATGAAAAAC	GACAAATTCT GAGCACCAGA CGTGAACGTG ATGTATGGTA TCATCCCTGA AAAGTGTGTG AATAAGGAGA CTCAGTGAGC CAAATCTGTCA CCTCTTGAAA CAGAAGATTC	ACGAGTGCAG AAATCCACTT AGCGCGGGGA AAGAGAAAAT AAGAACATCA AGGAAACCTT AGCTCTGTGA ATCAGAAAAT TTCATAGTGG GTGATGAGGA CCACTAAGGA	1740 1800 1860 1920 1980 2040 2100 2160 2220 2280
	GGTGTGTAAG TGGGGATGAC AACCTTTAGG GTACGAATGT GAAAATCCAT TATTCCTGGT CTTTACAGAT TCATTCTCGGA GCCATTCACT CGAAAAGGCG	TTTAGTGAGC GAAACCTTCC AAAGATAATC CCCAGCCCAG	TTCAGAAAAT TTCATAGTTC AGCGTGAACA CCCTTAATGA GGGAGACTTT ACCCATTTGA AAAGGCGTCA CCTTCATGCA TTGAAGGCAG AGAGTCATACC GCTCTAACCC	ATATGGCAAA TGCCCTGATT TGAACGTGAAA GTTTCAGAAA CCTTCATAGC AAACAAGGGT GAAAACTTAC AAGCTCAGAG AGGGTATGAG TATAACAAGA CTATGAAAAAC	GACAAATTCT GAGCACCAGA CGTGAACGTG ATGTATGGTA TCATCCCTGA AAAGTGTGTG AATAAGGAGA CTCAGTGAGC CAAATCTGTCA CCTCTTGAAA CAGAAGATTC	ACGAGTGCAG AAATCCACTT AGCGCGGGGA AAGAGAAAAT AAGAACATCA AGGAAACCTT AGCTCTGTGA ATCAGAAAAT TTCATAGTGG GTGATGAGGA	1740 1800 1860 1920 1980 2040 2100 2160 2220 2280
	GGTGTGTAAG TGGGGATGAC AACCTTTAGG GTACGAATGT GAAAATCCAT TATTCCTGGT CTTTACAGAT TCATTCTCGA GCCATTCACT CGAAAAGGCG AAATGTCTAC	TTTAGTGAGC GAAACCTTCC AAAGATAATG CCCAGCCCAG	TTCAGAAAAT TTCATAGTTC AGGTGAACA CCCTTAATGA GGGAGACTTT ACCCATTTGA AAAGGCGTCA CCTTCATGCA TTGAAGGCAG AGAGTCATAC GCCTTAACCC CATATGAGAG CATATGAGAG	ATATGGCAAA TGCCCTGATT TGAACGTGAA GTTTCAGAAA CCTTCATAGC AAACAAGGGT GAAAACTTAC AAGCTCAGAG AGGGTATGAG TATAACAAGA CTATGAAAAC GTCTGTTATT	GACAATTCT GAGCACCAGA COTIGAACGTG ATGTATGGTA TCATCCCTGA ANAGTGTTG AATAAGGAGA CTCAGTGAGC AAATCTGTCA CCTCTTGAAA CAGAAGATTC CATAGCTTAG	ACGAGTGCAG ANATCCACTT AGGCGGGGA ANGAGAANAT ANGANCCTT AGCTCTGTGA ATCAGAANAT TTCATAGTGG CTGATGAGGA CCACTAAGGA CCTCTGTGA	1740 1800 1860 1920 1980 2040 2100 2160 2220 2280 2340
	GGTGTGTAAG TGGGGATGAC AACCTTTAGG GTACGAATGT GAAAATCCAT TATTCCTGGT TCATTCTCGA TCATTCTCGA GCCATTCACT CGAAAAGGC AAATGTCTAC AGCTCAGAAA	TTTAGTGAGC GAAACCTTCC AAAGATAATG CCCAGCCCAG	TTCAGAAAAT TTCATAGTTC AGGTGAAC CCCTTAATGA GGGAGACTTT ACCCATTTGA AAAGGCGTCA CCTTCATGCA TTGAAGGCAG AGAGTCATAC GCTCTAACCA CATTAGAAG GTCAACCA TTGAAGGCAG TTGAAGGCAG TTGAAGGCAG TTGAAGGCAG TTGAAGGCAG TTGAAGGCAG TTGAAGGCAG	ATATGGCAAA TGCCCTGATT TGAACGTGAA GTTTCAGAAA CCTTCATAGC AAACATAGC AAACTTAC AAGGTCAGAG TATAACAAGA CTATGAAAAC GTCTGTTATT CAGTAAACCA	GACAAATTCT GAGCACCAGA COTGAACGTG ATGTATGGTA TCATCCCTGA AAAGTGTGTG AATAAGAGA CTCAGTGAGC CAATCTGTCA CCTCTTGAAA CAGAAGATTC CATAGCTTAG AAAGTAATGG	ACGAGTGCAG AAATCCACTT AGGCGGGGA AAGAGAAAAT AAGAACCTT AGCTCTGTGA ATCAGAAAAT TTCATAGTGG GTGATGAGGA CCACTAAGGA CCTCTGTGGA CAGAGTCTAC	1740 1800 1860 1920 1980 2040 2100 2160 2220 2280 2340 2400
75	GGTGTGTAAG TGGGGATGAC AACCTTTAGG GTACGAATGT GAAAATCCAT TATTCCTGGT TCATTCTCGA TCATTCTCGA GCCATTCACT CGAAAAGGC AAATGTCTAC AGCTCAGAAA	TTTAGTGAGC GAAACCTTCC AAAGATAATG CCCAGCCCAG	TTCAGAAAAT TTCATAGTTC AGGTGAAC CCCTTAATGA GGGAGACTTT ACCCATTTGA AAAGGCGTCA CCTTCATGCA TTGAAGGCAG AGAGTCATAC GCTCTAACCA CATTAGAAG GTCAACCA TTGAAGGCAG TTGAAGGCAG TTGAAGGCAG TTGAAGGCAG TTGAAGGCAG TTGAAGGCAG TTGAAGGCAG	ATATGGCAAA TGCCCTGATT TGAACGTGAA GTTTCAGAAA CCTTCATAGC AAACATAGC AAACTTAC AAGGTCAGAG TATAACAAGA CTATGAAAAC GTCTGTTATT CAGTAAACCA	GACAAATTCT GAGCACCAGA COTGAACGTG ATGTATGGTA TCATCCCTGA AAAGTGTGTG AATAAGAGA CTCAGTGAGC CAATCTGTCA CCTCTTGAAA CAGAAGATTC CATAGCTTAG AAAGTAATGG	ACGAGTGCAG ANATCCACTT AGGCGGGGA ANGAGAANAT ANGANCCTT AGCTCTGTGA ATCAGAANAT TTCATAGTGG CTGATGAGGA CCACTAAGGA CCTCTGTGA	1740 1800 1860 1920 1980 2040 2100 2160 2220 2280 2340 2400
75	GGTGTGTAAG TGGGGATGAC AACCTTTAGG GTACGAATGT GAAAATCCAT TATTCCTGGT TCATTACAGAT TCATTCTCGA GCCATTCACT CGAAAAGGCG AAATGTCTAC AGCTCAGAAA CATTCAGAAA CATTCAGAGC	TTTAGTGAGC GAAACCTTCC CAAGCCAG AAGGTGTGTG ACTAGAGGGA ACGTGTCCTTA GGCCGGGATG AAGAACCTCT GAATCTCAGA TTCACCATTA AGGCAAAAAT ACTCACAGTG TTCACAGTG TTCACAGTG TTCACAGTG TTCACAGTG	TTCAGAAAAT TTCATAGTTC AGGGTGACA CCCTTAATGA GGGAGACTTT ACCCATTTGA AAAGGGGTCA CCTTCATGCA AGAGTCATAC GCTCTAACCC CATATGAGGAG TAGCAGGGCC TGAACCATCA TGCAGGGCC TCAACCATCA	ATATGGCAAA TGCCCTGATT TGAACGTGAA GTTTCAGAAA CCTTCATAGC AAACAAGGGT AAAACATAGA AGGCTAGAG AGGCTATGAG AGGCTATGAG AGGCTATGAG CTATGAAAAC CTATGAAAAC GTCTGTTATT CAGTAAACCA GACAGTTCGT	GACAAATTCT GAGCACCAGA COTGAACGTG ATGTATGGTA TCATCCCTGA AAAGTGTGTGT AAATAAGGAGA CTCATCGACA AAATCTGTCA CAGAAGATTC CATAGCTTAG AAAGTAATGG GCTGGAGGGA	ACGAGTGCAG ANATCCACTI AGCGCGGGA ANGAGANANT ANGANATCACTT AGCTCTGTGA ATCAGANANT TTCATAGTGG GTGATGAGGA CCACTAAGGA CCTCTGTGGA ACAGGTCTAC ACACCTCTGA	1740 1800 1860 1920 1980 2040 2160 2220 2280 2340 2400 2460
	GGTGTGTAAG TGGGGATGAC AACCTTTAGG GTACGAATGT GAAAATCCAT TATTCCTGGT CCTTTACAGAT TCATTCTCGA GCCATTCACT CGAAAAGGCG AAATGTCTAC AGCTCAGAAA CATTCAGAGC AGGAAGGGAA	TTTAGTGAGC GAAACCTTCC AAAGATAATG CCCAGCCAG AAGGTGTGTG ACTAGAGGGA CAGTCCCTTA GGCCGGGATG AAGAACCTCT GAATCTCAGA TTCACCATTA GAGGCAAAAT AGTCACAGTG TTCGATGCTA TACAGTAGGT	TTCAGAAAAT TTCATAGTTC AGCTGAACA CCCTTAATGA GGGAGACTTT ACCCATTTGA CCTTCATGCA TTGAAGGCAG AGAGTCATAC GCTCTAACCC CATATGAGAG TAGCAGGGCC CATATGAGAG TAGCAGGGCC TCAACCATCA CTGTTATCCA	ATATGGCAAA TGCCCTGATT TGAACGTGAA GTTTCAGAAA CCTTCATAGC AAACAAGGGT GAAAACTTAC AAGCTCAGAG AGGGTATGAG TATAACAAGA CTATGAAAAC GTCTGTTATT CAGTAAACCA GAGAGTTOGT TAGCTTAGTG	GACAAATTCT GAGCACCAGA COTGAACGTG ATGTATGGTA TCATCCCTGA AAAGTGTGTG AATAAGGAGA CTCAGTGAGC AAATCTGTCA CCTCTTGAAA CAGAAGATTC CATAGCTTAG AAAGTAATGG GCTGGAGGA GCTTCCAAAC	ACGAGTGCAG ANATCCACTI AGGCGCGGA ANGAGAAAAT ANGAACATCA AGGAAACTT AGCTCTGTGA ATCAGAAAAT TTCATAGTGG GTGATGAGGA CCACTAAGGA CCTCTGTGA ACACCTCTGA ACACCTCTGA CTCCAAGAAG CTCCAAGAAG	1740 1800 1860 1920 1980 2040 2100 2220 2220 22340 2400 2460 2520
75	GGTGTGTAAG TGGGGATGAC AACCTTTAGG GTACGAATGT GAAAATCCAT TATTCCTGGT CCTTTACAGAT TCATTCTCGA GCCATTCACT CGAAAAGGCG AAATGTCTAC AGCTCAGAAA CATTCAGAGC AGGAAGGGAA	TTTAGTGAGC GAAACCTTCC AAAGATAATG CCCAGCCAG AAGGTGTGTG ACTAGAGGGA CAGTCCCTTA GGCCGGGATG AAGAACCTCT GAATCTCAGA TTCACCATTA GAGGCAAAAT AGTCACAGTG TTCGATGCTA TACAGTAGGT	TTCAGAAAAT TTCATAGTTC AGCTGAACA CCCTTAATGA GGGAGACTTT ACCCATTTGA CCTTCATGCA TTGAAGGCAG AGAGTCATAC GCTCTAACCC CATATGAGAG TAGCAGGGCC CATATGAGAG TAGCAGGGCC TCAACCATCA CTGTTATCCA	ATATGGCAAA TGCCCTGATT TGAACGTGAA GTTTCAGAAA CCTTCATAGC AAACAAGGGT GAAAACTTAC AAGCTCAGAG AGGGTATGAG TATAACAAGA CTATGAAAAC GTCTGTTATT CAGTAAACCA GAGAGTTOGT TAGCTTAGTG	GACAAATTCT GAGCACCAGA COTGAACGTG ATGTATGGTA TCATCCCTGA AAAGTGTGTG AATAAGGAGA CTCAGTGAGC AAATCTGTCA CCTCTTGAAA CAGAAGATTC CATAGCTTAG AAAGTAATGG GCTGGAGGA GCTTCCAAAC	ACGAGTGCAG ANATCCACTI AGCGCGGGA ANGAGANANT ANGANATCACTT AGCTCTGTGA ATCAGANANT TTCATAGTGG GTGATGAGGA CCACTAAGGA CCTCTGTGGA ACAGGTCTAC ACACCTCTGA	1740 1800 1860 1920 1980 2040 2100 2220 2220 22340 2400 2460 2520
75	GGTGTGTAAG TGGGGATGAC AACCTTTAGG GTACGAATGT TATTCCTGGT CTTTACAGAT TCATTCTCGA GCCATTCACT CGAAAAGGCG AAATGTCTTAC AGCTCAGAAA CATTCAGAGC AGGAGGGGAA TCACAATGGA	TTTAGTGAGC GAAACCTTCC AAAGATAATG CCCAGCCCAG	TTCAGAAAAT TTCATAGTTC AGGTGAACA CCCTTAATGA GGGAGACTTT ACCCATTIGA AAAGGCGTCA CCTTCATGCA TTGAAGGCAG GGACTCATACC CCATATGAGAG TAGCAGGGCC TCAACCATCA CTGTTATCCA TGGAATCTAA	ATATGGCAAA TGCCCTGATT TGAACGTGAA GTTTCAGAAA CCTTCATAGC AAACATAGC AAACTAGAG AGGGTATAGA AGGGTATAGA CTATGAAAA CTATGAAAAC GTCTGTTATT CAGTAAACC GAGGTTAGTG TAGCTTAGTG TAGGAAGGCA TAGGAAGTCCG TAGGAAGGGA	GACAAATTCT GAGCACCAGA COTGAACCTG ATGTATGGTA TCATCCCTGA AAAGTGTGTG CCAGTGAGC AAATCTGTCA CCTCTTGAAA CAGAAGATTC CATAGCTTAG AAAGTTATGG CATAGCTTAG CAGAGGATTC CATAGCTTAG CAGAGGATC CATAGCTTAG CATACCTCCAAAC GAATCCTCCAAAC GAATCCTCCA	ACGAGTGCAG ANATCCACTT AGGCGGGGA ANGAGAANAT ANGANCCTT AGCTCTGTGA ATCAGAANAT TTCATAGTGG CTGATAGGGA CCACTAAGGA CTCCTGTGGA ACACCTCTGCA ACACCTCTGCA ACACCTCTGCA ACACCTCTGCA ACACCTCTGCA ACACCTCTCAGAGAG TTTATATCTC	1740 1800 1860 1920 1980 2040 2100 2160 2220 2280 2340 2400 2460 2520 2580
75	GGTGTGTAAG TGGGGATGAC AACCTTTAGG GTACGAATGT GAAAATCCAT TATTCCTGGT TCATTCTCGA GCCATTCACT CGAAAAGGCG AAATGTCTAC AGCTCAGAAA CATTCAGAG CATTCAGAA CATTCAGAG AGAAGGGGAA AGAACGAAAAGAA AGACCTTAAT	TTTAGTGAGC GAAACCTTCC AAAGCATACT CCCAGCCCAG	TTCAGAAAAT TTCATAGTTC AGCOTGAACA CCCTTAATGA CGCAGTTGA AAAGGCGTCA CCTTCATGCA TTGAAGGCAG AGAGTCATAC GCTCTAACCC CATATGAAGA TAGCAGGGCC TCAACCATCA CTGTTATCCA AGAAGATCAA AGAAGATTCCA	ATATGGCAAA TGCCCTGATT TGAACGTGAA GTTTCAGAAA CCTTCATAGC AAACAAGGGT GAAAACTTAC AAGCTCAGAG AGGCTATGAG ATATAACAAGA CTATGAAAAC GTCTGTTATT CAGTAAACCA GAGAGTTCGT TAGCTTAGTG TGAGAAGGA TGCCAGAAGGA	GACAAATTCT GAGCACCAGA COTGAACGTG ATGTATGGTA TCATCCCTGA AAAGTGTGTGTG AAAATAGGAGA CTCAGTGAGC AAAATCTGTCA CAGAAGATTC CATAGCTTAG AAAGTAATGG GCTGGAGGGA GCTTCCAAAC GAATCCTCCA	ACGAGTECAG ANATCCACTI AGCGCGGGA ANGAGANANT ANGANACTTA AGGACATCTA AGCTCTGTGA ATCAGANANT TTCATAGTGG GTGATGAGGA CCACTAAGGA CCACTAAGGA CCACTAGGA CCACTAGGA CCACTAGGA CTGAGGA CTGAGGA CTGAGGA CTGAGGAGAG CTCAAGAGA CTCAAGAGAG CTCAAGAGAG CTCAAGAGAG CTTATATCTC AAGGGGCAG	1740 1800 1860 1920 1980 2040 2100 2220 2220 2340 2400 2520 2520 2580 2640
75	GGTGTGTAAG TGGGGATGAC AACCTTTAGG GTACGAATGT GAAAATCCAT TATTCCTGGT TCATTCTCGA GCCATTCACT CGAAAAGGCG AAATGTCTAC AGCTCAGAAA CATTCAGAG CATTCAGAA CATTCAGAG AGAAGGGGAA AGAACGAAAAGAA AGACCTTAAT	TTTAGTGAGC GAAACCTTCC AAAGCATACT CCCAGCCCAG	TTCAGAAAAT TTCATAGTTC AGCOTGAACA CCCTTAATGA CGCAGTTGA AAAGGCGTCA CCTTCATGCA TTGAAGGCAG AGAGTCATAC GCTCTAACCC CATATGAAGA TAGCAGGGCC TCAACCATCA CTGTTATCCA AGAAGATCAA AGAAGATTCCA	ATATGGCAAA TGCCCTGATT TGAACGTGAA GTTTCAGAAA CCTTCATAGC AAACAAGGGT GAAAACTTAC AAGCTCAGAG AGGCTATGAG ATATAACAAGA CTATGAAAAC GTCTGTTATT CAGTAAACCA GAGAGTTCGT TAGCTTAGTG TGAGAAGGA TGCCAGAAGGA	GACAAATTCT GAGCACCAGA COTGAACGTG ATGTATGGTA TCATCCCTGA AAAGTGTGTGTG AAAATAGGAGA CTCAGTGAGC AAAATCTGTCA CAGAAGATTC CATAGCTTAG AAAGTAATGG GCTGGAGGGA GCTTCCAAAC GAATCCTCCA	ACGAGTGCAG ANATCCACTT AGGCGGGGA ANGAGAANAT ANGANCCTT AGCTCTGTGA ATCAGAANAT TTCATAGTGG CTGATAGGGA CCACTAAGGA CTCCTGTGGA ACACCTCTGCA ACACCTCTGCA ACACCTCTGCA ACACCTCTGCA ACACCTCTGCA ACACCTCTCAGAGAG TTTATATCTC	1740 1800 1860 1920 1980 2040 2100 2220 2220 2340 2400 2520 2520 2580 2640
75 80	GGTETGTAAG TGGGGATGAC AACCTTTAGG GTACGAATGT GAAAATCCAT TATTCCTGGT CTTTACAGAT TCATTCTGGA GCCATTCACT CGAAAAGGCG AAATGTACA AGCTCAGAAA AGTCAGAGAA TCACAATGGA AGAACGGAA AGACCTTAAT TAAGAATCGC	TTTAGTGAGC GAAACCTTCC CAGCCAG AAGGTGTGTG ACTAGAGGGA CAGTCCCTTA GGCCGGGATC AAGACCTCT GAATCTCAGA TTCACCATTA GAGGCAAAAT AGTCACAGTG TTCACATGTA TTCACATGTA ATTAGATGGT AATGAATTGG GATAAATGGG AATGAATTGG GATAAGCGAC AACTATGAAG	TTCAGAAAAT TTCATAGTTC AGGOTGAACA CCCTTAATGA GGGAGACTTT ACCCATTTGA AAAGGCGTCA CCTTCATGCA TTGAAGGCAG GGTCTAACCC CATATGAAGAC TAGCAGGGC TAGCAGGGC TCAACCATCA CTGTTATCCA CTGTTATCCA CTGTTATCCA AGGAGTTCCA AGGAGTTCCA	ATATGGCAAA TGCCCTGATT TGRACGTGAA GTTTCAGAAA CCTTCATAGC AAACAAGGGT AAGCTCAGAG AGGGTATGAG AGTTGATAGAG CTATGAAAAC GTCTGTTATT CAGTAAACCA GAGAGTTAGTG TAGCTTAGTG TAGCTTAGTG TAGCTTAGTG TAGCTTAGTG TAGCTTAGTG TAGCTTAGTG TAGCTTAGTG TAGCTTAGTG TAGCTTAGTG TAGCAGAGGAA ACAGGAGTGTA	GACAAATTCT GAGCACCAGA COTGAACGTG ATGTATGGTA TCATCCCTGA AAAGTGTGTG CTCAGTGAGC AAATTGTCA CAGAAGATTCTCATAGCTTAGAA CAGAAGATTC CATAACTTAG GCTGGAGGGA GCTTCCAAAC GAATCCTCCA AACCCTTGTG TTCCGTGCCA	ACGAGTGCAG ANATCCACTI AGCGCGGGA ANGAGANANT ANGANACTTA AGGAACCTT ACTCTGTGA ATCAGANANT TTCATAGTGG GTGATTGAGGA CCACTAAGGA CCTCTGTGGA CAGAGTCTAC ACACCTCTGTA CTCCAAGANG TTTATATCTC ANGGGGCAG ANCCTCAGAA	1740 1800 1960 1920 2040 2100 2220 2220 2340 2400 2460 2520 2580 2640 2700
75 80	GGTGTGTAAG TGGGGATGAC AACCTTTAGG GTACGAATGT GAAAATCCAT TATTCCTGGT CCTTTACAGAT TCATTCTCGA GCCATTCACT CGAAAAGGCG AAATGTCTAC AGCTCAGAAA CATTCAGAGC AGGAAGGGAA TCACAATGGA AGACCTTAAT TAAGAATGCC AAGTGTTCCT	TTTAGTGAGC GAAACCTTCC AAAGATAATG CCCAGCCAG AAGGTGTGTG ACTAGAGGGA CAGTCCCTTA GGCCGGGATG AAGAACCTCT GAATCTCAGA TTCACCATTA GAGGCAAAAT AGTCACAGTG TTCGATGCTA TACAGTAGGT AATGAATGG GATAAGCGAC AACTATGAAG GGAGAGGGAT	TTCAGAAAAT TTCATAGTTC AGGTGAACA CCCTTAATGA GGGAGACTTT ACCCATTTGA ACAGGCAG CCTTCATGCA TTGAAGGCAG AGAGTCATAC CCATATGAGAG TAGCAGGGCC CTCAACCATCA TGGAATCTAA AGAAGATCTAA AGAAGATCTAA CTGTTATCCA TCGTCAT CTGTTCATCA CTGTTCATCA CTGTTCATCA CTGTTCATCA CTGTTCATCA CTGTTCATCA CTGTTGTGTGTT	ATATGGCAAA TGCCCTGATT TGAACGTGAA GTTTCAGAAA CCTTCATAGC AAACAAGGGT AAGACTCAGAG AGGGTATGAG TATAACAAGA CTATGAAAAC GTCTGTTATT CAGTAAACCA GAGAGTTCGT TAGCTTAGTG TGAGAAGGA TGCCAGAGAG ACAGAGGTGTA TAAGAAGGAT TAAGAAGGAT TAAGAAGGAT	GACAAATTCT GAGCACCAGA COTGAACCTG ATGTATGGTA TCATCCCTGA AAAGTGTTGTA CCTCTGTGAGC AAATCTGTCA CCTCTTGAAA CAGAAGATTC CATAGCTTAG AAACTAGTAG GATACTAGCTAG AAACTAGTAG GATACCTCCA AACCCTTCTCAAAC GAATCCTCCA AACCCTTGCCA CGGGGAATTCT	ACGAGTGCAG ANATCCACTT AGGGCGGGA ANGAGAAAAT ANGAACATCA AGGAAACCTT AGCTCTGTGA ATCAGAAAAT TTCATAGTGG GTGATGAGGA CCACTAAGGA CCTCTGTGGA CAGAGTCTAC ACACCTCTGA CTCCAAGAAG TTTATATCTC AAGGGGGCAGA CTCTCAGAA CTGTTCCCAG	1740 1860 1860 1920 1980 2040 2160 2220 2280 2240 2400 2460 2520 2580 2640 2700 2760
75	GGTGTGTAAG TGGGGATGAC AACCTTTAGG GTACGAATGT GAAAATCCAT TATTCCTGGT CCTTTACAGAT TCATTCTCGA GCCATTCACT CGAAAAGGCG AAATGTCTAC AGCTCAGAAA CATTCAGAGC AGGAAGGGAA TCACAATGGA AGACCTTAAT TAAGAATGCC AAGTGTTCCT	TTTAGTGAGC GAAACCTTCC AAAGATAATG CCCAGCCAG AAGGTGTGTG ACTAGAGGGA CAGTCCCTTA GGCCGGGATG AAGAACCTCT GAATCTCAGA TTCACCATTA GAGGCAAAAT AGTCACAGTG TTCGATGCTA TACAGTAGGT AATGAATGG GATAAGCGAC AACTATGAAG GGAGAGGGAT	TTCAGAAAAT TTCATAGTTC AGGTGAACA CCCTTAATGA GGGAGACTTT ACCCATTTGA ACAGGCAG CCTTCATGCA TTGAAGGCAG AGAGTCATAC CCATATGAGAG TAGCAGGGCC CTCAACCATCA TGGAATCTAA AGAAGATCTAA AGAAGATCTAA CTGTTATCCA TCGTCAT CTGTTCATCA CTGTTCATCA CTGTTCATCA CTGTTCATCA CTGTTCATCA CTGTTCATCA CTGTTGTGTGTT	ATATGGCAAA TGCCCTGATT TGAACGTGAA GTTTCAGAAA CCTTCATAGC AAACAAGGGT AAGACTCAGAG AGGGTATGAG TATAACAAGA CTATGAAAAC GTCTGTTATT CAGTAAACCA GAGAGTTCGT TAGCTTAGTG TGAGAAGGA TGCCAGAGAG ACAGAGGTGTA TAAGAAGGAT TAAGAAGGAT TAAGAAGGAT	GACAAATTCT GAGCACCAGA COTGAACCTG ATGTATGGTA TCATCCCTGA AAAGTGTTGTA CCTCTGTGAGC AAATCTGTCA CCTCTTGAAA CAGAAGATTC CATAGCTTAG AAACTAGTAG GATACTAGCTAG AAACTAGTAG GATACCTCCA AACCCTTCTCA AACCCTTCTCA AACCCTTGCAAC GAATCCTCCA CGCGAATTCT	ACGAGTGCAG ANATCCACTI AGCGCGGGA ANGAGANANT ANGANACTTA AGGAACCTT ACTCTGTGA ATCAGANANT TTCATAGTGG GTGATTGAGGA CCACTAAGGA CCTCTGTGGA CAGAGTCTAC ACACCTCTGTA CTCCAAGANG TTTATATCTC ANGGGGCAG ANCCTCAGAA	1740 1860 1860 1920 1980 2040 2160 2220 2280 2240 2400 2460 2520 2580 2640 2700 2760

				TTTTGGTGAA			2880
				GTGCTTTGCT			2940
				CTCTGGAAGC AACAAGTTAC			3000 3060
5				CAGACAATTT			3120
				GAAGTCTCAT			3180
				GGAGACCCAT			3240
				CCCTCAGAAG TGTGGATCTC			3300 3360
10				CAGTOGGGAG			3420
	CACCCATTCC	ATCAGCGAGT	ATCAGAGAGA	TTACACTGGA	GAGCAGCTGT	ATGAATGTCC	3480
				ATTCCTTTTC			3540
				TGATGATGGT GAATCCTGCT			3600 3660
15				TAGCTCTGCC			3720
				CCAGATGGCT			3780
				GACCGAAGAG			3840
				ACTTGCAGAT TCACACCTCA			3900 3960
20				TTGTGGTAAG			4020
		+		AGAAGAAGAA			4080
				CAATGTCCAT			4140
				GCCAGAAGTG			4200
25				TGAGCCAAAC TGGACAGCCA			4260 4320
				AGGTATTGAA			4380
				GGGAGATGCC			4440
				AGAGATTCAG			4500
30				CAGCACAGCA AAATGCCTTT			4560 4620
50				CAATCAAGCT			4680
				CCTGTCCCTC			4740.
				AAAACCTTCA			4800
35				TAATGTCAGT CAGATTGAAA			4860 4920
55				CAGTGTCTGC			4920
				GAAAACCCTA			5040
				GTGTAACGTA			5100
40				GTGATCACAT			5160
ŦU				TTACCTGGTA TTATATTTTT			5220 5280
				CAATATCTTT			5340
				GCATGATAGA			5400
45				TTTCTGCAGC			5460 .
43				AATATACGGA AAGTGGTTCT			5520 5580
				CAACTCAATA			5640
				CTTACATCTT			5700
50				TGAAGGTTGA			5760
50				CTTTCATCAC			5820 5880
				GCTAGTATCC			5940
	CTTAATTCTC	TTCGTTATTT	ATCTGACCCT	CTAACTCCAT	GTCTAACTTG	CATT	
55	TD 110						
55		123 Proteir cession #: E					
	1	11 .	21	31	41	51	
	1	1	1	ŀ		1 .	
60				1 PEKLKPWVR			60
OU				HSFSGDRDWD AYESRSQDAE			120 180
				RSKRSAYPST			240
	EDESSHGVIM	EKPIKDVSRS	SKSGRARESS	DRSQRFPRMS	DDNWKDISLN	KRESVIQQRV	300
65				FDTDGKGSIH			360
03				ECGRSFSVIS KSAALAEHRK			420 480
				SALIEHQKIH			540
·	ETFRPSPALN	EFQKMYGKEK	MYECKVCGET	FLHSSSLKEH	QKIHTRGNPF	ENKGKVCEET	600
70				QSSELSEHQK			660
70	-			PYENQKIPTK QRVRAGGNTS			720 780
				PARENPCEGG			840
				RAKKKYIEHR			900
75	GMLYECQECG	ECFAHSSDLT	EHQKIHDREK	PSGSRNYEWS	VIRSLAPTDP	QTSYAQEQYA	960
13				EKSHGEESQG			1020 1080
				FVDLTDLTDH SFLFEHQRIH			1140
				HSSALNEHMR			1200
80				ELADHVTVHK			1260
οU				EEEEEDEAAA AEPNGBAEGP			1320 1380
						QEIQVEEPYY	1440
				ANAFGECSGY			1500
85	CDVCGQLFND	RLSLARHQNT	HTG				
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	Nucleic Aci	124 DNA sec d Accession lence: 180	#: NM_0071	196			
_	1	11	21	31	41	51	
5	1	1	1	1	1	1	
				GGAGGAGAAG TACCAGGCAG			60 120
				CCCGCCCCTG			180
				CGTGGATGTT			240
10	CCTGGGCAGG						300
	CCCATTCGCA	GCCTTGGCAG	GCGGCCTTGT	TCCAGGGCCA	GCAACTACTC	TGTGGCGGTG	360
				CTGCCCACTG			420
				AAGATGGCCC			480
15				GCAGCGATGT CCCTGGGGTC			540 600
13	TGATGCTTCT	TCAACTGCGT	CCTCCCCAG	AGTGCACCGT	CARAGIGAAG	GGCACTGTCA	660
				TCAACTGTGC			720
				AGATCACAGA			780
••				ATTCTGGAGG			840
20				ACCCCTGTGG			900
				GGATCAAGAA		AGCAAGGGCT	960
	GATTCTAGGA	TAAGCACTAG	ATCTCCCTTA	ATAAACTCAC	AACICIC		
	Sec ID NO:	125 Protein	sequence				
25		ession #: N					
	1	11	21	31	41	51	
	1		1	1	1	L	
				DKVLGGHECQ			60
30				KDGPEQEIPV KCTVSGWGTV			120 180
20				DSGGPLVCDG			240
		WIKKIIGSKG	ooman rogo	2000121020			
35		126 DNA sec					
33		id Accession Lence: 171		/91.1			
	1	11	21	31	41	51	
	Ī	1	1	1	1	1	
40	TTGGCGGGCG	GAAGCGGCCA	CAACCCGGCG	ATCGAAAAGA	TTCTTAGGAA	CGCCGTACCA	60
40				CCTTCTGTCG			120
	TCCGCCCCTC	AGGTTCTTTT	TCTAATTCCA	AATAAACTTG ATGAAACTAT	TCCGACACGT	GGCTTTGCAA	180 240
				GAGAGATGGT			300
				TCAAAACGGA			360
45				ATGTGCTAGA			420
				TGTTTGACTA			480
				GTCAGATAGT			540
	ACAGCCAGGG	CTATGCTCAC	AGGGACCTCA	AGCCAGAAAA GTGCAAAACC	CARCCETARC	AACGATTACC	600 660
50	ATAAATTAAA	ATTICAL	ACTUTOCUTE	ATGCAGCACC	TGAGGGTAAC	CAAGGCAAAT	720
50	CATATCTTGG	ATCAGAGGCA	GATGTTTGGA	GCATGGGCAT	ACTGTTATAT	GTTCTTATGT	780
	GTGGATTTCT	ACCATTTGAT	GATGATAATG	TAATGGCTTT	ATACAAGAAG	ATTATGAGAG	840
	GAAAATATGA	TGTTCCCAAG	TGGCTCTCTC	CCAGTAGCAT	TCTGCTTCTT	CAACAAATGC	900
55				TGAAAAATCT			960
, c.				AAAGCAAGAA ACAGAAACAA			1020 1080
						CTAGCCAAGA	1140
	AGGCTCGGGG	AAAACCAGTT	CGTTTAAGGC	TTTCTTCTTT	CTCCTGTGGA	CAAGCCAGTG	1200
	CTACCCCATT	CACAGACATC	AAGTCAAATA	ATTGGAGTCT	GGAAGATGTG	ACCGCAAGTG	1260
60	ATAAAAATTA	TGTGGCGGGA	TTAATAGACT	ATGATTGGTG	TGAAGATGAT	TTATCAACAG	1320
	GTGCTGCTAC	TCCCCGAACA	TCACAGTTTA	CCAAGTACTG	GACAGAATCA	AATGGGGTGG	1380
	AATCTAAATC	TACTCCA	TOTATOCA	AGAACACCIGC	CTACTTTATC	AAGAACAAAG TTTCCTGAGC	1440 1500
	CAAAGACTCC	AGTTAATAAG	AACCAGCATA	AGAGAGAAAT	ACTCACTACG	CCAAATCGTT	1560
65	ACACTACACC	CTCAAAAGCT	AGAAACCAGT	GCCTGAAAGA	AACTCCAATT	AAAATACCAG	1620
	TAAATTCAAC	AGGAACAGAC	AAGTTAATGA	CAGGTGTCAT	TAGCCCTGAG	AGGCGGTGCC	1680
						AGAAAGGGAG	1740
						TATAATGTGA	1800 1860
70						ATTCTTCCAA	1920
						CAGTCAGATT	1980
						CCCGATGTGG	2040
						TTAGTGGAAG	2100
75						GATGAGTGTG TTCATTGGAA	2160 2220
, 5						TTAAACAAAA	2280
						CTGTCTTTTT	2340
	TAATCATGTG	GTTTTGTATA	TTAATAATT	TTGACTTTCT	TAGATTCACT	TCCATATGIG	2400
00	AATGTAAGCT	CTTAACTATO	TCTCTTTGT/	ATGTGTAATT	TCTTTCTGA	ATAAAACCAT	2460
80	TTGTGAATAT						
	Sea ID NO.	: 127 Protei	n semience				
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	WKDYDELLKY	YELHETIGTG	GFAKVKLACH	ILTGEMVAIK	IMDKNTLGSD	LPRIKTEIEA	60
	LKNLRHQHIC	QLYHVLETAN	KIFMVLEYCP	GGELFDYIIS	QDRLSEEETR	VVFRQIVSAV	120
	AYVHSQGYAH	RDLKPENLLF	DEAHKTKTID	FGLCAKPKGN	KDYHLQTCCG	SLAYAAPELI	180
5				DDNVMALYKK VEWQSKNPFI			240 300
,	MEDI'I EI'MOA	RISMANLLINH RISMANLLINH	DATE/ODINIE	RLRLSSFSCG	CASATORTO	REMNASI EDA	360
	TASDKNYVAG	1.TDYDWCEDD	LSTGAATPRT	SOFTKYWTES	NGVESKSLTP	ALCRTPANKI.	420
	KNKENVYTPK	SAVKNEEYFM	FPEPKTPVNK	NOHKREILTT	PNRYTTPSKA	RNOCLKETPI	480
				NOAHMEETPK			540
10	LTRSKRKGSA	RDGPRRLKLH	YNVTTTRLVN	PDQLLNEIMS	ILPKKHVDFV	QKGYTLKCQT	600
	QSDFGKVTMQ	FELEVCQLQK	PDVVGIRRQR	LKGDAWVYKR	LVEDILSSCK	V	
		128 DNA sec					
15			#: EOS sec	Insuce			
13	1	lence: 169-1 11	21	31	41	51	
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	GGGATCCTTT	CTGGAATGGA	GGTCTTATGA	GCTGCTATTG	AACACGGCAG	AGCCTGTTGG	60
				ACTGATTGAA			120
20	GCAAAGTTGA	GCACTACAGG	ACGTCGGGAC	TGGGCATTTC	CTTCCAACAT	GGCCGCCACT	180
				GCCGATTCTG			240
				CTCTGCAGGA			300
				CTGATTTTTG			360
25	CTCCTTCTTC	TCATGGTCTT	GCTCCGTTAC	GTGCCTCGCA TTTCTGGTGA	CACTCCCCTT	CTCCCCCATC	420 480
23				TŤCTTGTGCA			540
				ATTAGCTGCA			600
				CTGAGGACCC			660
				GTCTCCATCC			720
30				TGCCACGCAG			780
				AACCTCCTAG			840
				TGTGTCTTGG			900
				TTGGTGGTGG			960
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22				TCCAGTCACC			1080 1140
				CTGGCACCTG			1200
				GCCCAAGAGG			1260
				AACAAGGAGG			1320
40				AGATGGGAAC			1380
				CTGTGTTGCT			1440
				CCCGCCTTCT			1500
				TTGCTACAAT			1560
45				TCCCTCCCTC TTCTGACAGG			1620 1680
73				CCGCTCACTG			1740
				TAGCCAGGAC			1800
				TTTCTTTCTT			1860
				GGACAACAAT			1920
50				TCCTGCCTCA			1980
				TTTTATAATT			2040
				GACCTTGGGA			2100
				ATGCCTGGCC			2160
55				TGGAGAATTG			2220
55				CCCATCTCAT			2280 2340
				CAATTAGCGT			2400
				TCACTCCATA			2460
				ACAGGAAGGG			2520
60				TTTTTTTGAG			2580
	CCAGGCTGAA	GTCCAATCCC	ACAATCATGG	CTCACTGCAG	CCACCACCTC	CTGAGCTCAA	2640
						ACCACACCTG	
						TTGGACTGGA	2760
65						TTACAGGCGT	2820
UJ						CGGCCGGAAC ACGGGGAACT	2880 2940
						GTCATGTTTG	3000
						ACTTAGTTTT	3060
						TGGTCAGCTG	3120
70						CTTAACAAGC	3180
	CCAACTCCTT	ACGGTAATCC	TTTAAGGCCT	ATGTGATCTG	CCCTCACCCT	GGCTACACTC	3240
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						CTGCTTGGCT	3360
75						TGTCCAACCT	3420
13						TATTTTTAAA	3480
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						GCTGGGGAAA	3720
80	AAGAACCTAA	GGCCCTCCAC	TCACCAGGGT	TCCACATTCT	CTGTAGTCCA	GCTGGGAAAT	3780
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	CAGTGAACAC	ACTTGGCCTA	GGCCCCATCI	CAGGAGCCTT	CACATCTCCC	TGGGACCTGC	3960
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0.5	ATACATCTTC	CAGCCCTCAT	ACTCCTCCAC	. TCCCTTTTCA	TITCUTGAAC	ATTCCAACTT	4080

	CTATGCCTTT						4140
	CCTCACCCTT						4200
	TGCCCTGTGC ACATTTCCCT						4260 4320
5	GAAGTGCAAT	ATCACTAGAA	CATGTGAGAA	GAGAGGCATG	AAACCGAAGC	TGAGAGGGTT	4380
	TGAGATCTGG	AGCTACTCCT	TCCTCCACCC	AAACTTCAGA	AGGTGAAGGA	GATAGTGCAT	4440
	GTGAGTGAGC						4500
	AGTCCCAATC	TTGGATTCGA	CAGTTACAAG	AACCAATAAA	TTCCTTTCCT	TGTGG	
10	Seg ID NO:	129 Protein	sequence				
	Protein Acc						
	1	11	21	31	41	51	
	MAATASPOPL		CAMPADIA DE	I CDVD			60
15	LSGNLLLLMV						120
					SLLLATIVWA		180
	VFVQTHENPK						240
	RPAGQGRALK						300
20	AFLHCCFSPI GMNDLGERQS			LGWELLAPGIA	QASISSCSES	SILIAGEEMI	360
	O. Elib Dollarigo						
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	Nucleic Aci		_	74			
25	Coding sequ	lence: 246 11	21	31	41	51	
	ī	ī	ī	31 	i	Ī	
	AGGCGGACAA						60
	AGCCCGGGGC						120
30	GCTGGCTCGC						180 240
50	GGCAGCTGTT CGGCCATGAA						300
	AGAATAAGTT						360
	TCTACACCTC						420
35	CAGCTGCCCA						480
33	AAAGGGAGAG ATGCCGCCAG						540 600
	CTGAACTCAT						660
	ACATCCTGGG						720
40	ACATCCACCT						780
40	ACATGTTGTG GTCCGCTGGT						840 900
	GATCAAAGGA						960
					CTCCCGACCT		1020
4.5					CCTCCTCTCC		1080
45					GATTCTCCCT		1140
					AGGACTTGGG GCATCTCCTC		1200 1260
					TGTCTGGAAT		1320
<b>50</b>					ACTGCAGATT		1380
50					GCTGTTGGAA		1440
	TTTCACACCT	ATGACATACA	TGGGATAGCA	CCTGGGCCGC	CATGCACTCA	ATAAAGAATG	1500
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<i></i>	Seq ID NO:						
55	Protein Acc				41	51	
	i	11	21 	31 1	41	ì	
	MKKLMVVLSL	IAAAWAEEQN	KLVHGGPCDK	TSHPYQAALY	TSGHLLCGGV	LIHPLWVLTA	60
<b>~</b>	AHCKKPNLQV	FLGKHNLRQR	ESSQEQSSVV	RAVIHPDYDA	ASHDQDIMLL	RLARPAKLSE	120
60					HLVSREECEH		180
	LCAGDEKYGK IQAK	DSCQGDSGGP	LVCGDHLRGL	VSWGNIPCGS	KEKPGVYTNV	CRYTNWIQKI	240
	TVAN						
65	Seq ID NO:		-				
65			1 #: AY0380	71.1			
	Coding sequ	lence: 110	21	31	41	51	
	î	i	î.	ĭ	ī	ĩ	
<b>5</b> 0	ATGAGCAATC	AGTACCAGGA	GGAGGGCTGC	TCCGAGAGGC	CCGAGTGCAA	AAGTAAATCT	60
70						CCCGTGCAAA	120
						CGCCGACCCG	180 240
						TCAGGGTGOG	300
	GCAGCGGCGG	CGGCGGCGGC	GGCGGCGGCG	GCGGCAGCGG	CCGCCACGGC	CACGGCGGGT	360
75					GGCCCGGGGA		420
						CACGCTCAAG	
						GAACGGGGCG CGTCACGCAC	
						GGGTGGTGGC	
80	ACCGGCACCG	AGGACGACGA	GGAGGAGCTG	CTGGAGGACG	AAGAAGATGA	GGACGAGGAA	720
	GAGGAACTGC	TGGAGGACGA	CGAGGAGGAG	CTGCTGGAGG	ACCACCCCC	CGCGCTGCTC	780
	AAGGAGCCCC	GGCGCTGTCC	TGTGGCCGCC	ACTGGCGCCG	TGGCCGCAGC	AGCTGCCGCT GCACCCGGAA	840 900
						CGACTCGGAG	
85						CTACCAGCTG	

5	CTGGCCATGA GCCAAGTGGC CCGGGGCCGC CCGCACCACC TTCCCGAGCC GGCCTGAGCA TTCGGCAGGC CTGAGACAGC CTGAGACAGC	GGCTGGACTT GCAAGCGGGA TCTCCGCCAC CGGCGCTCGA TACCTCCGC CTTTCCTCGG TCTTTTCCAC CCACACCCGC CCGCAGACAG	GACCGAGGCC GAAGGCAGGC CCACCGGCTC CTCCGCTTGG TCCGGGCTGG AGCGGCAGTG AATGGCCCCC CGTGGAGGGC ACGCGCCTCT	CACTACCGG CGAGTCCAGG GGGCAGACCG ACTGCCGCTG GCCAGCCTG CTGACCAGC CTGACCAGCG GCAGTGGCAT AGCATAGCCG ATCCTGCCGG	TCTGGTTCCA ACCCCCTGG TGGACGCCAG CCGCCAGCGG CAGCTTTCAT CGTCGACCGC CGGGCGCCCT CGCTGAGGCT	GAACCGTCGG GCTGCCCTTCCCT CCCCTTCCCT CGCCGCCCCC GGCGCCGCCC CAGCCCGCCA GGCCGCGCCCCCC GGCCGCGCCCCCCCC	1080 1140 1200 1260 1320 1380 1440 1500 1560 1620 1680
15	Seq ID NO: Protein Acc	133 Protein	AK93901.1		41	51	
20	MSNQYQEEGC EKAVQGSPKS	SSAPFEAELH	LPPKLRRLYG	31 SILGRRSPCK PGGGRLLQGA	 MRLLGAAQSL AAAAAAAAAA	 PAPLTSRADP AAAAATATAG	60 120
20	PFVPPPPALD EELLEDDEEE DAEGKDGEDS	ELGGPGGVTH LLEDDARALL VCLSAGSDSE	PEERLGVAGG KEPRRCPVAA EGLLKRKQRR	AAAAWDTLK PGSAPAAGGG TGAVAAAAA YRTTFTSYQL	TGTEDDEEEL AVATEGGELS EELERAFQKT	LEDEEDEDEE PKEELLLHPE HYPDVFTREE	180 240 300 360
25	PHHPALDSAW FGRLFSTMAP	AAAAAAAA	FPSLPPPPGS LRQPTPAVEG	aqthppglpf aslppsgapl āvasgaladp	GLSTFLGAAV	FRHPAFISPA	420 480 540
20		134 DNA sec					
30	Nucleic Aci	id Accession 11	ı #: CAT clı 21	ster 31	41	51	
		 	GCAGATCATC	TCTCCAAATC	ATCACTTCTA	TCAAGCCTAT	60
25	TGCTTGAGCA	GTGTTATAGC	ACTCAGCCCT	CAGGGCAAAG	ATAAGTCTTC	ACCATTGTCA	120
35				TGCTGAATGG ATACTTATCA			180 240
				CTCAAGGAAA AATGTAGGTT			300 360
40	TAGAATAGAA	AAGCACCTTG	AAAACTGTAG	TCTGACTTAA	TAGACACAAA	TATAATGAAA	420
40			GTTATTTGAA AAAGCTGGAA	GGAAAAAGCA TTCTACC	GCAAAAGGCA	CAAGCTTCAG	480
	Seg ID NO:	135 DNA cor					
45	Nucleic Aci		#: NM_0067	199			
45	Nucleic Aci	id Accession	#: NM_0067	799 31	41 .	51 1	
45	Nucleic Aci Coding sequ 1   GCCGCGGGAG	id Accession mence: 199 11     AGGAGGCCAT	#: NM_0067 21 	31   GGGGCGCTGC	TGCTGGCGCT	 GCTGCTGGCT	60
	Nucleic Aci Coding sequ 1   GCCGCGGGAG CGGGCTGGAC	id Accession lence: 19  11  AGGAGGCCAT TCAGGAAGCC	#: NM_0067 21     GGGCGCGCGC   GGAGTCGCAG	31     GGGGCGCTGC GAGGCGCGCC	 TGCTGGCGCT CGTTATCAGG	 GCTGCTGGCT ACCATGCGGC	60 120 180
50	Nucleic Aci Coding sequ 1   GCCGCGGGAG CGGCTGGAC CGACGGTCA TGGCAGGGGA	id Accession sence: 19 11   AGGAGGCCAT TCAGGAAGCC TCACGTCGCG GCCTGCGCCT	#: NM_0067 21     GGGCGCGCGC GGAGTCGCAG CATCGTGGGT GTGGGATTCC	31   GGGGCGCTGC GAGGCGCGC GGAGAGGACG CACGTATGCG	TGCTGGCGCT CGTTATCAGG CCGAACTCGG GAGTGAGCCT	GCTGCTGGCT ACCATGCGGC GCGTTGGCCG GCTCAGCCAC	120 180 240
	Nucleic Aci Coding sequal CCCGCGGGAG GCCGCGGGAG CGACGGGTCA TGGCAGGGGA CGCTGGGCAC	id Accession sence: 19 11   AGGAGGCCAT TCAGGAAGCC TCACGTCGCG GCCTGCGCCT TCACGGCGGCCT	1 #: NM_0067 21 21 GGGCGCGCGC GGAGTCGCAG CATCGTGGGT GTGGGATTCC GCACTGCTTT	31   GGGGCGCTGC GAGGCGCGC GGAGAGGACG CACGTATGCG GAAACCTATA	 TGCTGGCGCT CGTTATCAGG CCGAACTCGG GAGTGAGCCT GTGACCTTAG	GCTGCTGGCT ACCATGCGGC GCGTTGGCCG GCTCAGCCAC TGATCCCTCC	120 180
50	Nucleic Aci Coding sequ 1   GCCGCGGGAG CGGCTGAC CGACGGTCA TGGCAGGGA CGCTGGGCAG TACTACACCC	id Accession sence: 19  11    AGGAGGCCAT TCAGGAAGCC TCACGTCGCG GCCTGCGCCT TCACGCTGCGT TCACGTTTGG GTTACTTCGT	H: NM_0067 63 21	31     GGGGCGCTGC GAGGCGCGC GAGAGGACG CACGTATGCG GAAACCTATG TCCATGCCAT TATCTGAGCC	TGCTGGCGCT CGTTATCAGG CCGAACTCGG GAGTGAGCCT GTGACCTTAG CCTTCTGGAG CTCGCTACCT	CTGCTGGCT ACCATGCGGC GCGTTGGCCG GCTCAGCCAC TGATCCCTCC CCTGCAGGCC GGGGAATTCA	120 180 240 300 360 420
	Nucleic Aci Coding sequ 1   GCCGCGGGAG CGGCTGGAC CGACGGTCA TGCCAGGGGA CGCTGGGCAC GGGTGGATGG TACTACACCC CCCTATGACA	id Accession ence: 199 11	H: NM_0067 63 21	31   GGGGCGCTGC GAGGCGCGC GAGAGGACG CACGTATGCG GAAACCTATA TCCATGCCAT TATCTGAGCC GCACCTGTCA	TGCTGGCGCT CGTTATCAGG CCGAACTCGG GAGTGAGCCT GTGACCTTAG CCTTCTGGAG CTCGCTACCT CCTACACTAA	GCTGCTGGCT ACCATGCGGC GCGTTGGCCG GCTCAGCCAC TGATCCCTCC CCTGCAGGCC GGGGAATTCA ACACATCCAG	120 180 240 300 360
50	Nucleic Aci Coding sequi    GCCGCGGGAG GCGCGCTGAC CGACGGTCA TGGCAGGGGATG TACTACACCC CCCTATGACA CCCATCTGTC GGCTGGGGT	id Accession lence: 19 11   AGGAGGCCAT TCAGGAAGCC TCACGTCGCG GCCTGCGCCT TCACGGCGGC TCACGTTGGT TCACGTTGGT TTGCTTTGGT TCCAGGCCTC ACATCAAAGA	H: NM_0067 63 21   GGGCGCGCGC GCACTGCTTG GCACTGCTTT CCAGCTGACT ATCGAATATC GAAGCTGTT ATCGAATATC GAAGCTGTT ATCGAATATC GAAGCTGTT CACATTTGAG GGATGAGGCA	31     GGGGCGCTGC GAGGCGGCGC GAAGAGGACC CACGTATGC GAAACCTATA TCCATGCCAT TATCTGAGCC GCACCTGTCA TTTGAGAACC CTGCCATCTC	TGCTGGCGCT TGCTGGCGCCT CGTATCAGG CAGACTCGG GAGTGACCTTAG CCTTCTGGAG CTCGCTACCTA CCTACACTAA GGACAGACTG CCCACACCCCT	GCTGCTGGCT ACCATGCGGC GCGTTGGCCG GCTCAGCCAC TGATCCCTCC CCTGCAGGCC GGGGAATTCA ACACATCCAG CTGGGTGACT CCAGGAAGTT	120 180 240 300 360 420 480 540 600
50 55	Nucleic Aci Coding sequ	id Accession lence: 19  11    AGGAGGCCAT TCAGGAAGCC TCACGTCGCG GCCTGCGCT TCACGGCGC TCACGTCTTGG TTGCTTTGGT TTGCCTTGGT TCCAGGCCTC ACATCAAACAA	H: NM_0067 63 21   GGGCGCGCGC GGAGTCGCAG CATCGTGGGT GTGGATTCC GCACTGCTTT CCAGCTGACT ATCGAATATC GAAGCTGTCT CACATTTGAG GCATTGAGG CTCTATGTGG CTCTATGTGC	31     GGGGCGCTGC GAGGCGGCGC GAGAGCGACC CACGTATGCG GAAACCTATA TCCATGCCAT TATCTGAGCC GCACCTGTCA	TGCTGGCGCT CGTTATCAGG CCGAACTCAG GAGTGAGCCT GTGACCTTAG CCTTCTGGAG CCTGCTACCT CCTACACTAA GGACAGACTG CCCACACCCT TCCTCAAGTA	CTGCTGGCT GCTGGCGG GCTTGGCCG GCTCAGCCAC TGATCCCTCC CCTGCAGGCC GGGGAATTCA ACACATCCAG CTGGGTGACT CCAGGAAGTT CCAGGAAGTT CAGGTTCCCC	120 180 240 300 360 420 480 540
50	Nucleic Aci Coding sequ 1   GCCGCGGGAG GCGGGGTGAC CGACGGTCA TGGCAGGGGA TGGCAGGGGA TACTACACCC CCCTATGACA CCCATCTGTC GGCTGGGGGT CAGGTGGCCA AAGGACATCT TTCGGTGACT	id Accession lence: 19 11   AGGAGGCCAT TCACGTCGCG GCCTGCGCT TCACGTCGCG TCACGTTTGG TTACTTCGT TTGCCTTGGT TCACGCCTC ACATCAAAGA TCATAAACAA TTGGAGACAT CAGGTGGACCAT	#: NM_0061 63 21   GGGCGCGCGC GGAGTCGCAG CATCGTTGGT TCAGATGTTT CAGATGATT ATCGAATATC GAAGCTGTCT ATCGAATATC GAATGAGCA CTCTATTGAG GGTTTGTGC CTTGGCCTGT	31   GGGGCGCTGC GAGGCGGCGC GAGAGCGACC CACGTATGCG GAAACCTATA TCCATGCCAT TATCTGAGCC GCACCTGTCA TTTGAGAACC CTGCCATCTC AACCACCTCT AACCACCTCT AACCACCTCT AACAAGAATG	TGCTGGCGCT CGTATCAGG CCGAACTCGG GAGTGAGCCT GTGACCTTAG CCTTCTGGAG CTCGCTACCTA CGACACCAC CCCACACCCT TCCTCAAGTA AAGGCGGGAA GACTGGTAGA	CONTROL OF THE PROPERTY OF THE	120 180 240 300 360 420 480 540 600 660 720 780
50 55	Nucleic Aci Coding sequi	id Accession lence: 19  11    AGGAGGCCAT TCAGGAGGC TCACGTCTGG GCTGCGCT TCACGGGGGCT TCACGGCGG TTCACGTTGG TTCACTTGGT TCACTTGGT TCCATTGGT TCCAGGCTC ACATCAAAGA TCATAAACAA TTGGAGACAT CAGGTGGAC CGGGAGTGGG TTGATGGGATTGG	H: NM_0067 63 21	31    GGGGCGCTGC GAGGCGCGCG GAGAGGACG CACGTATGCG GAAACCTATA TCTGAGCCAT TATCTGAGCACTCT CTGCCATCTCA ACCACTCTT GGCAATGCC AACCACTCT GGCAATGCC AACCAGAGAATG CCCAATCGC AACCAGACAGAATG	TGCTGGCGCT TGCTGGCGCT TGCTATCAGG CCGAACTCGG GAGTGAGCCT GTGACCTTAG CCTACACTAA GGACAGACTG CCCACACCCT TCCTCAAGTA AAGGCGGAA GACTGTGCTA CCGGTGTCTA CCGGTGTCTA GTGCCATGT	GCTGCTGGCT GCTGCTGGCG GCTTGGCCG GCTCAGCCAC TGATCCCTCC CCTGCAGGCC GGGGAATTCA ACACATCCAG CTGGGTGACT CCAGGAAGTT CCAGGAAGTT CCAGTTCCGC GGATGCCTGC TCAGATTGGA ACACAATATC CCAGCCAGAC	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50 55	Nucleic Aci Coding sequi Coding sequi Coding sequi Coding sequi GCCCCGGGAG CCGACGGAC CCGACGGATCA CCCATCGACA CCCATCTGTC CGCTGGCCA AAGGACATCT TTCGGTGACT GTCGTGAGCT ACCACCACT CCCTCTGAGCT ACCACACT CCCTCTGGCC CCCTCTGGCC	id Accession ence: 19  11    AGGAGGCCAT TCAGGAAGCC TCACGTCGCG GCTGCGCT TCACGGCGC TCACGTCGGT TCACGCGG GTTACTTCGT TCCAGGCCTC ACATCAAAGA TCATAAACAA TTGGAGACAT CAGGTGGAC CGGGGAGTGGG TTGACTGT CAGGTGGAC CGCTACTCTT	H: NM_0061 63 21   GGGCGCGCGC GGAGTCGCAGC GCACTGCTTT CCAGCTGATT ATCGAATATC GAAGCTGTCT CACATTTGAG GGATGAGCT CTCTATGTGC GCTTTGTGCT CTTGGCCTGT CTTGGCCTGT CTTGGCCTGT TTTCCCTCTT	31 GGGGCGCTGC GAGGCGGCGC GAGAGGACG CACGTATGCG GAAACCTATA TATCTGAGCA TATCTGAGCC TTTGAGAACC CTGCCATCTC GGCAATCTC GGCAATGCC AACACCTCTT GGCAATGGCC AACAGGATG ATGGCCCAGA CTCTGGCCTC	TGCTGGCGCT TGCTGGCGCT TGCTATCAGG CCCAACTTAG CCTTCTGGAG CCTACACTAA GGACAGACTG CCTACACTAA TCCTCAAGTA AAGGCGGAA GACTGTGGTA CCGTGCTACT CCGCATGCT CCGCATGCT TCCTCAAGTA TAGGCAGATGT TCCTCAAGTA TAGGCGGAA TGCGCATGTC TCCCCACTCCT TCCCCACTCCT	GCTGCTGGCT GCTGGCGG GCTTGGCCG GCTCAGCCAC TGATCCCTCC CCTGCAGGCC GGGGAATTCA ACACATCCAG CTGGGTGACT CCAGGAAGTT CAGGTTTCCGC GGATGCCTGC TCAGATTGGA CACCATACG CCAGCCAGAC GGGGCCAGCC	120 180 240 300 360 420 480 540 660 720 780 840 900 960
50 55	Nucleic Aci Coding sequ  1   GCCGCGGGAG GCGGCTGAC CGACGGTCA TGGCAGGGATG TACTACACCC CCCTATGACA CCCATCTGTC GGCTGGGGGT CAGGTCGCA AAGGACATCT TTCGGTGACT GTCGTGACT GTCGTGACT GTCGTGACT GTCGTCACCACACT TGAGCACACT TGAGCACACCT TGAGCCTACCC	id Accession lence: 19 11   AGGAGGCCAT TCAGGAAGCC TCACGTCGCG GCCTGCGCT TCACGCGGCT TCACGCGGCT TCACGCGCT TCACGCGCT TCACGCGCCT ACATCAAAGA TCAGAGCAT TCAGAGCAT CAGGTGGAC TCAGTCGAGCT TCAGTCAAACA TTGAGAGCAT TCAGTGGAC GCGCAGTCGG TTGAGTGAT TGAGTCAT TGAGCCATG	H: NM_0061 63 21 21 GGGCGCGCGC GCACTGCTTG TCAGCTGAT ATCGAATATC GAAGCTGTT ATCGAATATC GAAGCTGTT ATCGAATATC GCATTTTGAC GCATTTTGAC CTCTTGACT CTTGGCCTG CTGTGCTGCT TTTCCCTCTT CAGCCTGGT CTGCCTGT	31    GGGGCGCTGC GAGGCGCGCG GAGAGGACG CACGTATGCG GAAACCTATA TCTGAGCCAT TATCTGAGCACTCT CTGCCATCTCA ACCACTCTT GGCAATGCC AACCACTCT GGCAATGCC AACCAGAGAATG CCCAATCGC AACCAGACAGAATG	TGCTGGCGCT CGTTATCAGG CCGAACTCGG GAGTGAGCCT GTGACCTTAG CCTTCTGGAG CTCGCTACCT CCTACACTAA AGGACAGACT CCCACACCCT TCCTCAAGTA AAGGCGGGAA ACGCGGGTGTCTA CTGGCATCCT CTGCCACTCCT CTCCACTCCT CTCCACTCCT CTCCACTCCT CTCAGGCCCT CTCAGGCCCT CTCAGGCCCT CTCAGGCCCT CTCAGGCCCT CTCAGGCCCT CTCAGGCCCT CTCAGGCCCT	CAGGAAGTT CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	120 180 240 300 360 420 480 540 600 660 720 780 840 900
<ul><li>50</li><li>55</li><li>60</li></ul>	Nucleic Aci Coding sequi    GCGGCGGGAG GCGGCTGAC CGACGGGTCA TGGCAGGGGAC GGGTGGATGG TACTACACCC CCCTATGACA CCCATCTGTC GGCTGGGGT TAGGCAGACATCT TTCGGTGACT TCGGTGACT AGCACACT CCCTCCTGGC TGACCTCACC TGTCTTGTTT TGTCTTGTTT	id Accession lence: 19 11   AGGAGGCCAT TCAGGAAGCC TCACGTCGCG GCCTGCGCT TCACGCGGCT TCACGCGGCT TCACGCGCT TCACGCGCT TCACGCGCCT ACATCAAAGA TCAGAGCAT TCAGAGCAT CAGGTGGAC TCAGTCGAGCT TCAGTCAAACA TTGAGAGCAT TCAGTGGAC GCGCAGTCGG TTGAGTGAT TGAGTCAT TGAGCCATG	#: NM_0061 63 21   GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGTGGGGT	31   GGGGCGCTGC GAGGCGCGC GAGAGCGACC CACGTATGCG GAAACCTATA TCCATGCCAT TATCTGAGCC GCACCTGTCA TTTGAGAACC CTGCCATCTC AACAACTATC AACAAGAATG CCCAATCGCC AACAAGAATG CCCAATCGCC ATGGCCCAGA CTCTGGGCTC CCACTGCCAA	TGCTGGCGCT CGTTATCAGG CCGAACTCGG GAGTGAGCCT GTGACCTTAG CCTTCTGGAG CTCGCTACCT CCTACACTAA AGGACAGACT CCCACACCCT TCCTCAAGTA AAGGCGGGAA ACGCGGGTGTCTA CTGGCATCCT CTGCCACTCCT CTCCACTCCT CTCCACTCCT CTCCACTCCT CTCAGGCCCT CTCAGGCCCT CTCAGGCCCT CTCAGGCCCT CTCAGGCCCT CTCAGGCCCT CTCAGGCCCT CTCAGGCCCT	CAGGAAGTT CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	120 180 240 300 360 420 480 540 660 720 780 840 900 960
<ul><li>50</li><li>55</li><li>60</li></ul>	Nucleic Aci Coding sequil Coding sequil GCCGCGGGAG GCGGCGGAG CGACGGGTCA TGGCAGGGGATCA TGGCAGGGATCG TACTACACCC CCCTATGACA CCCATCTGTC GGCTGGGGGT CAGGTCGCA AAGGACATCT TTCGGTGAGCT TCCGTGACT GCCTCCTGGC TGAGCCTACC TGTCTTGTTT  Seq ID NO: Protein Aci	id Accession lence: 19 11 1 AGGAGGCCAT TCAGGAAGCC TCACGTCGCG GCCTGCGCCT TCACGGCGCC TCACGTCGGT TCACGCGCCT TCACGCGCCT TCACGCGCCT TCACGCCCT ACATCAAACAA TCAGAGACAT TCAGGACACT CAGGTCGC GCGAGTCGG TTAGTGAT TCAGTGGAC TCAGTCGCT TCAGTCGAC TCAGTCGCT TCAGTCGACT TCAGTCGACT TCAGTCGACT TCAGTCGAT TCAGTCGAT TCAGTCGCT TCAGTCGAT TCAGTCCATG GCTAATAAAC  136 Protei Cession #:	#: NM_0061 63 21 21 GGGCGCGCGC GCACTGCTTT CCAGCTGACT ATCGAATATC GAAGCTGTT ATCGAATATC GAAGCTGTT CACATTTGAG GCATTTGAG GCATTTGAG CTTATGAG CTCTATGTGC CTGGCCTGT CTTGGCCTGT CTTGGCCTGT CTGCCTGT TTCCCTCTT CAGCCTGGGG ACATTCCAGT  n sequence NP_006790	31  GGGGCGCTGC GAGGGGGCGCG GGAGAGGACG GAAACCTATA TCCATGCCAT TTTGAGGACC CTGCCATCTC AACCACCTCT AACCACCTCT AACCACCTCT CGCAATGGCC ACCAATGGCC ATGGCCCAGC ATGGCCCAGC ATGGCCCAGC ATGGCCCAGT TGATGCCTTGGGTA TGATGCCTTG	TGCTGGCGCT CGTTATCAGG CCGAACTCGG GAGGGACCTTAG CTGGCTACCT CCTTCTGGAG CTCGCTACCT CCTACAGTA AAGGCGGGAA AAGGCGGGAA CGCGTGTCTA CGGGGTGTCTA GTGGCATCTC GTGGCATCTC CCGGTGTCTA CCCACTCCT CCCACCCT CAGGGCATTC	CAGCAGAC  GCTGCTGGCT  GCTGCTGGCC  GCTCAGCCAC  GCTCAGCCAC  GCTCAGCCAC  GCGGAATTCA  ACACATCCAG  CTGGGGAATTCA  ACACATCCAG  GCTGGGTGACT  CCAGGAAGTT  CAGTTTCCGC  GGATGCCTGC  TCAGATTGGA  CACCAATATC  CCAGCCAGAC  GGGGCCGGTC  GGGTCTCTCT  TTCAAAA	120 180 240 300 360 420 480 540 660 720 780 840 900 960
<ul><li>50</li><li>55</li><li>60</li></ul>	Nucleic Aci Coding sequil Coding sequil GCCGCGGGAG GCGGCTGGAC CGACGGTCA TGGCAGGGGA TGGCAGGGGA TACTACACCC CCCTATGACA CCCATCTGTC GGCTGGGGGT CAGGTGGCA AAGGACATCT TTCGGTGACT GTCGTGACT TCCCTCCTGC TGAGCCTACC TGTCTTGTT  Seq ID NO: Protein Aci	id Accession lence: 19  11    AGGAGGCCAT TCACGGAGGC TCACGTCGCG GCCTGCGCT TCACGGCGG TCACGTTTGGT TTGCCTTGGT TGACTTCGT TTGCCTTGGT TCACAAAGA TCATAAACAA TTGAGACAT TCAGGGCCTC ACATAAACAA TTGAGTGGAC GGGAGTGGG TTGAGTGGAC TGAGTGAT TGAGTGAT TGAGTGAC TGAGTGAT TGAGTGAT TGAGTGAT TGAGTGAT TGAGTGAT TGAGTGAT TGAGTGAT TGAGTGAT TGAGTCGTT TGAGTCGAT TGAGTCGAT TGAGTCGAT TGAGTCGAT TGAGTCGAT TGAGTCGAT TGAGTCGAT TGAGTCGAT TGAGTCCAT TGAGCCCAT TGAGCCAT TGAGCCAT TGAGCCCAT TGAGCCAT T	#: NM_0061 63 21 21 GGGCGCGCGC GCACTGCTTT CCAGCTGACT ATCGAATATC GAAGCTGTCT ATCGAATATC GAATGATGCC GCATTGATT CACATTTGAC GGATTGAGC GCTTATTGAC GGTTTGTGC GTTTGTGCT CTTGGCCTGT CTGGCTGT CTGGCTGT CTGGCTGT CTGGCTGT CTGGCTGT CTGGCTGT CAGCCTGGGG ACATTCCAGT  n sequence NP_006790 21	31 31 31 31 31 32 33 33 31 31 31 31 31 31 31 31 31 31 31	TGCTGGCGCT CGTATCAGG CCGAACTCGG GAGTGAGCCT GGTGACCTTAG CCTTCTGGAG CTCGCTACCT CCTACACTAA GGACAGACTG CCCACACCCT TCCTCAAGTA AAGGCGGGAA AAGGCGGGAA GACTGGTACTA GTGCATGCT GTGCATCTC GTCAGCCT GTCAGGCCT CAGGGCATTC AAGGCCGT CAGGGCATTC AAGGCCGT CAGGGCATTC AAGGCCGT AAGGCCGT CAGGGCATTC	GCTGCTGGCT GCTGCTGGCC GCGTTGGCCG GCTCAGCCAC GCTCAGCCC CCTGCAGGCC GGGGATTCA ACACATCCAG CTGGGTGACT CCAGGAAGTT CAGTTTCCGC GGATGCCTGC TCAGATTGGA CACCAATATC CCAGCCAGAC GGGGCCGGTC GGTTCTCTTC TTCAAAA	120 180 240 300 360 420 540 660 660 720 780 840 900 960 1020
50 55 60 65	Nucleic Aci Coding sequil Coding sequil GCCGCGGGAG GCGGCGGAG CGACGGGTCA TGGCAGGGGATCA TGGCAGGGGATCG TACTACACCC CCCTATGACA CCCATCTGTC GGCTGGGGGT CAGGTCGCA AAGGACATCT TTCGGTGAGCT TCCGTGACT TCCTCCTGCC TGAGCCTACC TGTCTTGTTT  Seq ID NO: Protein Aci I MGARCALLLA	id Accession lence: 19  11    AGGAGGCCAT TCAGGAAGCC TCACGTCGCG GCCTGCGCCT TCACGCGGCC TCACGTTGGT TCCAGGCGCC ACATCAAAGA TCATAAACAA TTGAGAACAT TTGAGTGGACT TCAGTGGACT TCAGTGGACT TCAGTGGACT TCAGTGACACAC GGGAGTGGG TTGAGTGACT TGAGTGAT TGAGTGAT TGAGTGAT TGAGTGAT TGAGTCAT TGAGCCCATG GGTAATAAAC  136 Protei cession #: :  11    LLLARAGLRK	H: NM_0061 63 21 21 23 21 33 33 34 35 35 36 36 36 36 36 36 36 36 36 36 36 36 36	31   GGGGCGCTGC GAGGGGGCGC GGAGAGGAC GACATATGCG GAAACCTATA TCCATGCCAT TTTTGAGGACC CTGCCATCTC AACCACCTCT AACCACCTCT GGCAATGCCC AACAAGAATG CCCAATGGCC ATGGCCCAGA TCTTGGGCCC ATGGCCCAGA TGATGCCTTG CCACTGCCAA TGATGCCTTG  31   GGCGRRVITS	TGCTGGCGCT CGTTATCAGG CCGAACTCGG GAGTGAGCCT GTGACCTTAG CCTCCTCGGAG CTCGCTACCT CCTACACTAA AAGACCGGAA AAGACGGGAA ACGCGGGAT CCGGTGCTA CCGGTGCTA CCGGTGCTA CCGGTGCTA CCGGTGCTA CCGGTGTCTA CTGCCACTCC GTCAGGCCCT CAGGGCATTC  41 I RIVGGEDAEL	GCTGCTGGCT GCTGCTGGCT GCTTGCCG GCTTGGCCG GCTCAGCCAC TGATCCCTCC CCTGCAGGCC GGGGAATTCA ACACATCCAG CTGGGTGACT CCAGGAAGTT CAGTTTCCGC GGATGCCTGC TCAGGATTGGA CACCAATATC CCAGCCAGAC GGGGCCGGTC GGTTCTCTC TTCAAAA  51   GRWFWQGSLR	120 180 240 360 420 480 660 720 780 840 900 1020
50 55 60 65	Nucleic Aci Coding sequil Coding sequil GCCGCGGGAG GCGGCGGGAG CGGCTGGAC CGACGGTCA TGGCAGGGGA TACTACACCC CCCTATGACA ACCATTCGTC GGCTGGGGGT CAGGTGGCA AAGGACATCT TTCGGTGACT AGCACCACT TTCGTGAGCT AGCCACCACT TGTCTTGTT Seq ID NO: Protein Aci I MGARGALLLIA LWDSHVCGVS VSNIYLSPRY	id Accession lence: 19  11    AGGAGGCCAT TCACGAGGCGCT TCACGTCGCG GCCTGCGCT TCACGTCTGGT TCACGTTTGGT TTGCCTTGGT TTGCCTTGGT TGACTAAAGA TCAGAGACAT TCAGGGCCTC ACATCAAAGA TTGAGAGACAT TCAGGTGGAC GGGGAGTGGG TTGAGTGGAT TGAGTCAT TGAGTCAT TGAGTCAT  136 Protei cession #:  11    LLLARAGLRK LLSHRWALTA LGNSPYDIAL	#: NM_0061 63 21   GGGCGCGCGC GGAGTCGCAG CATCGTTGGT GTGGGATTCC GCACTGCTTT CAGCTGACT ATCGAATATC GAAGCTGTCT ATCGAATATC GGATGAGGCA CTCTATTGAG GGATTGAGC GGTTTGTGC GTTTGTGCT CTTGGCCTGT CTGGCTGG	31  GGGGCGCTGC GAGGCGGCGCG GAGAGCGCGCG GAAACCTATA TCCATGCCAT TATCTGAGCAT TATCTGAGAACC CTGCCATCTC GCAATCTC GCAATCCC AACAGAATG CCCAATCGC ATGGCCT ATGGCCTTG ATGGCCTTG ATGGCCTTG CCAATCGC ATGGCCTTG CCAATCGC ATGGCCTTG CCACTGCCAA TGATGCCTTG  31  GPCGRRVITS SDPSGMMVQF KHIQPICLQA	TGCTGGCGCT CGTTATCAGG CCGAACTCGG GAGTGAGCCT GGTGACCTTAG CCTTCTGGAG CTCGCTACCT CCTACACTAA GGACAGACT CCCACACCCT TCCTCAAGTA AAGGCGGGAA GACTGGGTA GTGGCATGTC CTCACTCT GTCAGCTCT GTCAGCATCT GTCAGCTCT GTCAGGCCT CAGGGCATTC  41   RIVGGEDAEL QLITMPSFW STFFEPENRTD	GCTGCTGGCT GCTGCTGGCC GCGTTGGCCG GCTCAGCCAC GCTCAGCCC CCTGCAGGCC GGGGAATTCA ACACATCCAG CTGGGTGACT CCAGGAAGTT CAGTTTCCGC GGATGCCTGC TCAGATTGGA CACCAATATC CCAGCCAGAC GGGGCCGGT GTTCTCTTC TTCAAAA  51    GRWPWQGSLR SLQAYYTRYF CAVTGWGYIK	120 180 240 300 360 420 540 660 720 780 840 900 960 1020
50 55 60 65	Nucleic Aci Coding sequil Coding sequil GCCGCGGGAG GCGGCTGGAC CGACGGGTCA TGGCAGGGGA TGGCAGGGTCA TGGCAGGGGA TACTACACCC CCCTATGACA ACCCATCTGTC GGCTGGGATC GTCGTGACT TTCGGTGACT TTCGGTGACT TTCGGTGACT TTCGTGACT TTCGTGACT TTCGTGACT TGCTCACC TGTCTTGTTT  Seq ID NO: Protein Aci I MGARGALLLA LWDSHVCGVS VSNIYLSPRY EDEALPSPHT	id Accession lence: 19  11    AGGAGGCCAT TCAGGAAGCC TCACGTCGCG GCCTGCGCCT TCACGGCGCC TCACGTTGGT TCCAGGCCT TCACGCGGC TCACGTCGGT TCACGCGCC ACATCAAAGA TCATAAACAA TTGAGACAT TCAGTGGAC TCAGTGGAC TCAGTGGAC TCAGTGGAC TCAGTGGAC TGAGTGGAC TGAGTGGAC TGAGTGGAC TGAGTGGAC TGAGTGGAC TGAGTGGAC TGAGTGGAC TGAGTGGAC TGAGTGGAC LGCACT TGAGCCCATG GGTAATAAAC  136 Protei LLLARAGLRK LLSHWALTA LCHEVQVAIIN YQIGVVSWGV	#: NM_0061 63 21 21 23 21 23 33 33 34 35 35 35 35 35 35 35 35 35 35 35 35 35	31  GGGGCGCTGC GAGGCGGCGCG GAGAGCGCGCG GAAACCTATA TCCATGCCAT TATCTGAGCAT TATCTGAGAACC CTGCCATCTC GCAATCTC GCAATCCC AACAGAATG CCCAATCGC ATGGCCT ATGGCCTTG ATGGCCTTG ATGGCCTTG CCAATCGC ATGGCCTTG CCAATCGC ATGGCCTTG CCACTGCCAA TGATGCCTTG  31  GPCGRRVITS SDPSGMMVQF KHIQPICLQA	TGCTGGCGCT TGCTGGCGCT CGTATCAGG CCGAACTCGG GAGTGAGCCT GTGACCTTAG CCTTCTGGAG CTCGCTACCT CCTACACTAA AAGCCGGAA AAGCGGGAA AAGCGGGAA CTGCATCT GTCACTCT GTCACTCT GTCACTCT GTCAGGCATTC  41   RIVGGEDAEL GQLTMPSFW TYPEPENRTD MVCAGNAQGG	GCTGCTGGCT GCTGCTGGCC GCGTTGGCCG GCTCAGCCAC GCTCAGCCAC GCGGAATTCA ACACATCCAG CCAGGAAGTT CAGTTTCCGC GGATTGCATC CCAGGAAGTT CAGTTTCCGC GCAGCAGAC TCAGCATATC CCAGCAGAC GGGCCGGC GGTTCTCTTC TTCAAAA  51   GRWPWQGSLR SLQAYYTRYF CWYTGWGYLK KDACFGDSCG	120 180 240 300 360 420 540 660 720 780 900 960 1020
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	Nucleic Aci Coding sequil Coding sequil GCGGCGGGGAG GCGGCGGGAG CGGCTGGAC CGACGGTCA TGGCAGGGGA TGGCAGGGGA TACTACACCC CCCTATGACA ACCATCTGTC GGCTGGGGGT CAGGTGGCA AAGGACATCT TTCGGTGACT GTCGTGACT TTCGTGACT GTCGTGACT GTCTGTGTT Seq ID NO: Protein Aci I MGARGALLLA LWDSHVCGV VSNIYLSPRY EDEALPSPHT PLACNENGLW FFPLLMALPL	id Accession lence: 19  11    AGGAGGCCAT TCACGGAGGC TCACGTCGCG GCCTGCGCT TCACGGCGGC TCACGTTTGGT TTGCCTTGGT TTGCCTTGGT TCACGACAC ACATCAAAGA TCATAAACAA TTGAGACAT TCAGGTGGAC GGGAGTGGG TTGAGTGGAC GGGAGTGGG TTGAGTGAT TGAGTCAT TGAGTCAT  136 Protei cession #:  11    LLLARAGLRK LLSHRWALTA LCHEVQVAIIN YQIGVVSWGV LGPV	#: NM_0061 63 21 21 GGGCGCGCGC GGAGTCGCAG CATCGTTGGT GTGGGATTCC GCACTGCTTT CCAGCTGACT ATCGAATATC GAAGCTGTCT ATCGAATATC GGATGAGGCA CTCTATTGAG GGTTTGTGC GTTTGTGCC GTTTGTGCC GTTTCCCTCTT CAGCCTGGGG ACATTCCAGT  n sequence NP_006790 21 PESQEAAPLS AHCFETYSDL VKLSAPTYT NSMCNHLFLK GCGRPNRPGV	31   GGGGCGCTGC GAGGGGGCGC GGAGAGGACG CACGTATGCG GAAACCTATA TCCATGCCAT TTTGAGGACC CTGCCATCTC AACCACCTCT AACCACCTCT AACCACCTCT CGCAATCGCC ATTGGGCAC ATTGGCCAGA TCTGGCCTAC ACTGCCATCTC AACAGAATG CCCACTGCCAA TGATGCCTAG TGATGCCTTG CCACTGCCAA TGATGCCTTG CCACTGCCAA TGATGCCTTG SDPSCMMVQF KHIQPICLQA YSFRRDIFGD	TGCTGGCGCT TGCTGGCGCT CGTATCAGG CCGAACTCGG GAGTGAGCCT GTGACCTTAG CCTTCTGGAG CTCGCTACCT CCTACACTAA AAGCCGGAA AAGCGGGAA AAGCGGGAA CTGCATCT GTCACTCT GTCACTCT GTCACTCT GTCAGGCATTC  41   RIVGGEDAEL GQLTMPSFW TYPEPENRTD MVCAGNAQGG	GCTGCTGGCT GCTGCTGGCC GCGTTGGCCG GCTCAGCCAC GCTCAGCCAC GCGGAATTCA ACACATCCAG CCAGGAAGTT CAGTTTCCGC GGATTGCATC CCAGGAAGTT CAGTTTCCGC GCAGCAGAC TCAGCATATC CCAGCAGAC GGGCCGGC GGTTCTCTTC TTCAAAA  51   GRWPWQGSLR SLQAYYTRYF CWYTGWGYLK KDACFGDSCG	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	Nucleic Aci Coding sequil Coding sequil GCGGCGGGAG GCGGCTGAC CGACGGGTCA TGGCAGGGGA TGGCAGGGGA TGGCAGGGGA TACTACACCC CCCTATGACA CCCATCTGTC TTCGGTGACT TTCGGTGACT TTCGGTGACT TCCTCTGGGC TGACCACACT TGTCTTGTTT  Seq ID NO: Protein Aci I MGARCALLLA LWDSHVCGVS VSNIYLSPRY EDEALPSPHT PLACNENGLW FFPLLMALPL  Seq ID NO: Nucleic Aci	id Accession lence: 19  11    AGGAGGCCAT TCAGGAAGCC TCACGTCGCG GCCTGCGCT TCACGCGGCG TCACTTCGT TTGCTTGGT TCCAGGCCT ACATCAAAGA TCATAAACAA TTGAGGAGCT CAGGTCGCT TCACGCTC GCGAGTCGG TCACTCAAAGA TCAGAGAGA TCAGAGAGA TCAGAGACA TCAGTACAAGA TCAGTACAAGA TCAGTAGACA TCAGTAGACAT CGCTACTCT TCAGCCATG GGTAATAAAC  136 Protei cession #:  11    LLLARAGLRK LLSIRWALTA LCNSPYDLIAL LQEVQVAIIN YQIGVVSWGV LGFV  137 DNA Se	#: NM_0061 63 21 21 GGGCGCGCGC GGAGTCGCAG CATCGTGGGT GTGGGATTCC GCACTGCTTT CCAGCTGACT ATCGAATATC GAAGCTGTCT CACATTTGAG GGATTGAGGCA CTCTATGTGC CTTATGTGC CTTATGTCC CTTATGTCC CTTATCTCC CTTTCCTCTT CAGCCTGT CTGCCTGT CAGCCTGGG ACATTCCAGT DESQUENCE NP_006790 21   PESQEAAPLS AHCFETYSDL VKLSAPVTYT NSMCNHLFLK GCGRPNRPGV  Quence n #: Eos se	31   GGGGCGCTGC GAGGCGCGC GAGAGGACG CACGTATGCG GAAACCTATA TCCATGCCAT TATCTGAGACC CTGCCATCTC AACCACTCT GGCAATGCC AACAGAATG CCCATCTC AACAGATG CCCATCGCA TGATGCCT ATGGCCATCGC AACAGATG CCCATCGCAA TGATGCCTTG  31   GPCGRRVITS SDPSCMMVQF KHIQPICLQA YSFRDIFGD YTNISHHFEW	TGCTGGCGCT TGCTGGCGCT CGTATCAGG CCGAACTCGG GAGTGAGCCT GGTGACCTTAG CCTCTCTGGAG CTCGCTACCT CCTACACTAA AAGGCGGAA AAGGCGGAA AAGGCGGAA GACTGGTA CTCAACTCA GTGGCATGTC CCACCCT TCTCAAGTA AAGGCGGAA AAGGCGGGAA GACTGGTA CCGACTCCT GTCAGGCATTC  41	GCTGCTGGCT GCTGCTGGCC GCGTTGGCCG GCTCAGCCAC GCTCAGCCC CCTGCAGGCC GGGGAATTCA ACACATCCAG CTGGGTGACT CCAGGAAGTT CAGTTTCCGC GGATGCCTGC TCAGATTGGA CACCAATATC CCAGCCAGAC GGGGCCGGTC GGTTCTCTTC TTCAAAA  51    GRWPWQGSLR SLQAYYTRYF CNVTGWGYIK KDACFGDSGG SQFDPSWPLL	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	Nucleic Aci Coding sequil Coding sequil GCGGCGGGAG GCGGCTGAC CGACGGGTCA TGGCAGGGGA TGGCAGGGGA TGGCAGGGGA TACTACACCC CCCTATGACA CCCATCTGTC TTCGGTGACT TTCGGTGACT TTCGGTGACT TCCTCTGGGC TGACCACACT TGTCTTGTTT  Seq ID NO: Protein Aci I MGARCALLLA LWDSHVCGVS VSNIYLSPRY EDEALPSPHT PLACNENGLW FFPLLMALPL  Seq ID NO: Nucleic Aci	id Accession lence: 19 11     AGGAGGCCAT TCAGGAAGCC TCACGTCGCG GCCTGCGCCT TCACGTCGGT TCACGTCGGT TCACGTCGGT TCACGTCGGT TCACGCGGC TCACGTCTGGT TCCAGGCCT TCACGCCT TCACGCCT TCACGCCT TCACGCCT TCACGCCT TCACGCCT TCACGCCT TCACTCT TCAGGCCC GCGAGTGGG TCAGTGGAC TCAGTGAT CCTACTCT TGAGCCCATG GGTAATAAAC  136 Protei     LLLARAGLRK LLSHWALTA LCHSPYDIAL LQEVQVAIN YQIGVVSWGV LGPV  137 DNA se lid Accessio	#: NM_0061 63 21 21 GGGCGCGCGC GGAGTCGCAG CATCGTGGGT GTGGGATTCC GCACTGCTTT CCAGCTGACT ATCGAATATC GAAGCTGTCT CACATTTGAG GGATTGAGGCA CTCTATGTGC CTTATGTGC CTTATGTCC CTTATGTCC CTTATCTCC CTTTCCTCTT CAGCCTGT CTGCCTGT CAGCCTGGG ACATTCCAGT DESQUENCE NP_006790 21   PESQEAAPLS AHCFETYSDL VKLSAPVTYT NSMCNHLFLK GCGRPNRPGV  Quence n #: Eos se	31   GGGGCGCTGC GAGGCGCGCG GGAGAGGACG CACGTATGCG GAAACCTATA TCCATGCCAT TTTGAGGACC CTGCCATCTC AACCACCTCT AACCACCTCT GGCAATGCCC AACAAGAATG CCCAATCGGC ATGGCCCAGA TGATGCCCTGCCAA TGATGCCTTG  31   GFCGRRVITS SDESGMIVLQA XSFRRDIFGD YTNISHHFEW	TGCTGGCGCT TGCTGGCGCT CGTATCAGG CCGAACTCGG GAGTGAGCCT GTGACCTTAG CCTTCTGGAG CTCGCTACCT CCTACACTAA AAGCCGGAA AAGCGGGAA AAGCGGGAA CTGCATCT GTCACTCT GTCACTCT GTCACTCT GTCAGGCATTC  41   RIVGGEDAEL GQLTMPSFW TYPEPENRTD MVCAGNAQGG	GCTGCTGGCT GCTGCTGGCC GCGTTGGCCG GCTCAGCCAC GCTCAGCCAC GCGGAATTCA ACACATCCAG CCAGGAAGTT CAGTTTCCGC GGATTGCATC CCAGGAAGTT CAGTTTCCGC GCAGCAGAC TCAGCATATC CCAGCAGAC GGGCCGGC GGTTCTCTTC TTCAAAA  51   GRWPWQGSLR SLQAYYTRYF CWYTGWGYLK KDACFGDSCG	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	Nucleic Aci Coding sequil Coding sequil GCCGCGGGAG GCGGCTGAC CGACGGTCA TGGCAGGGGA TGCTGGGCA TGCTGGCA ACCATTGTC GCTGGGCT AGCACACT TTCGTGACT AGCACACT TTCGTGACT AGCACACT TTCGTGACT AGCACACT TTCGTGACT AGCACACT TTCGTGACT TGTCTTGTT  Seq ID NO: Protein Aci I MGARGALLLA LWDSHVCGVS VSNITLSPRY EDEALPSPHT PLACKKNGLW FFPLLWALPL Seq ID NO: Nucleic Ac Coding seq I ATGGGCGCGCG	id Accession lence: 19  11    AGGAGGCCAT TCACGTCGCG GCCTGCGCT TCACGTCGCG GCTGCGCT TCACGTCGT TCACGTCGT TCACGTCGT TTACTTCGT TTGCCTTGGT TTGCCTTGGT TCCAGGCCTC ACATCAAAGA TCAGAGACAT TCAGGTGGAC CGGGAGTGGG TTGAGTGGAT CGTACTCTT TGAGCCCATG GGTAATAAAC  136 Protei cession #:  11    LLLARAGLRK LLSHRWALTA LCMSPYDIAL LQEVQVAIIN YQIGVVSWGV LGFV  137 DNA se id Accessio LUENCE: 19  11    CGCGGGGGCCCT	#: NM_0061 63 21 21 GGGCGCGCGC GGAGTCGCAG CATCGTTGGT GTGGGATTCC GCACTGCTTT CAGCTGACT ATOGAATATC GAAGCTGTCT ATOGAATATC GGATGAGGCA CTCTATTGAG GGATGAGGCA CTCTATGTGC GGTTTGTGCT CTTGGCCTGT CTGGCTGT CTGGCTGG	31   GGGGCGCTGC GAGGCGCGCG GAGAGGACG GAAACCTATA TCCATGCCAT TATCTGAGACC CTGCCATCTC AACCACTCT GGCAATGCCC AACAGAATG CCCATGCCAA TGAGCC AACAGAATG CCCATGCCAA TGATGCCT ATGGCCAATCGCC ATGGCCAA TGATGCCTTG  31   GPCGRRVITS SDPSCMMVQF KHIQPICLQA YSFRDIFGD YTNISHHPEW  quence 31   CTGCTGCTGCTGGCTGCTGCTGCTGCTGGCTAACAGGCTAGATGCCTTGGTTGCTGGTTGCTGGTTGCTGGTTGCTGGTTGCTGGTTGCTGGTT	TGCTGGCGCT CGTTATCAGG CCGAACTCGG GAGTGAGCCT GGTGACCTTAG CCTCCTGGAG CCTCCTCAGCTA AGACGGGAA AGACGGGAA AGACGGGAA AGACGGGAA AGACGGGAA CTCCACTCT GTCAACTTAA I   RIVGGEDAEL GQLTSMPSFW STPEPENRTD MVCACNAQGG IQKLMAQSGM  41   CTCGGGCTGGC	GCTGCTGGCT GCTGCTGGCC GCGTTGGCCG GCTCAGCCAC GCTCAGCCC CCTGCAGGCC GGGGAATTCA ACACATCCAG CTGGGTGACT CCAGGAAGTT CAGTTTCCGC GGATGCCTGC TCAGATTGGA CACCAATATC CCAGCCAGAC GGGGCCGGTC GGTTCTCTTC TTCAAAA  51    GRWPWQGSLR SLQAYYTRYF CNVTGWGYIK KDACFGDSGG SQFDPSWPLL	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020

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		144 Proteir					
45	Protein Acc	144 Protein cession #: 2 11		31	<b>41</b>	51 I	
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45 50	Protein Acc 1   MVDVKCLSDC AQDSDDSEGG Seq ID NO:	cession #: ) 11	RP_050184.1 21     FSPGPILPST   MGLSPKRETT	 RKLYEKKLVQ ARKTRLSRAG	 LLVSPPCAPP	1	60
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50	Protein Acci 1   MVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Acc Coding sequility   AGGTGAACAG TCCGCTGGCC TCCCCTGCTC TACCCGATTC	dession #: 2 11	(P_050184.1 21 i FSPGPILPST MGLSPKRETT Quence n #: NM_0022 2229 21 i CCAGCTCCGC CCCAGC TGGCGCCCCAG AGGAGGCCCGG	RKLYEKKLVQ ARKTRLSRAG	LLVSPPCAPP EKKVSQWA  41   GCTCTCGCCG CGGCCCCAC GTCTCCGCCT AGCCTCTCG	VMNGPRELDG  51   GGACCCCGCT GCCTGATGCT TCAACCTGGA GCTACTCGGT	60 120 180 240
50	Protein Acci 1   MVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Ac: Coding sequ 1   AGGTGAACAG TCCGCTGGCA CTGTGCGCTC TACCCGATTC CGCCCTCCAT	dession #: 2 11	RP_050184.1 21 FSPGPILPST MGLSPKRETT Guence 1 #: NM_0022 222 21 CCAGCTCCGC CCGGCCCAG TGGCGGCCGG AGCGGCAGCAG	RKLYEKKLVQ ARKTRLSRAG  204.1  31   CCCCTCACGC CCGCGCCCC CGGCTGCGTC GAACCCGGGC GCGCTACCTG	LLVSPPCAPP EKKVSQWA  41   GCTCTCGCCG CGCGCCCCAC GTCTCCGCCT AGCCTCTTCG CTCCTGGCTG	VMNGPRELDG  51   GGACCCGCT GCCTGATGCT TCAACCTGGA GCTACTCGGT GTGCCCCCCG	60 120 180 240 300
50	Protein Acci 1   MVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Ac: Coding sequi 1   AGGTGAACAG TCCGCTGGCA TCCCGCTGCCT TACCCGATTC CGCCCTCCAT GGAGCTCGCT CACTGCCCAC	dession #: 2  11    KLQNQLEKLG LQEHQAPESH  145 DNA secid Accession dence: 74 11    GTCCTCACGC GCCATGGGCC GCCATGGGCC GCCATGGGCC GCTTGATGG CTGGTAGTGA CGGCAGACAG GTGCCCGATG AAGGATGACT	(P_050184.1 21 i   FSPGPILPST MGLSPKRETT Quence i #: NM_0022 1229 21   CAGCTCCGC CCCGGCCCCAG TGGCGGCCCCAG AGGAGGCCGG AGGAGGCCGG AGCAGCAAGCA	RKLYEKKLVQ ARKTRLSRAG  204.1  31   CCCCTCACGC CCGCCGCCCC CGGCTGCGTC GAACCCGGGC GCGCTACCTG GCCCCACTGGT GAACATCACA	LLVSPPCAPP EKKVSQWA  41   GCTCTCGCCG GGCGCCCAC GTCTCCGCCT AGCCTCTTCG CTCCTGGCTG GCTGTGTACC GTGAAAAATG	VMNGPRELDG  51   GGACCCCGCT GCTGATGCT TCAACCTGGA GCTACTCGGT GTGCCCCCG TGTGCCCCCACT ACCCTGGCCA	60 120 180 240 300 360 420
50	Protein Acci        MVDVKCLSDC AQDSDDSEGG     Seq ID NO: Nucleic AccCoding sequit     AGGTGAACAG TCCGCTGGCA CTGCCATTC CGCCTCCAT CACCGATTCT CACTGCCAC TCACATTATT	dession #: 2  11    KLQNQLEKLG LQEHQAPESH  145 DNA secid Accession ence: 74    GTCCTCACGC GCCATGGGCC GCCTTGATGG CTGGTAGTGA CTGGTAGTGA CTGGCACAG GTGCCCGATG GAGGACAG GTGCCCGATG GAGGACATGT GAGGACATGT	RP_050184.1 21 i FSPGPILPST MGLSPKRETT Quence n #: NM_0022 222 21 ccagctccag CCGGCCCCAG AGGGGCCGG AGGGGCCGG AGGGGCCGG AGGGGCAGCA GCTACACCAA GTGAGCGGAT GGCGTTGGAGT	RKLYEKKLVQ ARKTRLSRAG  204.1  31    CCCCTCACGC CCGCCGCCCC CGGCTGCGTC GAACCCGGGC GCCTACCTG CCGGACTGGT GAACATCACTG GAACTGGT GAACTTGGCC	LLVSPPCAPP EKKVSQWA  41   GCTCTCGCCG CGGCCCCAC GTCTCCGCCT AGCCTCTTCG CTCCTGGCTG GCTGTACC GCTGTACC GCTGAAAATG AGCCAGGGCC	VMNGPRELDG  51   GGACCCCGCT GCCTGATGCT TCAACCTGGA GCTACTCGGT GTGCCCACT ACCCTGGCCAA CTGCAGGCAG	60 120 180 240 300 360
50 55 60	Protein Acci    MVDVKCLSDC AQDSDDSEGG  Seq ID NO: Nucleic Ac: Coding sequil   AGGTGAACAG TCCGCTGGCA CTGTGCGCTC TACCCGATTC TGGAGCTCGCAC TCACATTATT TAGTTCTGGTG GCGCATGGTG GCGCATGGTG GCGCATGGTG GCGCATGGTG GCGCATGGTG GCGCATGGTG	dession #: 2  11    KLQNQLEKLG LQEHQAPESH  145 DNA secid Accession dence: 74  11    GTCCTCACGC GCCATGGGCC GCCATGGATGA GGCAGAGAGA GTGCCCGATG AAGGACATGT TGTGCCCACC GGCAAGTGCC GGCAAGTGCC GGCAAGTGCC	RP_050184.1 21 i FSPGPILPST MGLSPKRETT TUENCE i #: NM_0022 3229 21   CCAGCTCCGC CCGGCCCCAG AGCAGGCCCAG AGCAGGCCGCA AGCAGGCCGCA AGCAGGCAG	RKLYEKKLVQ ARKTRLSRAG  204.1  31   CCCCTCACGC CCGCGCCCC CGGCTGCGTC GAACCCGGGC CCGGTACCTG GAACATCACA GACTGTGGCC GGTGCTGTGG CAATGACCTA	LLVSPPCAPP EKKVSQWA  41   GCTCTCGCCG GGCGCCCAC GTCTCCGCCT AGCCTCTTCG CTCTCGGCTG GCTGTTACC GTGAAAAATG AGCCAGGGCCA GAGCTCAGCTC	VMNGPRELDG  51   GGACCCCGCT GCCTGATGCT TCAACCTGGA GCTACTCGGT GTGCCCCCG TGTGCCCACT ACCCTGGCCA CTGCAGGCAG AAGACCAACGC CCAGTGATGA	60 120 180 240 300 360 420 480 540 600
50	Protein Acci    MVDVKCLSDC AQDSDDSEGG  Seq ID NO: Nucleic Accoding sequilated according sequilated acco	ession #: 2 11	(P_050184.1 21 i FSPGPILPST MGLSPKRETT Quence i #: NM_002: 1229 21 i CCAGCTCOGC CCGGCCCCAG AGGGCCCGA AGGAGGCCGG AGCAGGAGGCCGG GCTACACCAA GTACACCAA GTACACCAA GTACACCAA GTACACCAA ACTGCGAGGA ACGTCGAGGA ACGTCGAGGA ACGTCGAGGA ACGTCGAAGA ACGTCGCAAA ACGTCGCAAA	RKLYEKKLVQ ARKTRLSRAG  204.1  31   CCCCTCACGC CCGCGCCCC GGGTGCGTC GAACCCGGGC GCGCTACCTG CCGGACTGGT GAACATCACA ACTGTGGCC GGTGCTGTGG	LLVSPPCAPP EKKVSQWA  41   GCTCTCGCCG GGGCCCCAC GTCTCCGCCT AGCCTCTTCG CTCTAGATAATG AGCCAGGGCC TCAGGGTCAG GAGCTGGACT AGCCAGGGCC GAGCTAGACT GAGCTCAGCT GAGCTCAGCT GAGCTCAGCT GAGCTCAGCT GACTACTGG	VMNGPRELDG  51   GGACCCGGT GCTGATGGT TCAACCTGGA GCTACTCGGT GTGCCCCCG TGTGCCCCACT ACCCTGGCA CTGCAGGCAG AAGACCACGG CCAGTGATGAA AGACGGGCAT	60 120 180 240 300 360 420 480 540
50 55 60	Protein Acci    MVDVKCLSDC AQDSDDSEGG  Seq ID NO: Nucleic Ac: Coding sequi   AGGTGAACAG TCCGCTGGCA CTGTGCGCTC TACCGGATTC CACCTCCAT GGAGCTCGCTC CACTGCCAC TCACATTATT AGTTCTGGTC GCGCATGGTG CTGCCAGCTC CTGCCAGCTC CTGCCAGCTC TCGCCAGCTC TCGCCAGCTC TCGCCAGCTC TGCCTACAAC	dession #: 2  11    KLQNQLEKLG LQEHQAPESH  145 DNA secid Accession dence: 74  11    GTCCTCACGC GCCATGGGCC GCCATGGATGG CTGGTAGTGG GTGCCGATG AAGGATGACT GAGGACATGT TGTGCCACC GGCAAGTGCT TACCACACG GGCACAGCG TGGAAAGGAA	RP_050184.1 21 i FSPGPILPST MGLSPKRETT Guence i #: NM_0022 3229 21 i CCAGCTCCGC CCGGCCCCAG TGGCGGCCCAG AGCAGGCCGA AGCAGGCCGA AGCTACACCAA GTGAGCGGAT GGCTTCGAGT GCTACACCAA ACGTGCGAGG AGCAGCAGAG AGCAGCACAA ACGTGCGAGG AGCAGCACAA ACGTGCCAAG ACGTGCCAAG ACGTGCCAAC ACGTGCCAAC ACGTGCCACAA	RKLYEKKLVQ ARKTRLSRAG  204.1  31   CCCCTCACGC CCGCCGCCCC CGGCTGCGTC GAACCCGGGCT GCGACTGGT GAACATCACA GACTGTGGCC GGTGCTGGCC GGTGCTGGCC CAATGACACTA TAGCAACACT GATTCAGCGC	LLVSPPCAPP EKKVSQWA  41  GCTCTCGCCG GGCCCCAC GTCTCGGCT AGCCTCTTCG CTCCTGGCTG GCTGTTACC GTGAAAAATG AGCCAGGCC TCAGGGTCA GACTACCTGG GACTACCTGG GAGTACCTTGG AAGAAATTCAAGGGTCA GAGTACCTAC AAGAAGTGGG AAGAAGAGTGGG AAGAAGTGGG AAGAAGTGGG	S1 GGACCCGGT GGACCCCGT TCAACCTGGA GCTACTCGGT GTGCCCACT ACCCTGGCCA ACGCTGACCAGC ACGCTGATGATGA AGACCAGCG CCAGTGATGA AGACCAGCG AGACCAGCG AGACCAGCA AGACCAGCA AGACCAGCAT AGACCAGCA AGACCAGCAT AGACCACACT AGACCACAT AGACCACACT AGACCACCACT AGACCACACT AGACCACACT AGACCACACT AGACCACACT AGACCACCACT AGACCACCACT AGACCACCACT AGACCACCACT AGACCACT AGACCACCACT AGACCACCACT AGACCACCACT AGACCACT AGA	60 120 180 240 300 360 420 480 540 600 660 720 780
50 55 60 65	Protein Acci    MVDVKCLSDC AQDSDDSEGG  Seq ID NO: Nucleic Accoding sequilated According Sequilated Acco	dession #: 2  11    KLQNQLEKLG LQEHQAPESH  145 DNA secid Accession dence: 74  11    GTCCTCACGC GCCATGGGCC GCCATGGGCC GCCATGGGCC GTGCACGGC GTGCACGACAG GTGCCCGATG AAGGACAGCT TATGCCCACC GGCAAGTGCT TACCACAACG GGCACAGCG TGGAAAGGAA AAGGACCCAG	CP_050184.1 21 FSPGPILPST MGLSPKRETT GUENCE #: NM_0022 1229 CCAGCTCCGC CCCGCCCCAG AGCAGCAGCA AGCAGCAGCA GTCAGCAGCAGCA GTCAGCAGCA GTCAGCAGCA ACTGCAGCAG ACATGCAGA ACATGCAGA ACATGCAAA ACATGCAAA ACATGCAAAA AGGACCAAGA ACAGCAACAAAAAAAGAACCAAAGG	RKLYEKKLVQ ARKTRLSRAG  204.1  31   CCCCTCACGC CCGCGCCCC GGACTGCGT GAACCCGGGC GAACCCGGGC GAACATCACC GAACTCGGC GAACATCACC GATGTGGCC GATGTGGCC AATGACACA TAGCAACACA CCCAGAACACT	LLVSPPCAPP EKKVSQWA  41    GCTCTCGCCG GGCGCCCAC GTCTCCGCCT GCTCTCGGCTG GCTGTACC GTGAAAAATG AGCCAGGCC TCAGGGCC TCAGGGCC TCAGGGCC GTAAAAATG AGCAAGACT GATTACTGG ATTACTGG ATTACTGA ATTGGGTACA ATTGGGTACA	VMNGPRELDG  51   GGACCCCGCT GCCTGATGCT TCAACCTGGA GCTACTCGGT GTGCCCCCCG TGTGCCCACT ACCCTGGCCA CTGCAGGCAG AGACCAGCG CCAGTGATGA AGACGGCAT GCGCCCCCGG ACTATTCTGA CGATGCAGGT CCGCCCCCGG ACTATTCTGA CGATGCAGGT CGATGCAGGT CGATGCAGGT CGATGCAGGT CGATGCAGGT CGATGCAGGT CGATGCAGGT CGATGCAGGT CGATGCAGGT	60 120 180 240 300 360 420 480 540 600 720
50 55 60	Protein Acci    MVDVKCLSDC AQDSDDSEGG  Seq ID NO: Nucleic Ac: Coding sequil   AGGTGAACAG TCCGCTGGCA CTGTGCGCTC CACTGCCAT CGGACTCGCT CACTGCTC CACTGCTC CACTGCTC CTCACTTCT GCGCAGCT CTGCCAGCT CTGCCAGC	dession #: 2  11    KLQNQLEKLG LQEHQAPESH  145 DNA section decession tence: 74  11    GTCCTCACGC GCCATGGGCC GCCTTGATGG CTGGTAGTGA CGCAGACAG GTGCCCGATG AAGGACAG GTGCCCAACG GCAAGTGCT TACCACACC GGCAAGTGCT TACCACAACG TGGAAAGGA AAGGACCAGC TGGAAAGGA AAGGACCAGC ACCTGCACC GCGGTGTTCT	RP_050184.1 21 21 FSPGPILPST MGLSPKRETT Guence 1 #: NM_002: 3229 21   CCAGCTCCGC CCGGCCCCAG TGGCGGCCGAG AGCAGGCCGAG AGCAGGCAGA AGCTACACAA GTGAGCGGA GGCTTGGAGCA ACGTGCGAG AGAGTTGCAA ACGTGCGAGG AGAGTTCAC ACACTACAT ACGACTACAT ACGACCAAAACAT TGCTGAGCCA	RKLYEKKLVQ ARKTRLSRAG  204.1  31   CCCCTCACGC CCGCGCCCC GGCTGCGCC GAACCCGGGC GGCTACCTG CCGACTGGT CAACACAC CAGCACACAC CCAGAACACT GATTCAGGC AAACCTCTT GGACCATCT GATTCAGGC AAACCTCTT GGAGCAGGC GACCATTGT CGGACCAGGC GGAGCAGGC	LLVSPPCAPP EKKVSQWA  41   GCTCTCGCCG CGCGCCCCAC GTCTCCGCGT AGCCTCTTCG GCTGTACC GTGAAAAATG AGCCTGGACT GACTACCTGG GACTACCTGG ATACCTGG ATACCTGG ATTACCTGG ATTACGGTACA ATTACGGTACA ATTACGGTACA GACACCTGC GGACACCTGC	S1   GGACCCGCT GCCTGATGCT TCAACCTGGA GCTACTCGGT GTGCCCACT ACCCTGGCCA ACGCAGCAG AAGACCAGCG CAGTGATGA GCACCGGCAT ACCCTGGCA ACGCACT ACCCTGGCA ACGCACT ACCCTGGCA CAGTGATGA AGACCACGG CAGTGATGA GCACCCGG ACTTATCTGA CGATGCAGGT CACGCACCG GGAGGAGGCACA	60 120 180 240 300 360 420 480 540 660 720 780 840 900 960
50 55 60 65	Protein Acci    MVDVKCLSDC AQDSDDSEGG  Seq ID NO: Nucleic Accoding sequilated   AGGTGAACAG TCCGCTGGCC TACCCGATTC CGCCCTCCAT GAGCTCGCT CACTGCCAC TCACATTATT AGTTCTGGTC CGCGAGACC GTGCAGACC GTGCAGACC GTGCCAGCT TGCCTACAC TGCATAGTTAC AGGCAGCTT AGTATAGTTAC AGGCAGCTT ACATATGGGC GTATAGTTAC AGGCAGCTTC ACATATGGGC GGGCAGACC GTATAGTTAC AGGCAGCTTC ACATATGGGC GGTGCTGGAG GAACAATGAT	ression #: 2  11  KLQNQLEKLG LQEHQAPESH  145 DNA secid Accession lence: 74  11  GTCCTCACGC GCCATGGGCC GCCATGGGCC GCTTGATGG GTGCCCGATG AAGGACATG TGTGCCCGATG TGTACCACC GGCACAGGCT TACCACACC GGCACAGGCA TGGAAAGGA ATCCTGCACC GCGGTGTTCT GGCTCGCAGG GGGTGTTCT GGCTCGCAGGG GGGTGTTCT GGCTCGCAGGG GGGTGTGCAGGG GGGTGGCAGGG GGGTGGCAGGG GGGTGGCAGGG GGGTGGCAGG	CP_050184.1 21 FSPGPILPST MGLSPKRETT GUENCE #: NM_002: 1229 21   CCAGCTCCGC CCGGG AGGGGCCCAG AGGAGGCCGA AGCTACACCAA GTTACACCAA GTTACACCAA GTTACACCAA GTTACACCAA GTGAGTTGCAC ACAGTTACAC ACAGCTACAC ACGCCCCTA ACCTCCTGGT	RKLYEKKLVQ ARKTRLSRAG  204.1  31    CCCCTCACGC CCGCCGCCCC CGGCTGCCC CGGCTGCTG GAACCCGGC GCGACTGGT GAACATCAC GATGTGGC CAATGACTA CCAGAACACA CCAGAACACT CACATTCAGCGC TATCAGCGC TTTTGGCAGC TTTTGGCAGC GGGGCCCCCC GGGCCCCCC	LLVSPPCAPP EKKVSQWA  41    GCTCTCGCCG GGGCCCCAC GTCTCCGCCT GCTCTGGCTG GCTGTAAC GTGAAAAATG AGCCATGGCT CAGGGTCAG GAGTACCTGG GACTACCTGG GACTACCTGG GACTACCTGG GACTACCTGG GACTACCTGG GACTACCTGG GACTACCTG GACAATTGCCC GGACACTGC GCAATTGCCC TACTACTTCT	S1   GGACCCGCT GCCTGATGCT TCAACCTGGA GCTACTCGGT ACCCTGGCCAC ACCCTGGCCAC ACCCTGGCCAC ACCCTGGCCAC ACCCTGGCCAC ACCCTGGCCAC ACCCTGCCAG AGACCAGGCAT GCGCCCCCGG ACTTATCTGA CCATGATGAT CACGCACCC GGAGGAGGCAC TGGCAGACCT AGAGGAAAGA	60 120 180 240 300 420 480 540 660 720 780 960 960 1020 1080
50 55 60 65	Protein Acci    MVDVKCLSDC AQDSDDSEGG  Seq ID NO: Nucleic Ac: Coding sequil   AGGTGAACAG TCCGCTGGCA CTGTGCGCT CACTGCCAC TCACTCATTC GCGCTCCAT GGAGCTCGCT CACTGCTGCCAC TCACATTATT AGTTCTGGTC GCGCATGCTG CTGCCAGCTG GTGCCAGCTG GTGCCAGCTG GTGCCAGCTG GTGCTACAAC GTATAGTTAC ACATTATT ACATTATGGC GGACACTGGTG GGACACATGAT ACATATGGGC GGACACATGGTA GGAACATGGGC GGACACATGGAC GGACACATGGAC GGACACATGGAC GGACACATGGGC GGACACATGGGC GGACACATGGGC GGACACATGGGC GGACACATGGGC GGACACATGGGC GGACACATGGGC GGACACTAGGGC GGACACATGGGC GGACAATGGGG GGACAATGGGG	dession #: 2  11    KLQNQLEKLG LQEHQAPESH  145 DNA section dence: 74  11    GTCCTCACGC GCCTTGATGG CTGGTAGTGA GGCAGACAG GTGCCCGATG AAGGACAG GTGCCCGATG AAGGACAG GTGCCCACC GGCAAGTGCT TACCACACC GGCAAGTGCT TACCACACC GGCAAGTGCT TACCACACC GGCACTGGCACC GGCACTGCACC GGCACTGCACC GGCACCACC GCGTGTTCT GGCTCGCACG GGGTGGCAGG	RP_050184.1 21 21 FSPGPILPST MGLSPKRETT GUENCE 1 #: NM_002: 8229 21   CCAGCTCCGC CCGGCCCAG TGGCGGCCGA ACGTGCAGCA GCTACACCAA GTGAGCGAGC ACGTGCGAG ACATGTGAG ACATGTCAC ACATGTCAC ACAGCTACAT TGCTACACCA TGGCTCCAG TGGCGGCTCAC ACTGCAGC ACATGTCAC ACATGTCAC ACAGCTACAT AGGACCAAG ACATGTCAC ACAGCTACAT AGGACCAAG ACATGTCAC ACAGCTACAT AGGACCAAG ACATGCAA ACTTCCTGAT ACCTCCTGGT ATGTCTTCAT	RKLYEKKLVQ ARKTRLSRAG  204.1  31    CCCCTCACGC CCGCGCCCC GGACCGGGCC GAACCCGGGC GAACACTGGT TAGCAACACA CCAGAACACT GATTCAGGC AAACTCTAT CACCATTGTG GGAGGCAGGC TTTTGGCAGC GGGCCCCC GGACCCCC	LLVSPPCAPP EKKVSQWA  41   GCTCTCGCCG GGGCCCCAC GTCTCCGCGT GCTCTTCG GCTGTACC GTGAAAAATG GACTACCTG GACTACCTG GACTACCTG AGGAGTCGA ATGGGACT ATGGGACT CGGAGACTGC GCAATTGCCC TACTACTTCG GGAACCTCC GGAGACTCCT GGAACTCCC GGACCTCC GGACCTCC GGACCTCC GGACCTCC GGACCTCC GGACCTCCT GGACCTCCT GGACCTCCT	S1   GGACCCGCT GCCTGATGCT TCAACCTGGA GCTACTCGGT GTGCCCACT ACCCTGGCCA ACGCACGA AGACGGCAT AGACGGCAT AGACGGCAT GCGCCCCGG ACTATCTGA CGATGAAGA CGATGAAGA CGATGAAGA CGATGAAGA CGATGAAGA CGAGGACCT AGAGGAACT AGAGGAAACA TCCCTGCTCA	60 120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1080
50 55 60 65	Protein Acci    MVDVKCLSDC AQDSDDSEGG  Seq ID NO: Nucleic Accoding sequilated AGGGGAACAG TCCGCTGGCA TCCCGATTC GGCCTCCAT AGGTCTCCAT AGTTCTGGTC CACCACCAC TCACATTATT AGTTCTGGTC GCGCATGGT CTGCCAGCT GCGCAGCT GCGCAGCT GCATAGTT AGGCAGCT CTACAGC GTGCCAGCT GGTATAGTT AGGCAGCT CTGCTACAGC GTATAGTT AGGCAGCT CTCACTAC CGTGCTGGGG GAACAATGAT GGAACTAGGC GGTGCTGGGG GAACAATGAT CGGTACAGT CTGGTCACATC TGGTCACATC	ression #: 2  11  KLQNQLEKLG LQEHQAPESH  145 DNA secid Accession lence: 74  11  GTCCTCACGC GCCATGGGCC GCCATGGGCC GCCATGGGCC GCGACAGGCC GTGCACAGC GTGCCACAC AGGACAGG TGGCAGACAG TGGCACAGCG GGCACAGCG TGGAAGGA ATCCTGCAC GCGGTGTTC GGCTGCAG GGGTGCCAT ACCACAGC GCGTGTCT TACCACAC GCGTGTTCT TACCACAGG GGGTGCCAT ATCTTCACAC GGCTGCAGG GGTTGCCACAC GGGTGCCAT ACCAGGAT ATCTTTCTTCAC AACCAGGATG	CP_050184.1 21 FSPGPILPST MGLSPKRETT GUENCE ##: NM_0022 1229 CCAGCTCCGC CCCGGCCCCAG AGCAGCAGCA AGCAGCAGCA GTCACACCAA TCCTCAGGCACCAA ACGTCACACCAA ACGTCACAC ACGCTCCACTACACCAA ACGCTCCACTACACCAAACCAT TCCTGAGCCCAA ACCTCCTCGGT ACCTCCTCGGT ATGTCTTCAGGA	RKLYEKKLVQ ARKTRLSRAG   204.1   31	LLVSPPCAPP EKKVSQWA  41    GCTCTCGCCG GGCGCCCAC GTCTCCGCCT AGCCTCTTCG GCTGTTACC GTGAAAAATG AGCAAGGCCC TCAGGGTCAG GAGCTGCACT GACTACTTG GTGTACTCG GTGTACTCG GCGAGCTGCCC GCGAACTTGCCC GCGAACTTGCCC GCGAACTTGCCC TACTACTTCG GGAACCTCCT TACTTCG GGAACCTCCT	S1 GGACCCCGCT GCTGATGCT TCAACCTGGA GCTACTCGGT GTGCCCCCG TGTGCCCAC TGCAGGCAG AGACCAGG CCAGTGATGA AGACGGCAT ACCCTGGCCA TGCGCCCCG GGAGGAGCA CAGTGATGA CGATGATGA TCAGGCACT AGAGGAACA TCCCTGCTCA AGAGGAACA TCCCTGCTCA TGGCCAGCAT TTGAAGGCTT TTGAAGGCTT	60 120 180 240 300 420 480 540 660 720 780 840 900 960 1020 1080 1140 1260
50 55 60 65 70	Protein Acci    MVDVKCLSDC AQDSDDSEGG  Seq ID NO: Nucleic Ac: Coding sequility   AGGTGAACAG TCCGCTGGCC TACCCGATTC GGCCTCCAT GGAGCTCGCT CACTGCCAC TCACTATATT AGTTCTGGTC GCGCAGACC GTGCCAGACC GTGCCAGACC GTGCCAGACC GTATAGTTAC AGGCAGACT GGAATAGGG GGACAATGAT GGACTAGGAC CGTGCTGCAG GGACAATGAT GGAAGTAGGG CCCTCACTC GGGCAAAGTG GGGCAAAGTG	ression #: 2  11  KLQNQLEKLG LQEHQAPESH  145 DNA secid Accession lence: 74  11  GTCCTCACGC GCCATGGGCC GCCATGGGCC GCCTTGATGG GTGCCCGATG AAGGACATG TGTCCCGATG AAGGACATG TGTCCCACC GGCAAGTGCT GAGGACATG TGTCCCACC GGCAAGTGCT TACCACACG GGCACAGCG GGCACAGCG ATCCTGCACC GCGTGTTCT GGCTGGCAG ATCCTGCACC GCGTGTTCT GGCTCGCAG ATCCTGCACC GCGTGCACG GGGTGCCATCT CTTCTTCATC AACCAGGAT AACCAGGAT ATCCAGATG AACCAGGATG AACCAGATG AACCAGGATG AACCAGGATG AACCAGGATG AACCAGGATG AACCAGGATG AACCAGGATG AACCAGGATG AACCAGGATG AACCAGGATG AACCAGATG AACCAGAT	RP_050184.1 21 FSPGPILPST MGLSPKRETT GUENCE 1 #: NM_0022 229 21 CCAGCTCOGC CCAGCCCCAG AGCAGCCCCAG AGCAGCCCCAG AGCAGCAGCA AGCTACACCAA GTACACCAA GTACACCAA GTACACCAA GTACACCAA GTAGCAGGAT ACATCACA ACAGCTACAC ACAGCTACAC ACAGCTACAC TGCTGAGCCA TGCTGAGCCA ACATCTGCAT TGCTGAGCCA ACATCTCATGGAGCAAC ACATCTCATGGAGCAAC ACATCTCATGGACCAAGGCCCCAGTGG ACATTACACCA ACATCTCATGACCAA ACATCTCATGACCAACAC ACATCTCATGACCAACACACACACACACACACACACACAC	RKLYEKKLVQ ARKTRLSRAG  204.1  31    CCCCTCACGC CCGCGCCCC CGGCTGCTC GAACCCGGGC GAACATCAC CCAGACATGAC CAAACACA CCAGAACACA CCAGAACACA CCAGAACACT GATTCAGGGC GAACCTCTAT CACCATTGTG GGAGGCAGCC CTCTGCCTT TATTGCTGC TAAGGGGCT TATTGCTGT TAAGGGGCT TAAGGGGCT TAAGGGGCT TAAGGGGCT TAAGGGGCT TAAGGGGCTC TAAGGGGCTC TAAGGGGCTC TAAGGGGCTC TAAGGGGCTC TAAGGGGCTC TAAGGGGCTC TAAGGGGCTC TAAGGGGCTC TAAGGGCTC TAAGGGGCTC TAAGGGCTC TAAGGGGCTC TAAGGGCTC TAAGGGGCTC TAAGGGCTC TAAGGCTC TAAGGGCTC TAAGGCCT TAAGGGCTC TAAGGGCT TAAGGGCT TAAGGGCT TAAGGGCT TAAGGGCT TAAGGGCT TAAGGCT TAAGGCT TAAGGCT TAAGGCT TAAGGCC TAAGCC TAAGCC TAAGCT	LLVSPPCAPP EKKVSQWA  41    GCTCTCGCCG CGCCCCCAC GTCTCCGCCT AGCCTCTTCG CTCCTGGCTG GCTGAAAAATG AGCCAGGCC TCAGGGTCAG GAGCACGACT CAGGGTCAG AGCAGGGCC TCAGGGTCAG AGCAGGGCC TCAGGGTCAG AACAATGCCC GAGAACCTCG GCAAATGCCC GGAGACCTCCT GGTTATTCTG GGAACCTCCT GGTTATCTCG CTAGACACC CTTAGACAGC CTTAGACAGC	S1   GGACCCGCT GCCTGATGCT TCAACCTGGA GCTACTCGGT GTGCCCACT ACCCTGGCCA AGACCAGC AGAGCAGC AGAGCAGC AGAGCAGC AGAGCAGC AGAGCAGC ACTATCTGA CCAGGCACC GGAGGAGGC GGAGGAGGC AGAGGAAGA TCCCTGCTCA TGGCAGACCT TGGCAGACCT TGGCAGCCT TGGCAGCT TGCAGCGT TGCCAGCAGT TGCAGCGT TGCCAGCGT TCCCAGCAGGT CCCAGCAGGT CCCAGCAGGT	60 120 180 240 300 420 480 540 600 660 720 840 900 1020 1080 1140 1200
50 55 60 65 70	Protein Acci    MVDVKCLSDC AQDSDDSEGG  Seq ID NO: Nucleic Ac: Coding sequil   AGGTGAACAG TCCGCTGGCA CTGTGGGCT CACCGATTC GGAGCTCGCAC CACTGCAT CACATTATT AGTTCTGGTC GCGCATGGCA GTATAGTTAC GTGCAGCT CACATATAGT CACATATAGGC GGTGCTAGAAC GGTATAGT GGAACTAGGA GAACTAGGA CCCTTCACTC TCGTGACATC GGGCAAAGTG GATCCATGGA GCACATGGAT GCACATGCAT GCACATGGAT GCACATGCAT GCACAT	dession #: 2  11    KLQNQLEKLG LQEHQAPESH  145 DNA secid Accession dence: 74  11    GTCCTCACGC GCCATGGGCC GCCATGGATGA GGCAGAGAGA AGGACATGT TACCACACG GGCACAGGG GGCACAGGG TGGAAAGGA ATCCTGCACC GCGTGTTCT TACCACACG GGCACAGGG TGGAAAGGA ATCCTGCACC GCGTGTTCT TACCACAGGG TGGAAAGGA ATCCTGCACC CCGGTGTTCT TACCACAGGG GGTGCATGT TACACAGGG TGGAAAGGAA ATCCTGCACG GGGTGCATCT CTTCTTCATG AACCAGGATG TACATCTATC GAGAAGCTGG GTGGATGAGAG TGGAAAGTAGA	CP_050184.1 21 21 FSPGPILPST MGLSPKRETT FUENCE FSPGPILPST MGLSPKRETT FUENCE FSPGPILPST MGLSPKRETT FUENCE FSPGPILPST MGLSPKRETT FUENCE FSFGPILPST MGLSPKRETT FUENCE FSFGPILPST MGLSPKRETT FSFGSCCCAG FSFGCCCCAG AGCTCCGC AGCGCCCCAG AGCGCCCCAG AGCAGGCCCAG AGCACCAA ACTTCCAC ACAGCTACAC ACAGCTACAC ACAGCTACAC ACAGCTACAC ACAGCTACAC ACAGCTACAC ACAGCTACAC ACCCCAGTGG ACTTCTTACC GACTGCCCG ACTTCTACCC ACTCCCCGG ACTTCTACCC	RKLYEKKLVQ ARKTRLSRAG  204.1  31   CCCCTCACGC CCGCGCGCCC CGGCTGCGTC GAACCCGGGC GCGTACCTG GAACATCACA GATGTGGC CAATGACACA GATGACACT CAATGACACT CACCATTGT CACCATTGT CACCATTGT CACCATTGT TATGCAGC GAACCAGC CTTTTGGCAGC GAACCAGC CTTTTGCTGT TATTGCTGTC TAATGCGCC AGACCACT CACCATTGT CACCATTCT CACCATTGT CACCATTCT CACCATT CACCATTCT CACCATT	LLVSPPCAPP EKKVSQWA  41    GCTCTCGCCG GGCCCCAC GTCTCCGCCT AGCCTCTTCG GCTCTCTGCCG GTCTCTGCTAC GTCTAAAAATG AGCAGGCCC TCAGGGTCAG GAGCTGCACT GAGTACTTCG GAGTACTTCG GGAGACCTCC GGAGACCTCC GGAGACCTCC GGAGACCTCC GGTTATTCCC GGAGCCCCC TTACTTCG GGAGCCCCCT CTTACTTCG GGAGCCCCCT TCTTACTTCG GGAGCTCCCT CTTAGACAGC CTTAGACAGC TTCGGCTATT GTGGGAAGCCT	S1 GGACCCCGCT GCCCGGAGCCACT ACCCTGGACACGACCACGACGACCACGACCACGACCCAGACCCAGACCCAGACCCAGACCCAGACCCCAGACCCCAGACCCCAGACCCCAGACCCCAGACCACC	60 120 180 240 300 420 480 540 600 660 720 840 900 1020 1080 1140 1260 1320 1380 1440
50 55 60 65 70	Protein Acci    MVDVKCLSDC AQDSDDSEGG  Seq ID NO: Nucleic Accoding sequilated   AGGTGAACAG TCCGCTGGCA TCCCGATTC CGCCCTCCAT GGACTCGCT CACTGCCAC TCACATTATT AGTTCTGGTC CGCGCATGGT CGCGATGGT CGCGATGGT CGCGATGGT CGCGATGGT CGCATGATA AGTATAGTTAC AGGCAGCTT ACATTATT AGTATAGTTAC AGGCAGCTT CGTACAAC GGATGAGAC GGATGAGAC CGGTATAGGAC CGTATAGGAC CGGTATAGGAC CGATGACAC CGGCAAAGTG AATCCATGGA CACATGGAC CACTTACTC ACATCTGGAC CACTTACTC ACATCTGACAC CGGCAAAGTG AATCCATGGA CCATTTTGCTG	ression #: 2  11  KLQNQLEKLG LQEHQAPESH  145 DNA secid Accession lence: 74  15  GTCCTCACGC GCCATGGGCC GCCATGGGCC GCTTGATGG GTGCCCGATG AAGGACATGT TGTGCCCACT GAGACAGGT TGTACCACCC GGCAAGGGC TGGAAAGGA ATCCTGCACC GGGTGTTCT GGCTGGCAGG GGTGCCATCT GGCTGGCAGG GGTGCCATCT GGCTGGCAGG GGTGCCATCT CTCTTCATG AACCAGAGT TACACTATC CACACAGCT GGTAGCAGG GGTGCCATCT CTCTTCATG CACACAGCT CTCTCATC GACAGAGCTGG TACATCTATC GACAAGCTGG GTGGATGAGA CTGCGGGCCC CTCGCAGG CTGCAGG CTGCAGGAGCTGG CTGCAGGAGCTGG CTGCAGGAGCTGG CTGCAGGAGCTGG CTGCAGGAGCTGG CTGCAGGAGCTGG CTGCAGGAGCCCC CTCCACGCCCC CCCCCCCCCC	CP_050184.1 21 FSPGPILPST MGLSPKRETT GUENCE ##: NM_002: 1229 21 CCAGCTCOGC CCAGCCCCAG AGCAGGCCCAG AGCAGGCCGA AGCAGGCAG	RKLYEKKLVQ ARKTRLSRAG  204.1  31    CCCCTCACGC CCGCGCCCC CGGCTGCCCC CGGCTGCTC GAACCCGGGC GAACATCAC CCAGACACAC CCAGACACAC CCAGACACAC CCAGACACAC CCAGACACC GATTCAGCGC CTTTTGGCAGC GAGCCAGCC CTCTGCTTT TATTGCTGC TAACGGCC CTCTGCCTTT TATTGCTGT TAACGGCT CAGACCACT CACACTCTAC CACACTCTCAC CTCTGCCTTT CACACTCTCAC CGTTGGCCCC CAGACCTCTCAC CGTTGGCCCC CGACCACCC CGACCACCC CGACCACCC CGACCACCC CGACCCC CAGACCTCTCAC CACACTCCTC CACACTCCTCAC CACACTCCTC	LLVSPPCAPP EKKVSQWA  41    GCTCTCGCCG GGCCCCCAC GTCTCCGCCT AGCCTCTTCG GCTGTAAC GTGAAAAATG GACTACCTGG GACTACCTGG GACTACCTGG GACTACCTG GACTACCTG GACTACCTG GCAATTGCCC GGAAACTCC GGAACCTCC GTTATTATCTG GGAACCTCCT GTAGACAGG CTTAGACAGC CTTAGACAGC CTTAGACAGC CTCACAGAGACC CCACAGAGACC CCACAGAGACC CCACAGAGACC CCACAGAGACC CCACAGAGC CCACAGAGC CCACAGAGACC CCACAGAGAC CCCC CCACAGAGAC CCCC CCACAGAGAC CCCC CCACAGAGAC CCCC CCCC CCCC CCCC CCCC CCCC CCCC CCCC	S1   GGACCCGCT GCCTGATGCT TCAACCTGGA GCTACTCGGT GTGCCCACT ACCCTGGCCA AGACCAGCA AGACCAGCA AGACCAGCA CTGCAGCAGC AGAGCACCA GCGCACCA GCAGCACCA GCAGCACCA TGCCAGCACCA TGCCAGCACCA TGCAGACCT TGCAGACCT TGCAGACCT TGCAGCACCT TGCAGCACCT TGCAGCACCT TGCAGCACCT TGCAGCACCA TGCAGCACCT TGCAGCCCAG TGCTCAGACCA TGCTGCCCAG	60 120 240 300 360 420 480 540 660 720 780 900 960 1020 1080 1140 1200 1250 1320
50 55 60 65 70	Protein Acci    MVDVKCLSDC AQDSDDSEGG  Seq ID NO: Nucleic Ac: Coding sequil   AGGTGAACAG TCACCTGGCA CTGTGCGCT CACCGATTC GGAGCTCCCCCCCAT TCACATTATT AGTTCAGTC GCGCAGCT CTGCCAGCT CACTAGTAGT CGTGCAGCT CACTAGTAGG GAACAATGAT GGAGCAGCT TCGCAAGCT TCGCAAGCT CACTATGGG GAACAATGAT GGAACATGGG CCCTCACTC TCGTGACATC GGGCAAGTG GATCCATGGA GCAGATTGGT CCTTTGCTTAC CTTTGCTTAC CTTTCTTAC CTTTGCTTAC CTTTGCTTAC CTTTGCTTAC CTTTGCTTAC CTTTGCTTAC CTTTCTTAC CTTTGCTTAC CTTTCTTAC CTTTGCTTAC CTTTGCTTAC CTTTGCTTAC CTTTGCTTAC CTTTGCTTAC CTTTCTTAC CTTTCTTT	session #: 2  11  KLQNQLEKLG LQEHQAPESH  145 DNA secid Accession sence: 74  11  GTCCTCACGC GCCATGGGCC GCCATGGGCC GCCATGGACAG GTGGAAGAA AGGACATGT TACCACAACG GCACAACG GCACAACG GCACAACG GGCACAGC GGTGCACC GGCACACC GGCACACC GGCACCAC GGCTGCACC GGCTGCACC GGCTGCACC ACCAGGACC ACCAGACT ACCAGACT ACCAGACT ACCAGACT ACCAGACT ACCAGACT ACCAGACT ACCAGAGT AC	CP_050184.1 21 21 FSPGPILPST MGLSPKRETT MGCGCCAGG AGAGGCCCAG AGAGGCCAGG AGATGTGAG ACAGTACACCA ACAGTACACA ACAGTACACA ACAGTACACA ACAGTACACA ACAGTACACA ACAGTACAT TGCTGAGCCA TGCGCGCCTA ACCTCCTGGT ATGTTCTTCAT AGACTACGT GACTGCCTGG ACTTCTACCC GGCTGCTGG ACTTTTACCC GGCTGAGCCCCCGGCAACCC CCCGGGAACCCC CCCGGGAACCCC CCCGGAACCCC CCCGGAACCCC CCCGGAACCCC CCGGCAACCCC CCCGGCAACCCC CCGGCAACCCC CCGCGCAACCCC CCGCGCAACCCC CCGCGCAACCCC CCGCGCAACCCC CCGCGCAACCCC CCCGCGCAACCCC CCGCGCAACCCC CCCGCGCAACCCC CCCGCGCAACCCC CCCGCGCAACCCC CCCCCCC CCCCCCC CCCCCCC CCCCC CCCCC	RKLYEKKLVQ ARKTRLSRAG  204.1  31   CCCCTCACGC CCGCGCGCCC CGGCTGCGTC GAACCCGGGC GCGTACCTG GAACATCACA GACTGTGGC CAATGACACA GATTCAGCG CAATGACACT GATTCAGCG TTTTGGCAGC GAACCATGTT CACCATTGT CACCATGTT TATTGCTGT TATTGCTGT TATTGCTGC TAACGGCC CTCTGCCTTT TATTGCTGC GAACACTCAC GATTCACGC CAACACTCTCA CACATTCTC CAACTACACC CGTCGCCACC CGTCGCCACC CGTCGCACCTCT CAACTACAGG	LLVSPPCAPP EKKVSQWA  41    GCTCTCGCCG GGCCCCAC GTCTCGGCT GCTCTCGGCT GCTGTTACC GTGAAAAATG AGCCTGGTG AGCTGGACT GACTACCTGG GAGTACCTGG AAGAGTGGA ATGAGTACCT GGAAACATCA GGAACCTCCT GGATTATCTG GGAACCTCCT GGTTATCTG GGAACCTCCT TACTACTTG GGAACCTCCT TACTACTTG GGAACCTCCT TACTACTTG GGAACCTCCT TTCGGCTATT GTGGGAAGCC TCTAGACAGC CACAAGACCT TTGTGTGCAAG CGAAACATCA	S1   GGACCCGGT GCCTGATGCT TCAACCTGGA GCTACTCGGT GTGCCCAC TGTGCCCAC TGTGCCCAC TGTGCCCAC CTGAGCAG AGACCAGGA CAGTGATGA CAGTGATGA TCACTGGCA AGACGGCAT AGACGGCACT AGAGGAAGA TCACTGCAGCA TGGAGACCT AGAGGAAGA TCCCTGCTCA TTGAAGGCT TTGAAGGCT TTGAAGGCT TTGAAGGCT TTGAAGGT TTGAAGGT TTGAAGGT TTGAAGGT TTGAAGGT TTGAAGGT TTGCCAGCAGT TTGCCAGTGG TGTCCCAGTGG TGTGTGCCCAG TGTGTGCCCAG TGTGTGCCCAG TGTGGCCTA	60 120 180 240 300 420 480 540 600 660 720 1020 1020 1020 1140 1200 1260 1320 1440 1560 1560
50 55 60 65 70	Protein Acci    MVDVKCLSDC AQDSDDSEGG  Seq ID NO: Nucleic Ac: Coding sequity   AGGTGAACAG TCCGCTGGCA TCACCCTCAT CGCCCTCCAT CGACTCAT TAGTTCTGGCCAC TCACATTATT AGTTCTGGTC GCGCATGGTG CTGCCAGCTG GTGCCAGCTG CTGCCAGCTG CTGCAGACC GTATAGTTAC AGGCAGCTTC ACATATGGT AGTCCAGCTG CGGCAAGTGG GAACAATGGA GAACTAGGG CCCTCACTC CGGCAAAGTG CCCTCACTC CGGCAAAGTGA ACCATGGAC CCTTGCCTGCC CCTGCACTC CGCCAGCTGTG CTTGCTTGC CCTTGCTTGCCTG CCCTCTGCACC CCCTCACTC CCCTCTCACTC CCCTCTCACTC CCCTCTCCTCACTC CCCTCTCCTCACC CCCTCTCCTCCACC CCCTCTCCTCCACC CCCTCTCCTCCACC CCCTCCTCCACC CCCTCTCCTCCACC CCCTCCTCCACC CCCTCCACC CCCTCCACC CCCTCCACC CCCTCCACC CCCTCCACC CCCTCCACC CCCTCCACC CCCCTCCACC CCCCCCC CCCCCC CCCCCC CCCCCC CCCCCC	session #: 2  11  KLQNQLEKLG LQEHQAPESH  145 DNA secid Accession sence: 74  11  GTCCTCACGC GCCATGGGCC GCCATGGGCC GCCATGGGCC GCGATGGACAG GTGCCCGATG AAGGACAGT TAGGACAGCA GGCACAGGG TGGAAGGGA ATCCTGCACC GCGTGTTCT GGCTACGGC GGGTGCCATC CACCAGGG GGTGCCATC CACCAGGG GGTGCCATC CACCAGGG GGTGCCATC CACCAGGG GGTGCCATC CACCAGGG GGTGCCATC CACCAGGG GGTGCCATC CACCAGAGT TACCACAGGG CTTCTACT CACCAGAGT TACCACAGGG CTGGACCCTG AACCAGAGTG ACCAGAGTG ACCAGAGTG GCTGACAGGG CCTGCACAGGG CCTACACAGGG CCTACACAGG CCTACACACAC CCTACACAC CCTACACACAC CCTACACAC CCTAC	CP_050184.1 21 21 FSPGPILPST MGLSPKRETT FUENCE ##: NM_0022 229 221   CCAGCTCCGC CCCGGCCCCAG AGCAGGCCCCAG AGCAGGCCGAG AGCAGGCAG	RKLYEKKLVQ ARKTRLSRAG  204.1  31    CCCCTCACGC CCGCGCGCCC CGGCTGCCC CGGCTGGCT GAACCCGGCC GCGACTGGT GAACATCACA GATTCAGCC GATTCAGC CAATGACTA CCAGAACACT CACATTCAGCG TTTTGGCAGC CGGCCCCC GAACCAGGC CTCTGCCTT TATTGCTGTG TAAGGGCTC CAGACTCTCT CACATTCTG CAGACCTCTC CAGACCATCTCT CACATTCTG CAGACCTCTC CACATCTCTC CACATCTCTC CACACTCCC CACACTCCCC CCACACCCCC CCACACCCCC CCACACCCCC CCACACCCCC CCACACCCCC CCACACCCCC CACACCCCCC	LLVSPPCAPP EKKVSQWA  41    GCTCTCGCCG GGGCCCCAC GTCTCCGCCT CTCCTGGCTG GCTCTTGGCTG GCTGTATACC GAGTCACTAG AGCAGGCC TCAGGGTCAG AGCAGTGGAC AAGAGTGGAC TCAGGTTACTTG GAATTACCTG GCATTACTTG GGAACTTCC GGAGCTCCT CTTAGACAGC TTCGGCTATT TTGGGAAGCC CACAAGACCT CTTGGCAATC CCACAAGACCT CCACAAGACCT CCACAAGACCT CCACAAGACCT CCACAAGACCT CCCCATATT CTGGGAAGCC CACAAGACCT CCCCCATTTGCCC CCACAAGACCT CCCCCTTTGCCC CCCCCCCC CCCCCCCC CCCCCCC CCCCCCC CCCC	S1   GGACCCGCT GCCTGATGCT TCAACCTGGA GCTACTCGGT GTGCCCACT ACCCTGGCCA ACCCTGGCCA AGACCACGG AGACCACGG AGACCACGG AGACCACGG AGACCACGG ACTATCTGA CGATGAAGA TGCAGCACT AGAGGAACT TGGAGACCT TGGAGGACCT TGGAGGACCT TTGAAGGCTT TCCCAGCAGT TCCCAGCAGT TCCCAGCAGT TCCCAGCACT TCCCAGCAGT TCCCAGCAGT TCCCAGCAGT TCCCAGCAGT TCCCAGCAGT TCCCAGCAGT TCCCAGCAGCT TCCCAGCAGCT TCCAGCACGT TCCAGCACGT TCCAGCACGT TCGAGCCCAG TCGAGCCCAG TCGAGCCCAG TCGAGCCCAT TCGAGCCCAG TCGAGCCCAT TCGAGCCCAG TCGAGCCAG TCGAGCCCAG TCGAGCCCAG TCGAGCCCAG TCGAGCCCAG TCGAGCCCAG TCGAGCCAG TCGAGCCCAG TCGAGCCAG TCGAGCAG TCGAGCCAG TCGAGCCAG TCGAGCCAG TCGAGCCAG TCGAGCAG TCGAGCAG TCG	60 120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1140 1200 1260 1320 1380 1440 1500 1500
50 55 60 65 70	Protein Acci    MVDVKCLSDC AQDSDDSEGG  Seq ID NO: Nucleic Ac: Coding sequil   AGGTGAACAG TCCGCTGGCA CTGTGCGCTC CACTGCCAT GGAGCTCGCT CACTGCTAC AGGTTAGTT GCTCACTAC AGGTTAGTT GCGCAGCT GTGCCAGCT GCTACAAC GTATTAGTTAC AGGTGTAGAG GAACAATGAT TGGAACT GGAACTAGGA GCAAATGAT CATTGTCT GGGCAAAGT CACTCTGGAG GCCAGCTTGG CCTTGCTTAC CCTGTATTGCT CCTGTATGGAC CCCTCATCC CCTGTATTGCACC CCTGTATTGCACC CCTGTATTGCACC CCTGTATTGCACC CCTGTATGGACC CCTGTATTGCACC CCTGTATTGCACC CCTGTATGGACC CCTGTATGCACC CCTGTATGGACC CCTGTATGGACC CCTGTATGGACC CCTGTATGGACC CCTGTATGGACC CCTGTATGCACC CCTCACC	session #: 2  11    KLQNQLEKLG LQEHQAPESH  145 DNA secid Accession sence: 74  11    GTCCTCACGC GCCATGGGCC GCCATGGATGG CTGGATGGTAGTGA CGGCAGACAG GTGCCCGATG AAGGACATGT TATGCCCACC GGCAAGTGCT TACCACAACG TGGAAAGGAA AAGGACCAGG GTGCAGGC GGGACCAGCG TGGAAAGGAA AAGGACCAGG TGGAAAGGAA ATCCTGCACC GCGGTTGTTCT GCTGCAGG GGTGCCAGC GGTGCCATCT CTCTTCATG AACCAGGATG TACACAGGGT CTGGAAGGAAG CTGCGGGCCCT CAGCAGCCTG AACCAGGGT CCTGGACCTG CTGCACGGGCCTG AACCAGGGT CCTGGACCTG CTGCACGGGCCTG AACCAGGGT CCTGGACCTG CACCAGGGTTG CACGGCCTTC AACCTCCGTG CACCAGGGTTCT AACCTCCGTG CACCAGGGTTCT CACCAGGGTTCT CACCAGGGTTCT CACCAGGGTTCT CACCAGGGTTCT CACCAGGGTTCT CACCACGGCTTCT AACCTCCGTG CACCACGCTTCT CACCACGCTTCT CACCACGCTTCT CACCACCTGG CCCCTGCACCTGG CCCCCTGCACCTGGCCTC CACCACCTCTCTCTCCTGGCCCTC CACCACCTCTCTCTCCTGGTCCTCTCTCTCCTGGTCCTCCTCCTC	CP_050184.1 21 21 FSPGPILPST MGLSPKRETT GUENCE 1 #: NM_002: 3229 221   CCAGCTCCGC CCGGCCCAG TGGCGGCCCAG AGCAGGCCGA AGCAGGCCGA ACTACACCAA GTCAGCGAA GCTACACCAA GTGAGCGAG ACAGCTACAC ACGTCGCAG CCAAAAACAT TGCTGAGCCA TGGCGCCTA ACCTCCTGT TGCTGAGCCA ACCTCCTGT ACCTCCTGT ACCTCCTGT ACCTCCTGT CCAAAACAT CGCCAGTGG ACTTCCAC ACCCCGGCAGTCA CCACTGCCG ACCTCCTGGT ACTTCCTGT CCCTGGT ACTTCTCCC GCCCAGTGG ACTTCTCCC GCCCAGTCG ACCCCGGCC ACCCCGGCC ACCCCGGCC ACCCCGGCC ACCCCGGCC ACCCCCGCC ACCCCCGCC ACCCCCGCC ACCCCCGCC ACACCCCCCC ACCCCCGCC ACCCCCCCC	RKLYEKKLVQ ARKTRLSRAG  204.1  31    CCCCTCACGC CCGCGCCCC GGCTGCGCC GGCTGCGGC GGCTACCTG GAACACTGG CCGGACTGGT TAGGACACA GATTCAGAC GATTCAGGC GAACCATGTG GGAGCACGC TTTTGGCAGC GGACCCCC GAACCACTTCT GAACACAC CTCTGCCTTT TATTGCTGG TAAGGACAC CAGACACT CACATTGTG GGCCCCC CAACCAGGCG CTCTGCCTT TATTGCTGTG CACTACAGG CCCCCCC CGACCACC CGCCCCC CGCCCCC CGCCCCC CGACTCATC	LLVSPPCAPP EKKVSQWA  41    GCTCTCGCCG GCGCCCCAC GTCTCCGCCT AGCCTCTTCG GCTGTGTACC GTGAAAAATG AGCCTGGACT AAGCATGACTG GACTACTGG AAGGAGTCGA ATTGGTACT GGAAACTGC GGAACCTGC GGAACCTGC GGAACCTCC GGTTATCTG GGAACCTCC TTAACTACT GGAACCTCC TTAGCAAG TTGGCAAGC TTGGCAAGC TCTGCAAGACCT CCCACAAGACCT CGCTTTGCCAG CGAAACATCA CGCTTTGCCAG CGAAACATCA CGCTTTGCCAG ATCTCCATGA	S1  GGACCCGCT GCCTGATGCT TCAACCTGGA GCTACTCGGT ACCCTGGCCA ACGCCAC ACGCACCAC TCCACCAC TCCACCAC TCCACCAC TCCACCAC TCCACCAC TCCACCAC TCCACCAC TCCACCAC TCCACCCAC	60 120 180 240 360 420 480 540 660 720 960 1020 1080 1140 1260 1320 1380 1440 1500 1560 1620 1680

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                                                                                   2160
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        GCTCATCGCC TTTGAGGTCA TCGGGGTGAC CCTGCACACA AGGGACCTTC AGGTGCAGCT
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                                                                                   2400
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                                                                                   3000
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                                                                                   3120
        CGGCTTCTTC AAGCGAGCCC GCACTCGCGC CCTGTATGAA GCTAAGAGGC AGAAGGCGGA
                                                                                   3180
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                                                                                   3240
        CCCGCCCCCG GCCCACCTGG TGTGACTTCT TTAAGCGGAC CCGCTATTAT CAGATCATGC
                                                                                   3300
25
        CCAAGTACCA CGCAGTGCGG ATCCGGGAGG AGGAGCGCTA CCCACCTCCA GGGAGCACCC
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        CTCCCTGATC CCACCCCCC CTCCCCCAGT GTCCCCTTTC TTCCTATTTA TCATAAGTTA
TGCCTCTGAC AGTCCACAGG GGCCACCACC TTTGGCTGGT AGCAGCAGGC TCAGGCACAT
                                                                                   3480
                                                                                   3540
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                                                                                   3840
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35
                                                                                   3960
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                                                                                   4080
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        CAGATGTIGG GAGGATACAG AGGAGATGCC ACTICTCACT CACCACTACC AGCCAGCCTC CAGAAGGCCC CAGAGAGACC CTGCAAGACC ACGGAGGGAG CCGACACTTG AATGTAGTAA
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                                                                                   4320
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        AACAGCTCCC AGTTTGT
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        DMWLGVTVAS OGPAGRVLVC AHRYTQVLWS GSEDQRRMVG KCYVRGNDLE LDSSDDWQTY
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                                                                                    360
                                                                                    420
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RTSERSGEDA HEALLTLVVP PALLLSSVRP PGACQANETI FCELGNPFKR NORMELLIAP
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                                                                                     720
65
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                                                                                    840
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        SIPTINMENK TTWFSVDIDS ELVEELPAEI ELWLVLVAVG AGLLLLGLII LLLWKCGPFK
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75
                    11
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        AGGTGAACAG GTCCTCACGC CCAGCTCCGC CCCCTCACGC GCTCTCGCCG GGACCCCGCT
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                                                                                     300
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        CACTGCCCAC AAGGATGACT GTGAGCGGAT GAACATCACA GTGAAAAATG ACCCTGGCCA
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         TCACATTATT GAGGACATGT GGCTTGGAGT GACTGTGGCC AGCCAGGGCC CTGCAGGCAG
                                                                                     480
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        AGTTCTGGTC TGTGCCCACC GCTACACCCA GGTGCTGTGG TCAGGGTCAG AAGACCAGCG
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	TGCCTACAAC	TOON A ACCOM	NCNCCTACAT.	CATTCACCCC	AACCACTCCC	VCALAL VALACE	780
_							
5	GTATAGTTAC	AAGGACCCAG	AGGACCAAGG	AAACCTCTAT	ATTGGGTACA	CGATGCAGGT	840
	AGGCAGCTTC	ATCCTCCACC	CCAAAAACAT	CACCATTGTG	ACAGGTGCCC	CACGGCACCG	900
							960
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	GGTGCTGGAG	GGCTCGCAGG	TGGGCGCCTA	TTTTGGCAGC	GCAATTGCCC	TGGCAGACCT	1020
	GAACAATGAT	**********	- acmacancan	000000000	ma crea creace	ACACCA AACA	1080
10							
10	GGAAGTAGGG	GGTGCCATCT	ATGTCTTCAT	GAACCAGGCG	GGAACCTCCT	TCCCTGCTCA	1140
	CCCCTCACTC	CHALCALLA MAG	COCCACTO	CALCACACACACACACACACACACACACACACACACACA	CCTTTATCTC	TCCCCCACCAT	1200
	TGGTGACATC	AACCAGGATG	GATTTCAGGA	TATTGCTGTG	GGAGCTCCGT	TTGAAGGCTT	1260
	GGGCAAAGTG	<b>ምልሮ</b> ልሞርሞልሞር	ACACTACCTC	TARGEGETT	CTTAGACAGC	CCCAGCAGGT	1320
1.5	AATCCATGGA	GAGAAGCTGG	GACIGCCIGG	GTTGGCCACC	TTCGGCTATT	CCCTCAGTGG	1380
15	GCAGATGGAT	GTGGATGAGA	ACTTCTACCC	AGACCTTCTA	GTGGGAAGCC	TGTCAGACCA	1440
	00101110011	ana accordance	GGCCAGTCAT	CA A CA TO COMO	CACAACACC	WOOMOOOD A	1500
	GCCAGCTGTG	CTGGACCCTG	CACTTTGCAC	GGCCACCTCT	TGTGTGCAAG	TGGAGCTGTG	1560
			CCGGGAACCC				1620
	CITICCITAC	MACCAGAG 1G	CCGGGMACCC	CARCIACAGG	COMMONICA	cccrooccin	
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20			TCTCCATGCC				1740
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ريد	GCAGAAGCTG						2040
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			TGCTGCTGTC				2160
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			TCGGGGTGAC				2280
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	CCACTATACA	CTCCAGACCT	CGCTTAGCAT	CCTAAATCAC	CCCCTACAAA	CCTTTTTTCC	2400
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2.5			AAGTCAGCAA				2580
35	CACCCTCCAT	CCCAATCCCT	CCTGGCCCTG	CCGACCACCT	GGAGACCTTA	TCAACCCTCT	2640
-	CACCOTCOTT	0000110001		00011001001	001.01.00001	00000000000	
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<b>45</b> <b>50</b>	TGACTTCTTT CCGGGAGGAG GACCAGCTGG CCCCCAGTGT CCACCACCTT ATGCTGTCTG CGAGTGCACT	AAGCGGACCC GAGCGCTACC CAGACTCGGG CCCCTTTCTT TGGCTGGTAG GCCCTGGGGA GCATTCCTGT	GCTATTATCA CACCTCCAGG ACCAATACTA CCTATTTATC CAGCAGGCTC TCTTCCCACA GCCCTAGATG	GATCATGCCC GAGCACCCTG CTGACGTCCT ATAAGTTATG AGGCACATAC GGAGGGCCAG CACGTGGGGC	AAGTACCACG CCCACCAAGA CCCTGATCCC CCTCTGACAG ACCTCGTCAA CGCTGTGGAC CCACTGCTCG	CAGTGCGGAT AGCACTGGGT ACCCCCTCCT TCCACAGGGG GAGCATGCAC CTTACAACGC TGGACTGTGC	3180 3240 3300 3360 3420
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	TGACTTCTTT CCGGGAGGAG GACCAGCTGG CCCCCAGTGT CCACCACCTT ATGCTGTCTG CGAGTGCACT TGGTGCATCA AAAACAAGCC	AAGCGGACCC GAGCTTACC CAGACTCGGG CCCCTTTCTT TGGCTGGTAG GCCCTGGGGA GCCATTCCTGT CGGATGGTGC AAAGAGCCTC	GCTATTATCA CACCTCCAGG ACCAATACTA CCTATTTATC CAGCAGGCTC TCTTCCCACA GCCCTAGATG ATGGGCTCGC CCACCAGAGC	GATCATGCCC GAGCACCCTG CTGACGTCCT ATAAGTTATG AGGCACATAC GCAGGGCCAG CACGTGGGGC CGTGTCTCAG CGGGAGGAAA	AAGTACCACG CCCACCAAGA CCCTGATCCC CCTCTGACAG ACCTCGTCAA CCCTCTGGCAC CCCACTGGCCAG CCTCTGCCAG AGGCCCCTGC	CAGTGCGGAT AGCACTGGGT ACCCCCTCCT TCCACAGGG GAGCATGCAC CTTACAACGC TTGGACTGTGC CGCCAGCGCC AATGTGGTGA	3180 3240 3300 3360 3420 3480 3540 3600 3660
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	TGACTTCTTT CCGGGAGGAG GACCAGCTGG CCCCCAGTGT CCACCACCTT ATGCTGTTCTG CGAGTGCACT TGGTGCATCA AAACAAGCC CACCTCCCCT GTCAAAACTA CCCATGCCAG	AAGCGGACCC GAGCGCTACC CAGACTCGGG CCCCTTTCTT TGGCTGGTAG GCCCTCGGGA GCATTCCTGT CGGATGGTGC AAAGAGCCTC TTCACACCTG TTGACACGGA AGAGGTGGGGA AGAGGTGGGG	GCTATTATCA CACCTCCAGG ACCAATACTA CCTATTTATC CAGCAGGCTC TCTTCCCACA ACCCTAGATG ATGGGCTCGC CCACCAGAGC GATCCATCTT GCAGCCCCG ATCCTGCCTA	GATCATGCCC GAGCACCTCG CTGACGTCCT ATAAGTTATG AGGCACATAC GCAGGGCCAG CACGTGGGC CGTGTCTCAG GAGAGCACA GAGAGCCACA GAGAGCCACA AGGCTGGC AGGTTGTCTA	AAGTACCACG CCCACCAAGA CCCTGATCAC CCTCTGACAG ACCTCGTCAA CCCTGTGCAA CCCTCTGCCAG AGGCCCCTGC GTCACTGGAT TGGTGGGCCC CGGGGGCACT	CAGTGCGGAT AGCACTGGGT ACCACCTCT TCCACAGGGG GAGCATGCAC CTTACAACGC TGGACTGTGC CGCCAGCGCC AATGTGGTGA TGACTTTGCT TCCAATTGACAC TGGAGGACCT	3180 3240 3300 3360 3420 3480 3540 3600 3660 3720 3780 3840
50	TGACTTCTTT CCGGGAGGAG GACCAGCTGG CCCCCAGTGT CCACCACCTT ATGCTGTCTG CGAGTGCACT AAAACAAGCC CACCTCCCCT GTCAAAACTA GGCGTGCACA GGCGTGCTCA	ANGCGGACCC GAGGCTACC CAGACTCGGG CCCCTTTCTT TGGCTGGTAG GCCCTGGGGA GCATTCCTGT CGGATGGTGC ANAGAGCCTC TTCACACCTG CTGACAGGGA GAGGGTGGGG GACCCAACAG	GCTATTATCA CACCTCCAGG ACCAATACTA CCTATTTATC CAGCAGGCTC TCTTCCCACA GCCCTAGATG ATGGGCTCGC CCACCAGAGC GATCCATCTT GCAGCCCCCG ATCCTGCCTA CCAAAGGAACT CAAAGGAACT	GATCATGCCC GAGCACCTG CTGACGTCCT ATAAGTTATG AGGCACATAC GCAGGGCCAG CACGTCGGG CACGTCGGG CGGAGGAAA GAGAGCCACA GGCCCCTGG AGGTTGTCTA AGAAAGAAGA	AAGTACCACG CCCACCAAGA CCCTGATCAC CCTCTGACAG ACCTCGTCAA CCCTGTCGAC CCACTGCTCG CCTCTGCCAG AGGCCCCTGC GTCACTGGAT TGGTGGGCC CGGGGGCACT ACCCAGAAGG	CAGTGCGGAT AGCACTGGGT ACCCCTCCT TCCACAGGGG GAGCATGCAC CTTACAACGC TGGACTGTGC CGCCAGCGCC AATGTGGTGA TGACTTTGCT CCAATTGACA TGGAGGACCT CTTGCTTTCC	3180 3240 3300 3360 3420 3480 3540 3600 3660 3720 3780 3840 3900
50	TGACTTCTTT CCGGGAGGAG GACCAGCTGG CCCCCAGTGT CCACCACCTT ATGCTGTCTG CGAGTGCACT AAAACAAGCC CACCTCCCCT GTCAAAACTA GGCGTGCACA GGCGTGCTCA	ANGCGGACCC GAGGCTACC CAGACTCGGG CCCCTTTCTT TGGCTGGTAG GCCCTGGGGA GCATTCCTGT CGGATGGTGC ANAGAGCCTC TTCACACCTG CTGACAGGGA GAGGGTGGGG GACCCAACAG	GCTATTATCA CACCTCCAGG ACCAATACTA CCTATTTATC CAGCAGGCTC TCTTCCCACA GCCCTAGATG ATGGGCTCGC CCACCAGAGC GATCCATCTT GCAGCCCCCG ATCCTGCCTA CCAAAGGAACT CAAAGGAACT	GATCATGCCC GAGCACCTG CTGACGTCCT ATAAGTTATG AGGCACATAC GCAGGGCCAG CACGTCGGG CACGTCGGG CGGAGGAAA GAGAGCCACA GGCCCCTGG AGGTTGTCTA AGAAAGAAGA	AAGTACCACG CCCACCAAGA CCCTGATCAC CCTCTGACAG ACCTCGTCAA CCCTGTCGAC CCACTGCTCG CCTCTGCCAG AGGCCCCTGC GTCACTGGAT TGGTGGGCC CGGGGGCACT ACCCAGAAGG	CAGTGCGGAT AGCACTGGGT ACCCCTCCT TCCACAGGGG GAGCATGCAC CTTACAACGC TGGACTGTGC CGCCAGCGCC AATGTGGTGA TGACTTTGCT CCAATTGACA TGGAGGACCT CTTGCTTTCC	3180 3240 3300 3360 3420 3480 3540 3600 3660 3720 3780 3840 3900
50	TGACTTCTTT CCGGGAGGAG GACCAGCTGT CCACCACCTT ATGCTGTCTG CGAGTGCACT TGGTGCACA AAAACAAGCC CACCTCCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA TGCATCCTCT TGCATCTCTCT TGCATCTCTCT	ARGCGGACCC GAGCGCTACC CAGACTCGGG CCCTTTCTT TGGCTGGTAG GCCTTGGGGA GCATTCCTGT CGGATGGTGC AAAGAGCCTC CTGACACGGA AGAGTGGGG AGAGTGGGGA AGAGTGGGG GACCCAACAG TGAAGCCTC	GCTATTATCA CACCTCCAGG ACCAATACTA CCTATTTATC CAGCAGGCTC TCTTCCCACA GCCCTAGATG ATGGGCTCGC CACCAGAGC GATCCATCATT GCAGCCCCG ATCCTGCCTA CAAAGGAACT CTCCTTGGCC	GATCATGCCC GAGCACCCTG CTGACGTCCT ATAAGTTATG AGGCACATAC GCAGGGCCAG CACGTGGGGC CGTGTCTCAG AGGAGGACACA AGGAGGACACA AGCAGTGCTCCACA ACAAAGAAGA ACAAAGAAGA	AAGTACCACE CCCACCAAGA CCCTGATCCC CCTCTGACAG ACCTCGTCAA CCCTCGTCAC CCACTGCTCG CCACTGCTCG CTCTGCCAG ACGCCCTGC GTCACTGGT TGGTGGGCC CGGGGGCACT ACCCAGAAGG CTCGCAGGAGG CTCGCAGGAGG	CAGTGCGGAT AGCACTGGGT ACCCCTCCT TCCACAGGGG GAGCATCCAC CTTACAAAGC TGGACTGTGC GGCCAGCGCC AATGTGGTGA TGACTTTGCT CCAATTGACA TGGAGGACT CTTGCTTTCC GTGCAGCAGG	3180 3240 3300 3360 3420 3480 3540 3600 3720 3780 3840 3900 3960
50	TGACTTCTTT CCGGGAGGAG GACCAGCTGG CCCCCAGTGT CCACCACTT ATGCTGTCTC TGGTGCATCA AAAACAAGCC CACCTCCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA TGCATCTCTG AAGGAACAAA	ANGCGGACCC GAGCGCTACC CAGACTCGGG CCCCTTTCTT TGGCTGGTAG GCCTTGCGGA AAAGAGCTCT TTCACACCTG CTGACAGGA AGAGGTGGGG GACCCAACAG TGAAGCCTCT TGACAGGCAA	GCTATTATCA CACCTCCAGG ACCAATACTA CCTATTTATC CAGCAGGCTC TCTTCCCACC ATGGGCTGGC CACCAGAGC CATCCATCAT GCAGCCCCGG ATCCATCCTA CAAAGGAACT CTCTTGGCC CGGCAACGTA	GATCATGCCC GAGCACCCTG CTGACGTTCT ATAAGTTATG AGGCACATAC GCAGGGCCAG CACGTGGGGC CGTGTCTCAG CGGAGGAAA GAGACCCACA AGGTTGTCTA AGAAAGAAGA GCCTGGGC ACCTGGC ACAGACTGAA GCCTGGGCTGC	AAGTACCACG CCCACCAAGA CCCTCGACACG CCTCTGACAG ACCTCGTCAA CCCTGTCGAC CCCACTGCTCG CCTCTGCCAG AGGCCCTGC GTCACTGGAT TGGTGGGCC CGGGGGCACT ACCCAGAAGG ACTGCCAGGAA ACTGCCAGGAA	CAGTGCGGAT AGCACTGGGT ACCCCTCCT TCCACAGGG GAGCATGCAC CTTACAACGC TGGACTGTGC CGCCAGCGCC AATGTGGTGA TGACTTTGCT CCAATTGACA TGGAGGACCT CTTGCTTTCC GTGCAGCAGG GGCATGGCGG	3180 3240 3300 3420 3480 3540 3600 3720 3780 3840 3900 3960 4020
50 55	TGACTTCTTT CCGGGAGGAG GACCAGCTGG CCCCCAGTGT CCACCACCTT ATGCTGTTCTG CGAGTGCACT TGGTGCATCA AAACAAGCC CACCTCCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA TGCATCTCTCA AAGGAACAA GATCCTCCAC	ARGCGGACCC GAGGGCTACC GAGGCTACC CAGACTCCGG CCCCTTTCTT TGGCTGGTAG GCCTTGGGGA GCATTCCTGT CGGATGGTGC AAAGAGCCTC TTCACACCTG CTGACAGGA AGAGGTGGGG GACCCAACAG TGAAGGCTCT GACAGGCAA AGAGAGGCAGA AGAGAGGAGGAA	GCTATTATCA CACCTCCAGG ACCAATACTA CCTATTTATC CAGCAGGCTC TCTTCCCACA ATGGGCTCGC CCACCAGAGC GATCCATCTT GCAGCCCCG ATCCTGCCTA CAAAGGAACT CTCCTTGGCC CGGCAACGTA GGACCAATTC	GATCATGCCC GAGCACCTCG CTGACGTCCT ATAAGTTATG AGGCACATAC GCAGGGCCAG CACGTGGGCC CGTGTCTCAG GGGAGGAAA GAGAGCCACA AGGTTGTCTA AGAAAGAAGA ACAGACTGAG TGGACTGGCC TGGACTGGCCTCGGCCTCGGCCTCGAAGACTGAA	AAGTACCACG CCCACCAAGA CCCTGATCAC CCTCTGACAG ACCTCGTCAA CCCTGTGCAA CCCTGTGCAA CCCTCTGCCAG AGGCCCCTGC GTCACTGGAT CGGGGGCACT ACCCAGAAGG ACCTGCTGG GATGTTGCGGA ACTGCTGGGA ACTGCTGGGA ACTGCTGGGA ACTGCTGGGA ACTGCTGGGA ACTGTGCTGG	CAGTGCGGAT AGCACTGGGT ACCACCTCT TCCACAGGGG GAGCATGCAC CTTACAACGC CGCCAGCGCC AATGTGGTGA TGGACTTTGCT CCCAATTGACAC TGGAGCACCT CTTGCTTTCC GTGCAGCAGG GGCATGGGGG GGATACAGAG GGATACAGAG	3180 3240 3300 3460 3480 3540 3600 3720 3780 3840 3900 4020 4080
50 55	TGACTTCTTT CCGGGAGGAG GACCAGCTGG CCCCCAGTGT CCACCACCTT ATGCTGTTCTG CGAGTGCACT TGGTGCATCA AAACAAGCC CACCTCCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA TGCATCTCTCA AAGGAACAA GATCCTCCAC	ARGCGGACCC GAGGGCTACC GAGGCTACC CAGACTCCGG CCCCTTTCTT TGGCTGGTAG GCCTTGGGGA GCATTCCTGT CGGATGGTGC AAAGAGCCTC TTCACACCTG CTGACAGGA AGAGGTGGGG GACCCAACAG TGAAGGCTCT GACAGGCAA AGAGAGGCAGA AGAGAGGAGGAA	GCTATTATCA CACCTCCAGG ACCAATACTA CCTATTTATC CAGCAGGCTC TCTTCCCACA ATGGGCTCGC CCACCAGAGC GATCCATCTT GCAGCCCCG ATCCTGCCTA CAAAGGAACT CTCCTTGGCC CGGCAACGTA GGACCAATTC	GATCATGCCC GAGCACCTCG CTGACGTCCT ATAAGTTATG AGGCACATAC GCAGGGCCAG CACGTGGGCC CGTGTCTCAG GGGAGGAAA GAGAGCCACA AGGTTGTCTA AGAAAGAAGA ACAGACTGAG TGGACTGGCC TGGACTGGCCTCGGCCTCGGCCTCGAAGACTGAA	AAGTACCACG CCCACCAAGA CCCTGATCAC CCTCTGACAG ACCTCGTCAA CCCTGTGCAA CCCTGTGCAA CCCTCTGCCAG AGGCCCCTGC GTCACTGGAT CGGGGGCACT ACCCAGAAGG ACCTGCTGG GATGTTGCGGA ACTGCTGGGA ACTGCTGGGA ACTGCTGGGA ACTGCTGGGA ACTGCTGGGA ACTGTGCTGG	CAGTGCGGAT AGCACTGGGT ACCACCTCT TCCACAGGGG GAGCATGCAC CTTACAACGC CGCCAGCGCC AATGTGGTGA TGGACTTTGCT CCCAATTGACAC TGGAGCACCT CTTGCTTTCC GTGCAGCAGG GGCATGGGGG GGATACAGAG GGATACAGAG	3180 3240 3300 3420 3480 3540 3600 3720 3780 3840 3900 3960 4020
50	TGACTTCTTT CCGGGAGGAG GACCAGCTGT CCACCACTTT ATGCTGTCTG CGAGTGCACT TGGTGCACA AAAACAAGCC CACCTCCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA TGCATCCTCT AGGAACAAA GATCCTCCAC GAGATCCCAC	ARGCGGACCC GAGCGCTACC CAGACTCGGG CCCTTTCTT TGGCTGGTAG GCCTTGGGG GCCTGGGGA GCATTCCTGT CGGATGGTGC AAAGAGCCTC CTGACACGG AGAGGTGGGG GACCCAACAG TGAAGCCTC GACAGGCAAA AGAGGAGAGG	GCTATTATCA CACCTCCAGG ACCAATACTA CCTATTTATC CAGCAGGCTC TCTTCCCACA GCCCTAGATG ATGGGCTCGC CACCAGAGG GATCCATCTT GCAGCCCCG ATCCTGCCTA ACAAAGGAACT CTCCTTGGCC CGGCAACGTA CGGACCAATTC CCACTACCAG	GATCATGCCC GAGCACCTC GAGCACCTC ATAAGTTATG AGGCACATAC GCAGGGCCAG CACGTGGGGC CAGGTGCGGC CAGGTGCTCAG GAGAGCACAC AGCTTGCTCAG AGCACTTCCAC AGCACTTCCAC AGCACTTCCAC AGCACTGAC ACAGACTGAA GCCTGGGCTC TGGACAGACA CCAGCCTCCCA	AAGTACCACE CCCACCAAGA CCCTGATCCC CCTCTGACAG ACCTCGTCAA ACCTCGTCAC CCACTGCTCG CCTCTGCCAG ACGCCCTGC GTCACTGGAT TGGTGGGCC CGGGGGCACT ACCCCAGAAGG CTCGCAGGA ACTGTGTGGGA GATGTTTGGGA GAAGGCCCCA	CAGTGCGGAT AGCACTGGGT ACCCCTCCT TCCACAGGGG GAGCATGCAC CTTACAAAGC TGGACTGTGC GGCCAGCGCC AATGTGGTGA TGACTTTGCT CCAATTGACA TGGAGGACCT CTTGCTTTCC GTGCAGCAGG GGCATGCGGG GGCATGCGGG GGATACAGAG GAGAACCCT	3180 3240 3340 3360 3420 3480 3540 3600 3720 3780 3840 3900 4020 4080 4140
50 55	TGACTTCTTT CCGGGAGGAG GACCAGCTGG CCCCAGTGT CCACCACCTT ATGCTGTCTG CGAGTGCACCA TGGTGCATCA AAAACAAGCC CACCTCCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA TGGATCTCTG AAGGAACAAA GATCCTCCAC GAGATGCCAC	ANGCGGACCC GAGCGCTACC CAGACTGGGA CCCCTTTCTT TGGCTGGTAG GCCTGGGGA AGAGGCCTC TTCACACCTG TTCACACCTG TTCACACCTG GACAGCCACACAG GACAGCCCACACAG GACAGCCCTC GACAGGCAAA AGAGAGAGAG TGAAGCCTCT GACAGGAAA AGAGAGAGAG GACCTCT GACAGGAAA	GCTATTATCA CACCTCCAGE ACCAATACTA CCTATTTATC CAGCAGGCTC TCTTCCCACA GCCCTAGATG ATGGGCTCGC CAACAGAGC GATCCATCTT CCAGCACAGAGC CATCCTGCCTA ATACGAACT CTCCTTGGCC CGGCAACGTA GGACCATTC CCACTAGCAT CACATTC CCACTACCAG GACACTTGAA	GATCATGCCC GAGCACCCTC GAGCACCCTC ATAAGTTATG AGGCACATAC GCAGGGCCAG CACGTGGGGC CGTGTCTCAG GAGAGCACA GACGCCTGC AGATAGCCACA AGAAAGAAG GCCTGGCT TGAACAGACA CCCAGCCTCCA TGTACTCAA TGTAGTAATA	AAGTACCACE CCACCAAGA CCCTGATCCC CCTCTGACAG ACCTCGTCAA CGCTGTGGAC CCACTGCTCG CCTCTGCCAG AGGCCCTGC GTCACTGGAT TGGTGGGCC CGGGGGCACT ACCCAGAAGG CTCGCAGGAAGG ACTGTTGCGG AACTGTTGCGGA ACTGTTGCGGA ACTGTTGCGGA ACTGTTGCGGA ACTGTGCTGG GATGTTTGGGA GAAGGCCCCA GGCAGGGGG	CAGTGCGGAT AGCACTGGGT ACCCCTCCT TCCACAGGGG GAGCATGCAC CTTACAACGC TGGACTGTGC CGCCAGCGCC AATGTGGTGA TGACTTTGCT CCCATTGCTTCC CTTGCTTTCC CTGCACGGGG GGCATGCGG GGATACAGAG GAGAGACCCT CCTGCCACCC	3180 3240 3300 3360 3420 3480 3540 3600 3720 3720 3840 3900 3960 4020 4080 4140 4200
50 55	TGACTTCTTT CCGGGAGGAG GACCAGCTGG CCCCAGTGT CCACCACCTT ATGCTGTCTG CGAGTGCACCA TGGTGCATCA AAAACAAGCC CACCTCCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA TGGATCTCTG AAGGAACAAA GATCCTCCAC GAGATGCCAC	ANGCGGACCC GAGCGCTACC CAGACTGGGA CCCCTTTCTT TGGCTGGTAG GCCTGGGGA AGAGGCCTC TTCACACCTG TTCACACCTG TTCACACCTG GACAGCCACACAG GACAGCCCACACAG GACAGCCCTC GACAGGCAAA AGAGAGAGAG TGAAGCCTCT GACAGGAAA AGAGAGAGAG GACCTCT GACAGGAAA	GCTATTATCA CACCTCCAGE ACCAATACTA CCTATTTATC CAGCAGGCTC TCTTCCCACA GCCCTAGATG ATGGGCTCGC CAACAGAGC GATCCATCTT CCAGCACAGAGC CATCCTGCCTA ATACGAACT CTCCTTGGCC CGGCAACGTA GGACCATTC CCACTAGCAT CACATTC CCACTACCAG GACACTTGAA	GATCATGCCC GAGCACCCTC GAGCACCCTC ATAAGTTATG AGGCACATAC GCAGGGCCAG CACGTGGGGC CGTGTCTCAG GAGAGCACA GACGCCTGC AGATAGCCACA AGAAAGAAG GCCTGGCT TGAACAGACA CCCAGCCTCCA TGTACTCAA TGTAGTAATA	AAGTACCACE CCACCAAGA CCCTGATCCC CCTCTGACAG ACCTCGTCAA CGCTGTGGAC CCACTGCTCG CCTCTGCCAG AGGCCCTGC GTCACTGGAT TGGTGGGCC CGGGGGCACT ACCCAGAAGG CTCGCAGGAAGG ACTGTTGCGG AACTGTTGCGGA ACTGTTGCGGA ACTGTTGCGGA ACTGTTGCGGA ACTGTGCTGG GATGTTTGGGA GAAGGCCCCA GGCAGGGGG	CAGTGCGGAT AGCACTGGGT ACCCCTCCT TCCACAGGGG GAGCATGCAC CTTACAACGC TGGACTGTGC CGCCAGCGCC AATGTGGTGA TGACTTTGCT CCCATTGCTTCC CTTGCTTTCC CTGCACGGGG GGCATGCGG GGATACAGAG GAGAGACCCT CCTGCCACCC	3180 3240 3340 3360 3420 3480 3540 3600 3720 3780 3840 3900 4020 4080 4140
50 55	TGACTTCTTT CCGGGAGGAG GACCAGCTGG CCCCCAGTGT CCACCACTT ATGCTGTCTC TGGTGCATCA AAAACAAGCC CACCTCCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA TGCATCTCTG AAGGAACAAA GATCCTCCAC GAGATCCAC CAATCCACCAC CATCCCAC CCATCCCAC CACCCACC	ANGCGGACCC GAGCGCTACC GAGCGCTACC CAGACTCGGG CCCCTTTCTT TGGCTGGGA GCCTCGGGA AAGAGGCTCC TTCACACCTG CTGACAGGA AGAGGTGGG GACCCAACAG TGAAGCCTCT TGAAGCCTCT TGAAGCCTCT TGAAGCACTCT TGAAGCCTCT GACAGGCAA AGAGGGAGG TTCTCACTCA GGAGGGAGG GACCCAACCG GACCCACAGC GACCCACAGC GACCCACAGC GACCCACAGCT	GCTATTATCA CACCTCCAGG ACCAATACTA CCTATTTATC CAGCAGGCTC TCTTCCCACC ATGGGCTGGC CACCAGAGC CATCCATCTT GCAGCCCCG ATCCTGCCTA CAAAGGAACT CTCTTGGCC CGGCAACGTA GGACCAACTTC CCACTACCAG GAACCATCGA CAACTAGAA GAACCATGCG GACCACTGGAA GAACCATGCG	GATCATGCCC GAGCACCTCG CTGACGTCT ATAAGTTATG AGGCACATAC GCAGGGCCAG CACTGGGGC CGTGTCTCAG CGGAGGAAA GAGACCCACA AGGATGTCTCA AGAAAGAAGA ACCAGACTCAA GCCTGGCTC TGGACAGACA TGTAGTAATA TCAGGGGCCT TCAGGGCCCT	AAGTACCACG CCCACCAAGA CCCTCGACACG CCTCTGACAG ACCTCGTCAA CCCTGTCGACA CCCTGTCGCAG AGGCCCTGC GTCACTGGAT TGGTGGAC TGGTGGAC TGGTGGAC TGGTGGAC CCCAGAAGG CTCGCAGGA ACTGTGCTGG GATGTTGGGA GAAGGCCCCA GAAGGCCCAG AGAGGGGGAAGGAGGAAGG	CAGTGCGGAT AGCACTGGGT ACCCCTCCT TCCACAGGG GAGCATGCAC CTTACAACGC TGGACTGTGC CGCCAGCGCC AATGTGGTGA TGGACTTTGCT CCAATTGACA TGGAGGACCT CTTGCTTTCC GTGCAGCAGG GGCATGGCGG GGATACAGAG GAGAGACCCT CCTGCCACCCC TTCTTAGCTA	3180 3240 3300 3420 3480 3540 3660 3720 3780 3840 3960 4020 4080 4140 4200 4260
50 55	TGACTTCTTT CCGGGAGGAG GACCAGCTGT CCACCACCTT ATGCTGTCTG CGAGTGCACT TGGTGCATCA AAACAAGCC CACCTCCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA TGCATCTCTG AGGGACAAA GATCCTCCAC GGAAGACAC CCATCCACC CCATGCCAC CGAAGACCAC CCATCCACC CATCCACC CATCC	ANGCGGACCC GAGCGCTACC GAGCGCTACC CAGACTCGGG CCCTTTCTT TGGCTGGTAG GCCCTGGGGA GCATTCCTGT CGGATGGTGC AAAGAGCCTC CTGACAGGGA AGAGGTGGGG GACCCAACAG TGAAGCCTC GACAGGCAAA AGAGGGAAA AGAGGGGAAG TTCTCACTCA GGAGGGAGCC GGACCCAGCT TCTCTCTCCCAC	GCTATTATCA CACCTCCAGG ACCAATACTA CCTATTTATC CAGCAGGCTC CTCTCCCACA GCCCTAGATG ATGGGCTCGC CACCAGAGC GATCCATCTT GCAGCCCCG ATCCTGCCTA ATCCTGCCTA ATCCTGCCTA CCAACGAACGTA CCACTAGCACGC CGGCAACGTA CCACTACCAG GACCATTGAA GAACCATTGCC CCTGGCTCTG	GATCATGCCC GAGCACCTG CTGACGTCT ATAAGTTATG AGGCACATAC CACGTGGGG CACGTGGGG CACGTGGGG CAGGTGCACA GAGAGCACA GAGAGCACA AGATTGTCTAG GCCTGGGCT TGGACAGACA CCAGCCTCCA TGTAGTATATA TCAGGGGCCT CCCCCCCCCC	AAGTACCACE CCACCAAGA CCCTGATCCC CCTCTGACAG ACCTCGTCAA ACCTCGTCAC CCACTGCTCG CCACTGCTCG CTCACCAG AGGCCCCTGC GTCACTGGAT TGGTGGGCC CGGGGGCACT ACCCAGAAGG CTCGCAGGAA ACTGTGCTGG GATGTTGGGA GAAGGCCCCA GGCAGGGGGCAC AGAGGTGGAC ATGGGGAC ATGGGGAC ATGGGGAC ATGGGGAC AGAGGTGGAC ATGGGAC ATGGGAC ATGGGAC ATGGGCTGTG	CAGTGCGGAT AGCACTGGGT ACCCCTCCT TCCACAGGGG GAGCATGCAC CGCACAGGC TGGACTGTGC CGCCAGCGCC AATGTGGTGA TGACTTTGCT CCAATTGACA TGGAGACCT CTTGCTTTCC GTGCAGCAGG GGATACAGGG GGATACAGGG GAGAGACCT CCTGCCTACCT TTCTTGCCTACCT TTCTTACCTA TCCTAAGGCC TTCTTAGCTA TCCTTAAGGCC	3180 3240 3360 3420 3540 3540 3540 3780 3780 3780 3980 4020 4080 4140 4200 4260 4320
50 55 60	TGACTTCTTT CCGGGAGGAG GACCAGCTGT CCACCACCTT ATGCTGTCTG CGAGTGCACT TGGTGCATCA AAACAAGCC CACCTCCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA TGCATCTCTG AGGGACAAA GATCCTCCAC GGAAGACAC CCATCCACC CCATGCCAC CGAAGACCAC CCATCCACC CATCCACC CATCC	ANGCGGACCC GAGCGCTACC GAGCGCTACC CAGACTCGGG CCCTTTCTT TGGCTGGTAG GCCCTGGGGA GCATTCCTGT CGGATGGTGC AAAGAGCCTC CTGACAGGGA AGAGGTGGGG GACCCAACAG TGAAGCCTC GACAGGCAAA AGAGGGAAA AGAGGGGAAG TTCTCACTCA GGAGGGAGCC GGACCCAGCT TCTCTCTCCCAC	GCTATTATCA CACCTCCAGG ACCAATACTA CCTATTTATC CAGCAGGCTC CTCTCCCACA GCCCTAGATG ATGGGCTCGC CACCAGAGC GATCCATCTT GCAGCCCCG ATCCTGCCTA ATCCTGCCTA ATCCTGCCTA CCAACGAACGTA CCACTAGCACGC CGGCAACGTA CCACTACCAG GACCATTGAA GAACCATTGCC CCTGGCTCTG	GATCATGCCC GAGCACCTG CTGACGTCT ATAAGTTATG AGGCACATAC CACGTGGGG CACGTGGGG CACGTGGGG CAGGTGCACA GAGAGCACA GAGAGCACA AGATTGTCTAG GCCTGGGCT TGGACAGACA CCAGCCTCCA TGTAGTATATA TCAGGGGCCT CCCCCCCCCC	AAGTACCACE CCACCAAGA CCCTGATCCC CCTCTGACAG ACCTCGTCAA ACCTCGTCAC CCACTGCTCG CCACTGCTCG CTCACCAG AGGCCCCTGC GTCACTGGAT TGGTGGGCC CGGGGGCACT ACCCAGAAGG CTCGCAGGAA ACTGTGCTGG GATGTTGGGA GAAGGCCCCA GGCAGGGGGCAC AGAGGTGGAC ATGGGGAC ATGGGGAC ATGGGGAC ATGGGGAC AGAGGTGGAC ATGGGAC ATGGGAC ATGGGAC ATGGGCTGTG	CAGTGCGGAT AGCACTGGGT ACCCCTCCT TCCACAGGGG GAGCATGCAC CGCACAGGC TGGACTGTGC CGCCAGCGCC AATGTGGTGA TGACTTTGCT CCAATTGACA TGGAGACCT CTTGCTTTCC GTGCAGCAGG GGATACAGGG GGATACAGGG GAGAGACCT CCTGCCTACCT TTCTTGCCTACCT TTCTTACCTA TCCTAAGGCC TTCTTAGCTA TCCTTAAGGCC	3180 3240 3300 3420 3480 3540 3660 3720 3780 3840 3960 4020 4080 4140 4200 4260
50 55 60	TGACTTCTTT CCGGGAGGAG GACCAGCTGT CCACCACCTT ATGCTGTCTG CGAGTGCACT TGGTGCATCA AAAACAAGC CACCTCCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA TGCATCCTG AAGGAACAAA GATCCTCCAC GAGATCCACC GCAAGACCAC CATCCAGCCA TCCTTGGCTT TCATTCAGGAA TCCTTGGCTT CATTTGAGAA	ANGCGGACCC GAGCGCTACC CAGACTGGGA CCCCTTTCTT TGGCTGGTAG GCCCTGGGGA GCATTCCTGT CGGATGGTGC AAAGAGCCTC CTGACACGGA AGAGGTGGGG GACCCAACAG TGAAGCCTC GACAGGAA AGAGGAGGAG TGTAGGCAACAG GGAGGAGGAGGAG GGACCCACAG TCTCTCACTCA CGAGGGAAC GGAGGGAGC GCCCAGCT TCTCTGCCAG GCTGAGGCTA	GCTATTATCA CACCTCCAGG ACCAATACTA CCTATTTATC CAGCAGGCTC TCTTCCCACA GCCCTAGATG ATGGGCTCGC GATCCACACT GCACCACAGGC ATCCTGCCTA ACAAGGAACT CTCCTTGGCC CGGCAACGTA GGACCAATTG GAACCAATTGA GAACCATTGA GAACCATTGA GAACCATTGA GAACCATGCG GACACTTGAA GAACCATGCG GCTTCCAAAAA	GATCATGCCC GAGCACCCTG CTGACGTCCT ATAAGTTATG AGGCACATAC GCAGGGCCAG CACGTGGGGC CGTGTCTCAG GGAGGACAA AGAAGAAGA GCCTGGGT AGAAGAAGA GCCTGGGCTC TGGACAGAAC TGAGCCTCCA TGTAGTAATA TCAGGGGCCT CCTCCCTGA	AAGTACCACE CCCACCAAGA CCCTGATCCC CCTCTGACAG ACCTCGTCAA CGCTGTGGAC CCACTGCTCG CTCTGCCAG AGGCCCCTGC GTCACTGGAT TGGTGGGCCC CGGGGGCACT TCCCAGAAGG CTCGCAGAAGG AACTGTTGGGA ACTGTTGGGA ACTGTTGGGA ACTGTTGGGA ACTGTTGGGA GAAGGCCCCA GAAGGTGGAG ATGGGGTGTGGCC CCCTGCCTGCCTGCCTGCCTGCCTGCC	CAGTGCGGAT AGCACTGGGT ACCCCTCCT TCCACAGGGG GAGCATCCAC CTTACAAAGC TTGGACTGTGC CGCCAGCGCC AATGTGGTGA TGACTTTGCT CCAATTGACA TGGAGGACCT CTTGCTTTCC GTGCAGCAGG GGATACAGAG GGATACAGAG GAGAGACCCT CCTGCCACCC TTCTTAGCTA TCCTTAAGGCC TTCGCCAGCCC TTGGCAGCCC TTGGCAGCCC TTGGCAGCCC TTGGCAGCCC TTGGCAGCCC TTGGCAGCCC	3180 3240 3300 3420 3480 3540 3540 3720 3780 3980 4020 4080 4140 4200 4260 4320 4380
50 55	TGACTTCTTT CCGGGAGGAG GACCACCTGG CCCCCAGTGT CCACCACTTT ATGCTGTCTG CGAGTGCACTCA AAAACAAGCC CACCTCCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA TGGATCCTCG GAGGACAAA GATCCTCGC GCAAGACCAC CATCCAGCCA TCCTTGGCTCA CGAAGACCAC CATCCAGCCA TCCTTTGGGTT CATTTGAGGA ACTCCCCAGC	ANGCGGACCC GAGCGCTACC CAGACTCGGG CCCCTTTCTT TGGCTGGTAG GCCTGGGGA GCATTCCTGT CGGATGGTGC AAAGAGCCTC TTCACACCTG CTGACAGGA AGAGGTGGGG GACCCAACAG TTCACACAGA AGAGAGGAGG TTCTCACTCA GGAGGGAGG GACCCAGCT TCTTGCCAG GACCCAGCT CCTGGCAG	GCTATTATCA CACCTCCAGG ACCAATACTA CCTATTTATC CAGCAGGCTC TCTTCCCACA GCCCTAGATG ATGGGCTCGC GATCCATCTT GCAGCCCCGG ATCCTGCCTA ATCCTGCCTA CAAAGGAACT CTCCTTGGCC CGGCAACGTA GGACCAATTC CCACTACCAG GACCATACCAG GACCATTGAA GAACCATGCA GACCATGCA GACCATGCA GACCATGCA CCTGGCTCTGAA TCCCATAGTAA TCCCATAGTAA	GATCATGCCC GAGCACCTC ATAAGTTATG AGGCACATAC GCAGGGCCAG CACGTGGGC CGTGTCTCAG CGGGAGGAAA GAGACCACA AGCACACACACACAC	AAGTACCACG CCCACCAAGA CCCTGATCAC CCTCTGACAG ACCTCGTCAA ACCTGGTCAA ACGCTGCTCG CCTCTGCCAG AGGCCCTGC GTCACTGGAC TGGTGGGCC CGGGGGCACT ACCCAGAAGG CTCGCAGAAGG ACTGTGCTGG AATTTTGGGA AGAGGCCCCA GGCAGGGGGA ACTGTGCTGG AATTTTGGA AGAGGCCCCA GGCAGGGGGA ACTGTGCTGG GAATTCCCTC GAATTCCCTC	CAGTGCGGAT AGCACTGGGT ACCCCTCTT TCCACAGGGG GAGCATGCAC CTTACAACGC TGGACTGTGC CGCCAGCGCC AATGTGGTGA TGGACTGCT CCTACTGCTTTCC CTGCTTTCC GTGCAGCGG GGATACAGAG GAGAGACCT CCTGCCACCC TTCTTAGCTA TCCTAGCCCC TTCTTAGCCCC CTGCCACCCC TTGCTAGGCCC CCCCCCTCTTG	3180 3240 3360 3420 3540 3540 3540 3780 3780 3780 3980 4020 4080 4140 4200 4260 4320
50 55 60	TGACTTCTTT CCGGGAGGAG GACCACCTGG CCCCCAGTGT CCACCACTTT ATGCTGTCTG CGAGTGCACTCA AAAACAAGCC CACCTCCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA TGGATCCTCG GAGGACAAA GATCCTCGC GCAAGACCAC CATCCAGCCA TCCTTGGCTCA CGAAGACCAC CATCCAGCCA TCCTTTGGGTT CATTTGAGGA ACTCCCCAGC	ANGCGGACCC GAGCGCTACC CAGACTCGGG CCCCTTTCTT TGGCTGGTAG GCCTGGGGA GCATTCCTGT CGGATGGTGC AAAGAGCCTC TTCACACCTG CTGACAGGA AGAGGTGGGG GACCCAACAG TTCACACAGA AGAGAGGAGG TTCTCACTCA GGAGGGAGG GACCCAGCT TCTTGCCAG GACCCAGCT CCTGGCAG	GCTATTATCA CACCTCCAGG ACCAATACTA CCTATTTATC CAGCAGGCTC TCTTCCCACA GCCCTAGATG ATGGGCTCGC GATCCACACT GCACCACAGGC ATCCTGCCTA ACAAGGAACT CTCCTTGGCC CGGCAACGTA GGACCAATTG GAACCAATTGA GAACCATTGA GAACCATTGA GAACCATTGA GAACCATGCG GACACTTGAA GAACCATGCG GCTTCCAAAAA	GATCATGCCC GAGCACCTC ATAAGTTATG AGGCACATAC GCAGGGCCAG CACGTGGGC CGTGTCTCAG CGGGAGGAAA GAGACCACA AGCACACACACACAC	AAGTACCACG CCCACCAAGA CCCTGATCAC CCTCTGACAG ACCTCGTCAA ACCTGGTCAA ACGCTGCTCG CCTCTGCCAG AGGCCCTGC GTCACTGGAC TGGTGGGCC CGGGGGCACT ACCCAGAAGG CTCGCAGAAGG ACTGTGCTGG AATTTTGGGA AGAGGCCCCA GGCAGGGGGA ACTGTGCTGG AATTTTGGA AGAGGCCCCA GGCAGGGGGA ACTGTGCTGG GAATTCCCTC GAATTCCCTC	CAGTGCGGAT AGCACTGGGT ACCCCTCTT TCCACAGGGG GAGCATGCAC CTTACAACGC TGGACTGTGC CGCCAGCGCC AATGTGGTGA TGGACTGCT CCTACTGCTTTCC CTGCTTTCC GTGCAGCGG GGATACAGAG GAGAGACCT CCTGCCACCC TTCTTAGCTA TCCTAGCCCC TTCTTAGCCCC CTGCCACCCC TTGCTAGGCCC CCCCCCTCTTG	3180 3240 3300 3420 3480 3540 3540 3720 3780 3980 4020 4080 4140 4200 4260 4320 4380
50 55 60	TGACTTCTTT CCGGGAGGAG GACCACCTGG CCCCCAGTGT CCACCACTTT ATGCTGTCTG CGAGTGCACTCA AAAACAAGCC CACCTCCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA TGGATCCTCG GAGGACAAA GATCCTCGC GCAAGACCAC CATCCAGCCA TCCTTGGCTCA CGAAGACCAC CATCCAGCCA TCCTTTGGGTT CATTTGAGGA ACTCCCCAGC	ANGCGGACCC GAGCGCTACC CAGACTCGGG CCCCTTTCTT TGGCTGGTAG GCCTGGGGA GCATTCCTGT CGGATGGTGC AAAGAGCCTC TTCACACCTG CTGACAGGA AGAGGTGGGG GACCCAACAG TTCACACAGA AGAGAGGAGG TTCTCACTCA GGAGGGAGG GACCCAGCT TCTTGCCAG GACCCAGCT CCTGGCAG	GCTATTATCA CACCTCCAGG ACCAATACTA CCTATTTATC CAGCAGGCTC TCTTCCCACA GCCCTAGATG ATGGGCTCGC GATCCATCTT GCAGCCCCGG ATCCTGCCTA ATCCTGCCTA CAAAGGAACT CTCCTTGGCC CGGCAACGTA GGACCAATTC CCACTACCAG GACCATACCAG GACCATTGAA GAACCATGCA GACCATGCA GACCATGCA GACCATGCA CCTGGCTCTGAA TCCCATAGTAA TCCCATAGTAA	GATCATGCCC GAGCACCTC ATAAGTTATG AGGCACATAC GCAGGGCCAG CACGTGGGC CGTGTCTCAG CGGGAGGAAA GAGACCACA AGCACACACACACAC	AAGTACCACG CCCACCAAGA CCCTGATCAC CCTCTGACAG ACCTCGTCAA ACCTGGTCAA ACGCTGCTCG CCTCTGCCAG AGGCCCTGC GTCACTGGAC TGGTGGGCC CGGGGGCACT ACCCAGAAGG CTCGCAGAAGG ACTGTGCTGG AATTTTGGGA AGAGGCCCCA GGCAGGGGGA ACTGTGCTGG AATTTTGGA AGAGGCCCCA GGCAGGGGGA ACTGTGCTGG GAATTCCCTC GAATTCCCTC	CAGTGCGGAT AGCACTGGGT ACCCCTCTT TCCACAGGGG GAGCATGCAC CTTACAACGC TGGACTGTGC CGCCAGCGCC AATGTGGTGA TGGACTGCT CCTACTGCTTTCC CTGCTTTCC GTGCAGCGG GGATACAGAG GAGAGACCT CCTGCCACCC TTCTTAGCTA TCCTAGCCCC TTCTTAGCCCC CTGCCACCCC TTGCTAGGCCC CCCCCCTCTTG	3180 3240 3300 3420 3480 3540 3540 3720 3780 3980 4020 4080 4140 4200 4260 4320 4380
50 55 60	TGACTTCTTT CCGGGAGGAG GACCAGCTGT CCACCACTT ATGCTGTCTG CGAGTGCACT TGGTGCATCA AAACAAGCC CACCTCCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA AGACCAC AGACCAC AGACCAC CACTCCCCC CGAGATCCCAC CGCAGCCAC CATCCACCAC CATCCACCAC CATCCACCAC CATCCACCAC CATCCACCAC CATCCACCAC CATCCACCAC CATCCACCAC TCCTTTGGCTT CATTTGAGAA ACTCCCCAGC TGCCTTCTTT	ARGCGGACCC GAGCGCTACC CAGACTGGGA CCCTTTCTT TGGCTGGTAG GCCCTGGGA GCATTCCTGT CGGATGGGA AAAGACCTTC CTGACACGGA AGAGGTGGGG GACCCAACAG TGAAGGCTCT GACAGGAAA AGAGGAGAGG	GCTATTATCA CACCTCCAGG ACCAATACTA CCTATTTATC CAGCAGGCTC CTCTCCCACA GCCCTAGATG ATGGGCTCGC CACCAGAGC GATCCATCTT GCAGCCCCG ATCCTGCCTA ACCAGGAACT CTCCTTGGCC CGGCAACGTA GAACCATTGCA GACCATTGAA GAACCATGCG GACCACTTGAC GACCATTGAC GACCATTGAC GACCATTGAC GACCATTGAC GACCATTGAC CCTGGCTCTG GTTCCAAAAA TCCATGGTAC TTCTCACCGC	GATCATGCCC GAGCACCTC ATAAGTTATG AGGCACATAC GCAGGGCCAG CACGTGGGC CGTGTCTCAG CGGGAGGAAA GAGACCACA AGCACACACACACAC	AAGTACCACG CCCACCAAGA CCCTGATCAC CCTCTGACAG ACCTCGTCAA ACCTGGTCAA ACGCTGCTCG CCTCTGCCAG AGGCCCTGC GTCACTGGAC TGGTGGGCC CGGGGGCACT ACCCAGAAGG CTCGCAGAAGG ACTGTGCTGG AATTTTGGGA AGAGGCCCCA GGCAGGGGGA ACTGTGCTGG AATTTTGGA AGAGGCCCCA GGCAGGGGGA ACTGTGCTGG GAATTCCCTC GAATTCCCTC	CAGTGCGGAT AGCACTGGGT ACCCCTCTT TCCACAGGGG GAGCATGCAC CTTACAACGC TGGACTGTGC CGCCAGCGCC AATGTGGTGA TGGACTGCT CCTACTGCTTTCC CTGCTTTCC GTGCAGCGG GGATACAGAG GAGAGACCT CCTGCCACCC TTCTTAGCTA TCCTAGCCCC TTCTTAGCCCC CTGCCACCCC TTGCTAGGCCC CCCCCCTCTTG	3180 3240 3300 3420 3480 3540 3540 3720 3780 3980 4020 4080 4140 4200 4260 4320 4380
50 55 60	TGACTTCTTT CCGGGAGGAG GACCAGCTGT CCACCACCTT ATGCTGTCTG CGAGTGCACCA TGGTGCATCA AAAACAAGCC CACCTCCCCC GTCAAAACTA CCCATGCCAG GGCGTGCTCA AGGAACAAA GATCCTCCAC GAGATGCACA CATCCAGCA TCCTTGGCAG TCCTTGGCAGCA TCCTTGGCAGCA ACTCCAGCCA TCCTTGGCAT CATTTGAGAA ACTCCCCAGC TGCCTTCTTT Seq ID NO:	ARGCGGACCC GAGCGCTACC CAGACTGGGA CCCCTTTCTT TGGCTGGTAG GCCTTGCTG GGATGCTGC AAAGAGCCTC CTGACAGGA AGAGGTGGG GACCCAACAG GACCAACAG GACAGCACC GACAGGAAA AGAGAGAG	GCTATTATCA CACCTCCAGA CACCTCCAGA CACTATTATC CAGCAGGCTC CACCAGAGGCTC CACCAGAGGC CACCAGAGGC CACCAGAGAGC CACCAGAGAC CTCTTGCCTA ATCTGCCTA ATCTGCCTA CAAAGGAACT CTCCTTGGCC CGGCAACGTA GAACCATTGA GAACCATTGA GAACCATGGG CCACTACCAG GACACTTGAA TCCATGGCTCG GTTCCAAAAA TCCATGGTAC TTCTCACCGC  T Sequence	GATCATGCCC GAGCACCTC ATAAGTTATG AGGCACATAC GCAGGGCCAG CACGTGGGC CGTGTCTCAG CGGGAGGAAA GAGACCACA AGCACACACACACAC	AAGTACCACG CCCACCAAGA CCCTGATCAC CCTCTGACAG ACCTCGTCAA ACCTGGTCAA ACGCTGCTCG CCTCTGCCAG AGGCCCTGC GTCACTGGAC TGGTGGGCC CGGGGGCACT ACCCAGAAGG CTCGCAGAAGG ACTGTGCTGG AATTTTGGGA AGAGGCCCCA GGCAGGGGGA ACTGTGCTGG AATTTTGGA AGAGGCCCCA GGCAGGGGGA ACTGTGCTGG GAATTCCCTC GAATTCCCTC	CAGTGCGGAT AGCACTGGGT ACCCCTCTT TCCACAGGGG GAGCATGCAC CTTACAACGC TGGACTGTGC CGCCAGCGCC AATGTGGTGA TGGACTGCT CCTACTGCTTTCC CTGCTTTCC GTGCAGCGG GGATACAGAG GAGAGACCT CCTGCCACCC TTCTTAGCTA TCCTAGCCCC TTCTTAGCCCC CTGCCACCCC TTGCTAGGCCC CCCCCCTCTTG	3180 3240 3300 3420 3480 3540 3540 3720 3780 3980 4020 4080 4140 4200 4260 4320 4380
50 55 60	TGACTTCTTT CCGGGAGGAG GACCAGCTGT CCACCACCTT ATGCTGTCTG CGAGTGCACCA TGGTGCATCA AAAACAAGCC CACCTCCCCC GTCAAAACTA CCCATGCCAG GGCGTGCTCA AGGAACAAA GATCCTCCAC GAGATGCACA CATCCAGCA TCCTTGGCAG TCCTTGGCAGCA TCCTTGGCAGCA ACTCCAGCCA TCCTTGGCAT CATTTGAGAA ACTCCCCAGC TGCCTTCTTT Seq ID NO:	ARGCGGACCC GAGCGCTACC CAGACTGGGA CCCCTTTCTT TGGCTGGTAG GCCTTGCTG GGATGCTGC AAAGAGCCTC CTGACAGGA AGAGGTGGG GACCCAACAG GACCAACAG GACAGCACC GACAGGAAA AGAGAGAG	GCTATTATCA CACCTCCAGA CACCTCCAGA CACTATTATC CAGCAGGCTC CACCAGAGGCTC CACCAGAGGC CACCAGAGGC CACCAGAGAGC CACCAGAGAC CTCTTGCCTA ATCTGCCTA ATCTGCCTA CAAAGGAACT CTCCTTGGCC CGGCAACGTA GAACCATTGA GAACCATTGA GAACCATGGG CCACTACCAG GACACTTGAA TCCATGGCTCG GTTCCAAAAA TCCATGGTAC TTCTCACCGC  T Sequence	GATCATGCCC GAGCACCTC ATAAGTTATG AGGCACATAC GCAGGGCCAG CACGTGGGC CGTGTCTCAG CGGGAGGAAA GAGACCACA AGCACACACACACAC	AAGTACCACG CCCACCAAGA CCCTGATCAC CCTCTGACAG ACCTCGTCAA ACCTGGTCAA ACGCTGCTCG CCTCTGCCAG AGGCCCTGC GTCACTGGAC TGGTGGGCC CGGGGGCACT ACCCAGAAGG CTCGCAGAAGG ACTGTGCTGG AATTTTGGGA AGAGGCCCCA GGCAGGGGGA ACTGTGCTGG AATTTTGGA AGAGGCCCCA GGCAGGGGGA ACTGTGCTGG GAATTCCCTC GAATTCCCTC	CAGTGCGGAT AGCACTGGGT ACCCCTCTT TCCACAGGGG GAGCATGCAC CTTACAACGC TGGACTGTGC CGCCAGCGCC AATGTGGTGA TGGACTGCT CCTACTGCTTTCC CTGCTTTCC GTGCAGCGG GGATACAGAG GAGAGACCT CCTGCCACCC TTCTTAGCTA TCCTAGCCCC TTCTTAGCCCC CTGCCACCCC TTGCTAGGCCC CCCCCCTCTTG	3180 3240 3300 3420 3480 3540 3540 3720 3780 3980 4020 4080 4140 4200 4260 4320 4380
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	TGACTTCTTT CCGGGAGGAG GACCAGCTGG CCCCAGTGT CCACCACCTT ATGCTGTCTG CGAGTGCACCA TGGTGCATCA AAAACAAGCC CACCTCCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA AAGGAACAAA GATCCTCGG GAAGACCAC GAAGACCAC CATCCAGCA TCCTTGGCTT CATTTGAGAA ACTCCCCAGC TGCCTTCTTT Seq ID NO: Protein Ac	ARGCGGACCC GAGCGCTACC CAGACTCGGG CCCCTTTCTT TGGCTGGTAG GCCTTGGGGA GCATTCCTGT CGGATGGTGC AAAGAGCCTC TTCACACCTG CTGACAGGA AGAGGTGGGG GACCCAACAG TGAAGCCTC TTCACTCAC GGAGGGAGG GACCCAGCT CTTGTGCAG GCTGAGGCA CCCAGCCT CTTTGCCAG CCTAGCCTG TCTTTGCCAG CCTAGCCCTG TCTTTGCCAG CCTAGCCCT CTTTTGCCAG CCTAGCCCT CTTTTGCCAG CCTAGCCCT CTATATAGGC  148 Proteicession #:	GCTATTATCA CACCTCCAGG ACCAATACTA CCTATTTATC CAGCAGGCTC TCTTCCCACA GCCCTAGATG ATGGGCTCGC GATCCATCAT CCACCAGAGC GATCCATCAT CTCTGCCTA ATCCTGCCTA CACAAGGAACT CTCCTTGGCC CGGCAACGTA GGACCAATTC CCACTACCAG GACCATTGAA GAACCATGCA GACCATGCA TCCTGGCTCTG TTCTCCAAAA TCCATGGTAC TTCTCACCGC  n sequence NP_005492.1	GATCATGCCC GAGCACCTCG GAGCACCTCG ATAAGTTATG AGGCACATAC GCAGGGCCAG CACGTGGGGC CGTGTCTCAG CGGGAGGAAA GAGACCACA AGCACCTCGC ACGCTCGC CGCCTCCA CCAGCCTCCA CCAGCCTCCA CCAGCCTCCA CCAGCCTCCA CCAGCCTCCA CCAGCCTCCA CCAGCGCCCCCCCCCC	AAGTACCACE CCACCAAGA CCCTGATCCC CCTCTGACAG ACCTCGTCAA ACCTCGTCAC CCACTGCTCG CCTCTGCCAG AGGCCCTGC GTCACTGGAT TGGTGGGCC CGGGGGCACT ACCCAGAAGG ACTGTGCTGG GATGTTGGGA ACTGTGCTGG GATGTTGGGA ACTGTGCTGG GATGTTGGGA ACTGTGCTGG GATGTTGGGA ACTGTGCTGG GATGTTGGGA ACGGGGGGGCCCA GGCAGGGGGGC AGAGGTGGAC ATGGGCTTGCTG GAATTCCCTC CAGCTCCCAG	CAGTGCGGAT AGCACTGGGT ACCCCTCCT TCCACAGGG GAGCATGCAC CTTACAACGC TGGACTGTGC CGCCAGCGCC AATGTGGTGA TGGACTTGCT CCAATTGACA TGGAGGACCT CTTGCTTTCC GTGCAGCCG GGATACAGAG GAGAGACCCT CCTGCCACCC TTCTTAGCTA TCCTAAGGCC TCCTAGCAGCCC TCCTAGCCCT TTGGCAGCCC TCCTAGCCCC TTGGCAGCCC TTGGCAGCCC TTGGCAGCCC	3180 3240 3300 3420 3480 3540 3540 3720 3780 3980 4020 4080 4140 4200 4260 4320 4380
50 55 60	TGACTTCTTT CCGGGAGGAG GACCAGCTGT CCACCACCTT ATGCTGTCTG CGAGTGCACCA TGGTGCATCA AAAACAAGCC CACCTCCCCC GTCAAAACTA CCCATGCCAG GGCGTGCTCA AGGAACAAA GATCCTCCAC GAGATGCACA CATCCAGCA TCCTTGGCAG TCCTTGGCAGCA TCCTTGGCAGCA ACTCCAGCCA TCCTTGGCAT CATTTGAGAA ACTCCCCAGC TGCCTTCTTT Seq ID NO:	ARGCGGACCC GAGCGCTACC CAGACTGGGA CCCCTTTCTT TGGCTGGTAG GCCTTGCTG GGATGCTGC AAAGAGCCTC CTGACAGGA AGAGGTGGG GACCCAACAG GACCAACAG GACAGCACC GACAGGAAA AGAGAGAG	GCTATTATCA CACCTCCAGA CACCTCCAGA CACTATTATC CAGCAGGCTC CACCAGAGGCTC CACCAGAGGC CACCAGAGGC CACCAGAGAGC CACCAGAGAC CTCTTGCCTA ATCTGCCTA ATCTGCCTA CAAAGGAACT CTCCTTGGCC CGGCAACGTA GAACCATTGA GAACCATTGA GAACCATGGG CCACTACCAG GACACTTGAA TCCATGGCTCG GTTCCAAAAA TCCATGGTAC TTCTCACCGC  T Sequence	GATCATGCCC GAGCACCTC ATAAGTTATG AGGCACATAC GCAGGGCCAG CACGTGGGC CGTGTCTCAG CGGGAGGAAA GAGACCACA AGCACACACACACAC	AAGTACCACG CCCACCAAGA CCCTGATCAC CCTCTGACAG ACCTCGTCAA ACCTGGTCAA ACGCTGCTCG CCTCTGCCAG AGGCCCTGC GTCACTGGAC TGGTGGGCC CGGGGGCACT ACCCAGAAGG CTCGCAGAAGG ACTGTGCTGG AATTTTGGGA AGAGGCCCCA GGCAGGGGGA ACTGTGCTGG AATTTTGGA AGAGGCCCCA GGCAGGGGGA ACTGTGCTGG GAATTCCCTC GAATTCCCTC	CAGTGCGGAT AGCACTGGGT ACCCCTCTT TCCACAGGGG GAGCATGCAC CTTACAACGC TGGACTGTGC CGCCAGCGCC AATGTGGTGA TGGACTGCT CCTACTGCTTTCC CTGCTTTCC GTGCAGCGG GGATACAGAG GAGAGACCT CCTGCCACCC TTCTTAGCTA TCCTAGCCCC TTCTTAGCCCC CTGCCACCCC TTGCTAGGCCC CCCCCCTCTTG	3180 3240 3300 3420 3480 3540 3540 3720 3780 3980 4020 4080 4140 4200 4260 4320 4380
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	TGACTTCTTT CCGGGAGGAG GACCAGCTGG CCCCAGTGT CCACCACCTT ATGCTGTCTG CGAGTGCACCA TGGTGCATCA AAAACAAGCC CACCTCCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA AAGGAACAAA GATCCTCGG GAAGACCAC GAAGACCAC CATCCAGCA TCCTTGGCTT CATTTGAGAA ACTCCCCAGC TGCCTTCTTT Seq ID NO: Protein Ac	ARGCGGACCC GAGCGCTACC CAGACTCGGG CCCCTTTCTT TGGCTGGTAG GCCTTGGGGA GCATTCCTGT CGGATGGTGC AAAGAGCCTC TTCACACCTG CTGACAGGA AGAGGTGGGG GACCCAACAG TGAAGCCTC TTCACTCAC GGAGGGAGG GACCCAGCT CTTGTGCAG GCTGAGGCA CCCAGCCT CTTTGCCAG CCTAGCCTG TCTTTGCCAG CCTAGCCCTG TCTTTGCCAG CCTAGCCCT CTTTTGCCAG CCTAGCCCT CTTTTGCCAG CCTAGCCCT CTATATAGGC  148 Proteicession #:	GCTATTATCA CACCTCCAGG ACCAATACTA CCTATTTATC CAGCAGGCTC TCTTCCCACA GCCCTAGATG ATGGGCTCGC GATCCATCAT CCACCAGAGC GATCCATCAT CTCTGCCTA ATCCTGCCTA CACAAGGAACT CTCCTTGGCC CGGCAACGTA GGACCAATTC CCACTACCAG GACCATTGAA GAACCATGCA GACCATGCA TCCTGGCTCTG TTCTCCAAAA TCCATGGTAC TTCTCACCGC  n sequence NP_005492.1	GATCATGCCC GAGCACCTCG GAGCACCTCG ATAAGTTATG AGGCACATAC GCAGGGCCAG CACGTGGGGC CGTGTCTCAG CGGGAGGAAA GAGACCACA AGCACCTCGC ACGCTCGC CGCCTCCA CCAGCCTCCA CCAGCCTCCA CCAGCCTCCA CCAGCCTCCA CCAGCCTCCA CCAGCCTCCA CCAGCGCCCCCCCCCC	AAGTACCACE CCACCAAGA CCCTGATCCC CCTCTGACAG ACCTCGTCAA ACCTCGTCAC CCACTGCTCG CCTCTGCCAG AGGCCCTGC GTCACTGGAT TGGTGGGCC CGGGGGCACT ACCCAGAAGG ACTGTGCTGG GATGTTGGGA ACTGTGCTGG GATGTTGGGA ACTGTGCTGG GATGTTGGGA ACTGTGCTGG GATGTTGGGA ACTGTGCTGG GATGTTGGGA ACGGGGGGGCCCA GGCAGGGGGGC AGAGGTGGAC AGAGGTGGAC ATGGGCTTCCTG GAATTCCCTC CAGCTCCCAG	CAGTGCGGAT AGCACTGGGT ACCCCTCCT TCCACAGGG GAGCATGCAC CTTACAACGC TGGACTGTGC CGCCAGCGCC AATGTGGTGA TGGACTTGCT CCAATTGACA TGGAGGACCT CTTGCTTTCC GTGCAGCCG GGATACAGAG GAGAGACCCT CCTGCCACCC TTCTTAGCTA TCCTAAGGCC TCCTAGCAGCCC TCCTAGCCCT TTGGCAGCCC TCCTAGCCCC TTGGCAGCCC TTGGCAGCCC TTGGCAGCCC	3180 3240 3300 3420 3480 3540 3540 3720 3780 3980 4020 4080 4140 4200 4260 4320 4380
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	TGACTTCTTT CCGGGAGGAG GACCAGCTGT CCACCACCTT ATGCTGTCTG CGAGTGCACT TGGTGCATCA AAAACAAGC CACCTCCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA TGCATCCTG AAGGAACAAA GATCCTCCAC GAAGACCAC CATCCAGCCA TCCTTGGCTT CATTTGAGAA ACTCCCAGC TCCTTTGGTT CATTTGAGAA ACTCCCCAGC TGCCTTCTTT Seq ID NO: Protein Act	ARGCGGACCC GAGCGCTACC CAGACTGGGA CCCCTTTCTT TGGCTGGTAG GCCCTGGGGA GCATTCCTGT CGGATGGTGC AAAGAGCCTC CTGACACGGA AGAGGTGGGG GACCCAACAG TGAAGCCTC GACAGGAAA AGAGAGAGGG TGTACACCG GCCCACGC TCTCTGCCAG GCTGAGGCAC CCAGCCCCT GTATATAGGC  148 Protei ccssion #: 11	GCTATTATCA CACCTCCAGG ACCAATACTA CCTATTTATC CAGCAGGCTC CTCTTCCCACA GCCCTAGATG ATGGGCTCGC GATCCACCT GCAGCCCCG ATCCTGCCTA CAAAGGAACT CTCCTTGGCC CGGCAACGTA GAACCATTGA GAACCATTGA GAACCATTGA GAACCATTGA GAACCATGCG GCTTCCAAAAA TCCATGGTCT GTTCCAACGC IN SEQUENCE NP_005492.1	GATCATGCCC GAGCACCCTC GAGCACCCTC ATAAGTTATG AGGCACATAC GCAGGGCCAG CACGTGGGGC CGTGTCTCAG GGCGGCTGC AGGAGGACAA AGAAAGAAGG ACAGACTGAA GCCTGGGCTC TGGACAGACA TGTAGTAATA TCAGGGGCCT CCCTCCTCCC CCTCCTCCTGA TGTAGCAGGGG GACCAATAAA	AAGTACCACE CCCACCAAGA CCCTGATCCC CCTCTGACAG ACCTCGTCAA CGCTGTGGAC CCACTGCTCG CCTCTGCCAG AGGCCCCTGC GTCACTGGAT TGGTGGGCCC CGGGGGCACT TCCCAGAAGG CTCGCAGAAGG CTCGCAGAAGG AACTGTGCTGG GAAGTTGGGC GGCAGGGGGC AGAGGTGGAG ACGGCTCCCAG ATTCCCTC CAGCTCCCAG 41	CAGTGCGGAT AGCACTGGGT AGCACTGGT TCCACAGGGG GAGCATCAC CTTACAAAGC TGGACTGTGC CGCCAGCGCC AATGTGGTGA TGACTTTGCT CCAATTGACA TGGAGGACT CTTGCTTTCC GTGCAGCAGG GGATACAGGG GGATACAGGG GGATACAGGG GGAGACCCT CCTGCCACCC TTCTTAGCTA TCCTAAGGCC TTCGCAGCCC CCCCCTCTTG TTTGT	3180 3240 3360 3420 3540 3540 3600 3720 3780 3840 3960 4020 4020 4140 4260 4380 4440
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	TGACTTCTTT CCGGGAGGAG GACCAGCTGG CCCCAGTGT CCACCACTT ATGCTGTCTG CGAGTGCACT TGGTGCATCA AAAACAAGCC CACCTCCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA AAGGAACAAA GATCCTCCAC GAAGACCAC GAAGACCAC CATCCAGCA TCCTTTGGCTT CATTTGAGAA ACTCCCCAGC TGCCTTCTTT Seq ID NO: Protein Act 1   MGPGPSRAPR	ARGCGGACCC GAGCGCTACC CAGACTCGGG CCCCTTTCTT TGGCTGGTAG GCCCTGGGGA AGAGGCTTC CTGACAGGGA AGAGGTGGGG GACCCAACAG GACAGCAACAG GACAGAGGAGG GACCCAACAG GACAGGGAAA AGAGAGGAGG GACCCAACAG GCAGGGCAACA GGAGGGAG	GCTATTATCA CACCTCCAGG ACCAATACTA CCTATTTATC CAGCAGGCTC TCTTCCCACA GCCCTAGATG ATGGGCTCGC GATCCATCTT CCACCAGAGC GATCCATCTT CCACCAGAGC ATCCTGCCTA ACAAGGAACT CTCCTTGGCC CCGCAAACGTA GCACCATGCA GACCATTCACAG GACCATTCCAACAG GACCATTCCAACAG TCCTAGCTCTG TTCTCCACCGC  n sequence NP_005492.1 21 LMVAAGGCVV	GATCATGCCC GAGCACCTCG GAGCACCTCG ATAAGTTATG AGGCACATAC GCAGGGCCAG CACGTGGGGC CGTGTCTCAG CGGAGGAAA GAGACCACA GCCTCGCC AGGTTGCTCA GCAGCTCCA CCAGCCTCCA CCAGCCTCCA CCAGCCTCCA CCAGCCTCCA CCAGCCTCCA CCAGCCTCCA TCAGCAGCA TCAGCACA TCAGCAGCA TCAGCAGCA TCAGCAGCA TCAGCAGCA TCAGCAGCA TCAGCAGCACA TCAGCAGCAC TCAGCAC TCAGCAGCAC TCAGCAGCAC TCAGCAGCAC TCAGCAGCAC TCAGCAGCAC TCAGCAC TCAGCAGCAC TCAGCAC TCAGCAGCAC TCAGCAC TCA	AAGTACCACE CCCACCAAGA CCCTGATCCC CCTCTGACAG ACCTCGTCAA CGCTGTGGAC CCACTGGTCAC CGCTGTGGAC CCTCTGCCAG AGGCCCTGC CGTCATGGAC TGGTGGGCC CGGGGGCACT ACCCAGAAGG CTCGCAGGAAGG ACTGTGCTGG AATGTTGGGA ACAGGGGAAGG CTCGCAGGAGG ACAGGGGGA ACAGGGGGA ACAGGGGGA ACAGGGGGAC AGAGGTGGAG ATGGCTCCCAG ATTCCCTC CAGCTCCCAG  41   VVKEAGNPGS	CAGTGCGGAT AGCACTGGGT AGCACTGGGT ACCCCTCTT TCCACAGGGG GAGCATGCAC CTTACAACGC TGGACTGTGC CGCCAGCGCC AATGTGGTGC CCAATTGACA TGGAGACCT CTTGCTTTGC TGTGCC GGCAGCGGG GGATACAGAG GAGAGACCCT CCTGCCACCC TTCTTAGCTA TCCTAAGGCC TTCTTAGCTA TCCTTAGGCTA TCCTTAGGCTA TCCTTAGGCTA TCCTTAGGCTC TTTGTTTTGT	3180 3240 3360 3420 3540 3540 3600 3720 3780 3840 3900 4020 4020 4020 4260 4320 4340 4440
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	TGACTTCTTT CCGGGAGGAG GACCAGCTGG CCCCAGTGT CCACCACTT ATGCTGTCTG CGAGTGCACT TGGTGCATCA AAAACAAGCC CACCTCCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA AAGGAACAAA GATCCTCCAC GAAGACCAC GAAGACCAC CATCCAGCA TCCTTTGGCTT CATTTGAGAA ACTCCCCAGC TGCCTTCTTT Seq ID NO: Protein Act 1   MGPGPSRAPR	ARGCGGACCC GAGCGCTACC CAGACTCGGG CCCCTTTCTT TGGCTGGTAG GCCCTGGGGA AGAGGCTTC CTGACAGGGA AGAGGTGGGG GACCCAACAG GACAGCAACAG GACAGAGGAGG GACCCAACAG GACAGGGAAA AGAGAGGAGG GACCCAACAG GCAGGGCAACA GGAGGGAG	GCTATTATCA CACCTCCAGG ACCAATACTA CCTATTTATC CAGCAGGCTC TCTTCCCACA GCCCTAGATG ATGGGCTCGC GATCCATCTT CCACCAGAGC GATCCATCTT CCACCAGAGC ATCCTGCCTA ACAAGGAACT CTCCTTGGCC CCGCAAACGTA GCACCATGCA GACCATTCACAG GACCATTCCAACAG GACCATTCCAACAG TCCTAGCTCTG TTCTCCACCGC  n sequence NP_005492.1 21 LMVAAGGCVV	GATCATGCCC GAGCACCTCG GAGCACCTCG ATAAGTTATG AGGCACATAC GCAGGGCCAG CACGTGGGGC CGTGTCTCAG CGGAGGAAA GAGACCACA GCCTCGCC AGGTTGCTCA GCAGCTCCA CCAGCCTCCA CCAGCCTCCA CCAGCCTCCA CCAGCCTCCA CCAGCCTCCA CCAGCCTCCA TCAGCAGCA TCAGCACA TCAGCAGCA TCAGCAGCA TCAGCAGCA TCAGCAGCA TCAGCAGCA TCAGCAGCACA TCAGCAGCAC TCAGCAC TCAGCAGCAC TCAGCAGCAC TCAGCAGCAC TCAGCAGCAC TCAGCAGCAC TCAGCAC TCAGCAGCAC TCAGCAC TCAGCAGCAC TCAGCAC TCA	AAGTACCACE CCCACCAAGA CCCTGATCCC CCTCTGACAG ACCTCGTCAA CGCTGTGGAC CCACTGGTCAC CGCTGTGGAC CCTCTGCCAG AGGCCCTGC CGTCATGGAC TGGTGGGCC CGGGGGCACT ACCCAGAAGG CTCGCAGGAAGG ACTGTGCTGG AATGTTGGGA ACAGGGGAAGG CTCGCAGGAGG ACAGGGGGA ACAGGGGGA ACAGGGGGA ACAGGGGGAC AGAGGTGGAG ATGGCTCCCAG ATTCCCTC CAGCTCCCAG  41   VVKEAGNPGS	CAGTGCGGAT AGCACTGGGT AGCACTGGT TCCACAGGGG GAGCATCAC CTTACAAAGC TGGACTGTGC CGCCAGCGCC AATGTGGTGA TGACTTTGCT CCAATTGACA TGGAGGACT CTTGCTTTCC GTGCAGCAGG GGATACAGGG GGATACAGGG GGATACAGGG GGAGACCCT CCTGCCACCC TTCTTAGCTA TCCTAAGGCC TTCGCAGCCC CCCCCTCTTG TTTGT	3180 3240 3360 3420 3540 3540 3600 3720 3780 3840 3960 4020 4020 4140 4260 4380 4440
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	TGACTTCTTT CCGGGAGGAG GACCAGCTGG CCCCAGTGT CCACCACTT ATGCTGTCTG CGAGTGCACT TGGTGCATCA AAAACAAGCC CACTCCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA AGACCAC ATGCATCTCTG AAGGAACAAA GATCCTCCAC GCAAGACCAC CATCCAGCT CCTTGGCTT CATTTGAGAA ACTCCCCAGC TGCCTTCTTT CATTTGAGAA ACTCCCCAGC TGCCTTCTTT Seq ID NO: Protein Act 1   MGPGPSRAPR QTERQQRYLL	ARGCGGACCC GAGCGTACC CAGACTGGGA CCCTTTCTT TGGCTGTAG GCCCTGGGA GCATTCCTGT CGGATGGTGC AAAGAGCCTC CTGACAGGGA AGAGGTGGGG GACCCAACAG TGAAGCCTC GACAGGGAAA AGAGGGAAG TTCTCACTCA GGAGGGAAG TTCTCACTCA GGAGGGAGGAG CCCAGCT TCTTGTGCAG GCTGAGGCTA CCCAGCCT TATATAGGC 148 Prote: cession #: 11   APRIMLCALA LAGAPRELAV	GCTATTATCA CACCTCCAGG ACCAATACTA CCTATTTATC CAGCAGGCTC CAGCAGGCTC GCCCTAGATG ATGGGCTCGC CACCAGAGGC CCACCAGAGC ATCCTGCCTA ACCATCTTGCCTA ACCATCAGACC CCACCAGAGACT CTCCTTCGCC CGGCAACGTA GGACCATTGA GGACCATTGAA GAACCATTGCA GACCATTGAC CCACTACCAG GCACCTTGACCAG TCCATGGTCTG GTTCCAAAAA TCCATGGTAC TTCTCACCGC  n Sequence n Sequence n Sequence p005492.1 21   LMVAAGGCVV PDGYTNRTGA	GATCATGCCC GAGCACCTG CTGACGTCT ATAAGTTATG AGGCACATAC GCAGGGCCAG CACGTGGGG CACGTGGGG CAGGTGCTCAG GCCGCTGGC AGGATGACAA AGAAAGAAGA GCCTGGGCTC CTGGACAGACA CCAGCCTCCA TGTAGTAATA TCAGGGGCTC CCCTCCCCC CCTCCCCCC CTCTCCTGA TGTAGCAGAA  31  SAFNLDTRFL VYLCPLTAHK	AAGTACCACE CCCACCAAGA CCCTGATCCC CCTCTGACAG ACCTCGTCAA ACCTCGTCAC CCTCTGCCAG ACGCCCTGCCAG ACGCCCTGCCAG ACGCCCTGCCAG ACGCCCTGCCAGAAGG CTCGCAGAAGG CTCGCAGAAGG CTCGCAGAAGG CAATGCCCA GAAGGCCCCA GGCAGGAGGA ACTGCTGG GAATTCCCCAG ACAGCTCCCAG ACAGCTCCCAG CCCTGCCTG CAGCTCCCAG  41    VVKEAGNPGS DDCERNNITV	CAGTGCGGAT AGCACTGGGT AGCACCTCCT TCCACAGGGG GAGCATGCAC CGCCAGCGCC TGGACTGTGC CGCCAGCGCC AATGTGGTGA TGACTTTGCT CCAATTGACA TGGAGACCT CTTGCTTTCC GTGCAGCAG GGATACAGGG GGATACAGGG GGATACAGGG GAATACAGG TCCTTAGCTA TCCTAAGGCC TTCTTAGCTA TCCTAAGGCC TTCTTAGCTA TTTTGT  51   LFGYSVALHR KNDPGHHITE	3180 3240 3360 3420 3480 3540 3540 3780 3780 39840 3990 4020 4080 4120 4260 4260 4320 4340 4440
50 55 60 65 70	TGACTTCTTT CCGGGAGGAG GACCAGCTGT CCACCACTTT ATGCTGTCTG CGAGTGCACT TGGTGCATCA AAAACAAGC CACCTCCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA TGCATCCTGG AAGGAACAAA GATCCTCCAG GAAGACCAC CATCCAGCCA TCCTTGGCTT CATTTGAGAA ACTCCCCAGC TGCTTCTTT Seq ID NO: Protein Act I MGPGPSRAPR QTERQORYLL DMMLGVTVAS	ARGCGGACCC GAGCGCTACC CAGACTGGGA CCCTTTCTT TGGCTGGTAG GCCTTGGGGA GCATTCCTGT CGGATGGTGC AAAGAGCCTC CTGACACGGA AGAGGTGGGG GCACTACACAG TGAAGCCTC GACAGCAACAG TGAAGCCTC GACAGCAACAG TCTCTCACTCA GGAGGGAGCC GACCCCACCT GACAGCCCT TCTTGTCCTCA CCAGCCCT TCTTGTGCGCT TCTTGTGCGCT TCTTGTGCGCT TCTTGTGCTC TCTTGTGCCT TCTTGTGCCT TCTTGTGCCT TCTTGTGCCT TCTTGTGCCT TCTTGTGCCT TATATAGGC  148 Protei 1 1 1 1 APRIMICALA APRIMICALA LAGAPRELAV QGPAGRVIVC	GCTATTATCA CACCTCCAGG ACCATACTA CAGCAGGCTC CAGCAGGCTC CCACCAGAGCTC GCACCACAGGC GATCCACCT GCACCACAGGC ATCCTGCCTA ACAAGGAACT CTCCTTGGCC CGGCAACGTA GAACCATGCA GACCATTGA GAACCATGCA GACCATGCA GACCATGCA GACCATGCA GACCATGCA CCACTACCAG GACCATTGA TCCATGGTC GTTCCAACAA TCCATGGTAC TTCTCACCGC  I Sequence NP_005492.1  LMWAAGGCVV PDGYTNRTGA ARRYTQVLWS	GATCATGCCC GAGCACCCTG CTGACGTCT ATAAGTTATG AGGCACATAC GCAGGGCCAG CACGTGGGGC CGTGTCTCAG GGAGGACACA GGCGCTGGC AGGTTGTCTA AGAAGAAGA GCCTGGCTC TGGACAGAC TGGACAGAC TGGACACAC TGTAGTAATA TCAGGGGCT TCCCCTCCCC	AAGTACCACE CCCACCAAGA CCCTGATCCC CCTCTGACAG ACCTCGTCACAG ACCTCGTCACAG ACGCTGCTCG CCTCTGCCAG AGGCCCCTGC GTCACTGGTT TGGTGGGCCC CGGGGGCACT TCGCAGGAACG CTCGCAGAAGG ACTGTGCTGG GATGTTTGGGA ACTGTGTGGA ACTGTGCTGG GAAGGTGGAG ACTGTCCCAG AGAGGTGGAC CCCTGCCTG CAGCTCCCAG  41    VVKEAGNPGS DDCERMITTV KCYVRCMDLE	CAGTGCGGAT AGCACTGGGT AGCACTGGT ACCCCTCTT TCCACAGGGG GAGCATCAC CTTACAAAGC TGGACTGTGC CGCCAGCGCC AATGTGGTGA TGACTTTGCT CCAATTGACA TGGAGGACT CTTGCTTTCC GTGCAGCAGG GGCATGCGGG GGATACAGAG GAGAGACCT TCCTAGCTACC TTCTTAGCTA TCCTAAGGCC TTCTTAGCTA TCCTAAGGCC TTCTTAGCTA TTTGT  51   LFGYSVALHR KNDPGHHIIE LDSSDDWGTY	3180 3240 3360 3420 3540 3600 3720 3780 3980 4020 4080 4140 4200 4240 4320 4380 4440
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	TGACTTCTTT CCGGGAGGAG GACCAGCTGT CCACCACTTT ATGCTGTCTG CGAGTGCACT TGGTGCATCA AAAACAAGC CACCTCCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA TGCATCCTGG AAGGAACAAA GATCCTCCAG GAAGACCAC CATCCAGCCA TCCTTGGCTT CATTTGAGAA ACTCCCCAGC TGCTTCTTT Seq ID NO: Protein Act I MGPGPSRAPR QTERQORYLL DMMLGVTVAS	ARGCGGACCC GAGCGCTACC CAGACTGGGA CCCTTTCTT TGGCTGGTAG GCCTTGGGGA GCATTCCTGT CGGATGGTGC AAAGAGCCTC CTGACACGGA AGAGGTGGGG GCACTACACAG TGAAGCCTC GACAGCAACAG TGAAGCCTC GACAGCAACAG TCTCTCACTCA GGAGGGAGCC GACCCCAGCT CCAGCCCT GTATATAGGC  148 Protei CCAGCCCT 11 APRIMICALA APRIMICALA LAGAPRELAV QGPAGRVIVC	GCTATTATCA CACCTCCAGG ACCATACTA CAGCAGGCTC CAGCAGGCTC CCACCAGAGCTC GCACCACAGGC GATCCACCT GCACCACAGGC ATCCTGCCTA ACAAGGAACT CTCCTTGGCC CGGCAACGTA GAACCATGCA GACCATTGA GAACCATGCA GACCATGCA GACCATGCA GACCATGCA GACCATGCA CCACTACCAG GACCATTGA TCCATGGTC GTTCCAACAA TCCATGGTAC TTCTCACCGC  I Sequence NP_005492.1  LMWAAGGCVV PDGYTNRTGA ARRYTQVLWS	GATCATGCCC GAGCACCCTG CTGACGTCT ATAAGTTATG AGGCACATAC GCAGGGCCAG CACGTGGGGC CGTGTCTCAG GGAGGACACA GGCGCTGGC AGGTTGTCTA AGAAGAAGA GCCTGGCTC TGGACAGAC TGGACAGAC TGGACACAC TGTAGTAATA TCAGGGGCT TCCCCTCCCC	AAGTACCACE CCCACCAAGA CCCTGATCCC CCTCTGACAG ACCTCGTCACAG ACCTCGTCACAG ACGCTGCTCG CCTCTGCCAG AGGCCCCTGC GTCACTGGTT TGGTGGGCCC CGGGGGCACT TCGCAGGAACG CTCGCAGAAGG ACTGTGCTGG GATGTTTGGGA ACTGTGTGGA ACTGTGCTGG GAAGGTGGAG ACTGTCCCAG AGAGGTGGAC CCCTGCCTG CAGCTCCCAG  41    VVKEAGNPGS DDCERMITTV KCYVRCMDLE	CAGTGCGGAT AGCACTGGGT AGCACTGGT ACCCCTCTT TCCACAGGGG GAGCATCAC CTTACAAAGC TGGACTGTGC CGCCAGCGCC AATGTGGTGA TGACTTTGCT CCAATTGACA TGGAGGACT CTTGCTTTCC GTGCAGCAGG GGCATGCGGG GGATACAGAG GAGAGACCT TCCTAGCTACC TTCTTAGCTA TCCTAAGGCC TTCTTAGCTA TCCTAAGGCC TTCTTAGCTA TTTGT  51   LFGYSVALHR KNDPGHHIIE LDSSDDWGTY	3180 3240 3360 3420 3480 3540 3540 3780 3780 39840 3990 4020 4080 4120 4260 4260 4320 4340 4440
50 55 60 65 70	TGACTTCTTT CCGGGAGGAG GACCAGCTGT CCACCACTTT ATGCTGTCTG CGAGTGCACCA TGGTGCATCA AAAACAAGCC CACCTCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA AGGAACAAA GATCCTCCAC GAGATGCCAC GAAGACCAC CATCCAGCA TCCTTGGCAC TCCTTGGCTT Seq ID NO: Protein Act I MGPGPSRAPR QTERQORYLL DMHLGVTVAS HNEMCNSNTD	ARGCGGACCC GAGCGCTACC CAGACTGGGA CCCCTTTCTT TGGCTGGTAG GCCTTGCTG GAGACGGAC GAATCCTGT CGGATGGGA AAAGACCTC CTGACACGGA AGAGGTGGGG GACCCAACAG GACCAACAG GACACAACAG GACACAACAG GACGCAACAG GACGCAACAG TTCTCACACAG GACGGAGGAGC ACCCAGCT CCAGCCCCT GTATATAGGC 11 APRIMICALA LAGAPRELAV QGPAGRVLVC QGAGGTACACACAG AGGAGGACL CCAGCCCLCT CTGACAGCCCCT GTATATAGGC ACCCAGCCCCT GTATATAGGC LL AGGAGGAGACAGACCAGCCCCT GTATATAGGC LL AGGAGGACACACAGCCCCT GTATATAGGC LL AGGAGGCTACACCCCT CCAGCCCCT GTATATAGGC LL AGGAGGCTACACCCCT CCAGCCCCT CCAGCCCT CCAGCCCCT CCAGCCCT CCAGCCCCT CCAGCCCCT CCAGCCCT CCAGCCT CCAGCCT CCAGCCCT CCAGCCCT CCAGCCCT CCAGCCT CC	GCTATTATCA CACCTCCAGE ACCAATACTA CCTATTTATC CAGCAGGCTC CTCTTCCCACA GCCCTAGATG ATGGGCTCGC CACCAGAGC CCACCAGAGC CTCTTGCCACA ATCCTGCCTA ACAAGGAACT CTCCTTGGCC CGGCAACATTC CCACTACAG GAACCATTCA GAACCATTGAA GAACCATGCAG GTTCCAAAAA TCCATGGTCT GTTCCAACGC NP_005492.1 21 LMVAAGGCVV PDGYTNRTGA AHRYTQVLWS TSGGFTQNTV	GATCATGCCC GAGCACCCTC CTGACGACCCTC ATAAGTTATG AGGCACATTAC GCAGGGCCAG CACGTGGGGC CGTGTCTCAG GAGGACAAA GAGAGCCACA AGGATTGCTA AGAAAGAAG ACAGACTGAA GCCTGGCTC TGGACAGAAA TCAGGGGCCT CCTCCTCCTGA TGTAGCAGGA TGTAGCAGGG GACCAATAAA  31   SAFNLDTRFL VYLCPLTAHK GSEDQRRMVG YFGAPGAYNM	AAGTACCACE CCCACCAAGA CCCTGATCCC CCTCTGACAG ACCTCGTCACAG ACCTCGTCACAG ACCTGGTCGC CCTCTGCCAG AGGCCCTGC CTCACTGGTCT TGGTGGGCCC CGGGGGCACT ACCCAGAAGG CTCGCAGGAAAGG CTCGCAGGGA ACTGTGCTGG GATTTTGGGG GATGTTGGGG GAAGGTGGAG TCCCCTGCCTG GAATTCCCTC CAGCTCCCAG  41  VVKEAGNPGS DDCERNNITY KCYVRGDLE KGNSTMIQRK	CAGTGCGGAT AGCACTGGGT AGCACTGGT ACCCCTCTT TCCACAGGGG GAGCATGCAC CTTACAACGC TGGACTGTGC GGCCAGGGCC AATGTGGTGA TGGACTTTGCT TCTGCTTTCC GTGCAGCAGG GGATACAGAG GGATACAGAG GAGAGCCCT CCTGCCACCC TTCTTAGCTA TCCTAAGGCC TTCTTAGGTA TCCTAAGGCC TTGGCACCC TTGGCACCC TTGTTAGGTA TCCTAAGGCC TTGGCACCC TTGGCACC TTGGCACCC TTGGCACC TTGGCACCC TTGGCACC TTGGCACCC TTGGCACC TTG	3180 3240 3360 3420 3540 3540 3600 3720 3780 3960 4020 4020 4140 4260 4380 4440
50 55 60 65 70	TGACTTCTTT CCGGGAGGAG GACCACCTGG CCCCCAGTGT CCACCACCTT ATGCTGTCT TGGTGCATCA AAAACAAGCC CACCTCCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA TGGATCTCAG GAAGACCAC CATCCCAG GCAAGACCAC CATCCAGCA TCCTTGGCTT CATTTGAGAA ACTCCCCAGC TGCTTCTT Seq ID NO: Protein Ac:	ARGCGGACCC GAGCGCTACC CAGACTCGGG CCCTTTCTT TGGCTGGTAG GCCTTGGGGA GCATTCCTGT CGGATGGTGC AAAGAGCCTC TTCACACCTG GACACCTG GACACCTG GACAGGA AGAGGTGGG GACCCAACAG GACACCACAG TTCTCACTCA GGAGGGAGG TTCTCACTCA GGAGGGAGC GACCCAGCT TCTTGCCAG GTGAGGCTA CCCAGCCCT GTATATAGGC  148 Protei 1285101 #: 1 1 APRIMICALA LAGAPRELAV GYLAGGTMCQLG GYTMQVGSFI GYTMQVGSFI GYTMQVGSFI GYTMCVGSFI	GCTATTATCA CACCTCAGG ACCACTAGAT ACCATTTATC CAGCAGGCTC TCTTCCCACA ACCACAGAGC GATCCATCTT CAGCAGAGC GATCCATCT CACACAGAGC ATCCTGCCTA ATCCTGCCTA ATCCTGCCTA CACAGAGACT CTCTTGGCC CGGCAACGTA GGACCATTC CCACTACCAG GACCATTCA GAACCATCAG GACCATTGAA GAACCATGCA CTTGCTCAAAA TCCATAGTAC TTCTCACCGC I Sequence NP_005492.1 21   LMVAAGGCVV PDGYTNRTGA AHRYTQVLWS TSGGFTQNTV LHPRNITIVT	GATCATGCCC GAGCACCTIG CTGACGTCT ATAAGTTATG AGGCACATAC CGAGGGCCAG CACGTGGGGC CGTGTCTCAG CGGGAGGAAA AGAGCCACA AGCACTGAG ACCACACACACACACACACACACACACACACACACA	AAGTACCACE CCACCAAGA CCCTGATCCC CCTCTGACAG ACCTCGTCAA ACCTCGTCACAG ACCTCGTCAC CCACTGCTCG CCTCTGCCAG AGGCCCTGC GTCACTGGAT TGGTGGGCC CGGGGGCACT ACCCAGAAGG ACTGTGCTGG GATGTTGGGA ACTGTGCTGG GATGTTGGGA ACTGTGCTGG GATGTTGGA ACTGTGCTGG GATGTTGGA ACTGTGCTGG GATTTCCCCAG AGGCTCCCAG  41  VVKEAGNPGS DDCERMNITV KCYVRENDLE KGNSYMIQRK VFLLSQEAGG	CAGTGCGGAT AGCACTGGGT AGCACTGGGT ACCCCCTCTT TCCACAGGGG GAGCATGCAC CTTACAACGC TGGACTGTGC CGCCAGCGCC AATGTGGTGA TGGACTGCTTC CCTATCGCTTTCC CTGCACTCGGGGGGAGACCT CTTGCTTTCC CTGCTCCCC TTCTTAGCTA TCCTAAGGCC TCCTAGCCACCC TTCTTAGCTA TCCTAGGCCC CCCCTCCTTG TTTGT  S1 LFGYSVALHR KNDPGHHIIE LDSSDDMGTY EWDLSSYSYK DLERRQVLEG	3180 3240 3360 3420 3540 3540 3600 3780 3840 3960 4020 4020 4140 4260 4320 4380 4440
50 55 60 65 70	TGACTTCTTT CCGGGAGGAG GACCAGCTGG CCCCCAGTGT CCACCACTTT ATGCTGTCTG CGAGTGCACTC TGGTGCATCA AAAACAAGCC CACTCCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA TGCATCTCG GAAGACACA CATCCCAG GCAAGACCAC CATCCAGCCA TCCTTTGGGTT CATTTGAGAA ACTCCCCAGC TGCCTTCTTT Seq ID NO: Protein Ac:	ARGCGGACCC GAGCGCTACC CAGACTCGGG CCCTTTCTT TGGCTGGTAG GCCTTGGGGA GCATTCCTGT CGGATGGTGC AAAGAGCCTC TTCACACCTG GACACCTG GACACCTG GACAGGA AGAGGTGGG GACCCAACAG GACACCACAG TTCTCACTCA GGAGGGAGG TTCTCACTCA GGAGGGAGC GACCCAGCT TCTTGCCAG GTGAGGCTA CCCAGCCCT GTATATAGGC  148 Protei 1285101 #: 1 1 APRIMICALA LAGAPRELAV GYLAGGTMCQLG GYTMQVGSFI GYTMQVGSFI GYTMQVGSFI GYTMCVGSFI	GCTATTATCA CACCTCAGG ACCACTAGAT ACCATTTATC CAGCAGGCTC TCTTCCCACA ACCACAGAGC GATCCATCTT CAGCAGAGC GATCCATCT CACACAGAGC ATCCTGCCTA ATCCTGCCTA ATCCTGCCTA CACAGAGACT CTCTTGGCC CGGCAACGTA GGACCATTC CCACTACCAG GACCATTCA GAACCATCAG GACCATTGAA GAACCATGCA CTTGCTCAAAA TCCATAGTAC TTCTCACCGC I Sequence NP_005492.1 21   LMVAAGGCVV PDGYTNRTGA AHRYTQVLWS TSGGFTQNTV LHPRNITIVT	GATCATGCCC GAGCACCTIG CTGACGTCT ATAAGTTATG AGGCACATAC CGAGGGCCAG CACGTGGGGC CGTGTCTCAG CGGGAGGAAA AGAGCCACA AGCACTGAG ACCACACACACACACACACACACACACACACACACA	AAGTACCACE CCACCAAGA CCCTGATCCC CCTCTGACAG ACCTCGTCAA ACCTCGTCACAG ACCTCGTCAC CCACTGCTCG CCTCTGCCAG AGGCCCTGC GTCACTGGAT TGGTGGGCC CGGGGGCACT ACCCAGAAGG ACTGTGCTGG GATGTTGGGA ACTGTGCTGG GATGTTGGGA ACTGTGCTGG GATGTTGGA ACTGTGCTGG GATGTTGGA ACTGTGCTGG GATTTCCCCAG AGGCTCCCAG  41  VVKEAGNPGS DDCERMNITV KCYVRENDLE KGNSYMIQRK VFLLSQEAGG	CAGTGCGGAT AGCACTGGGT AGCACTGGT ACCCCTCTT TCCACAGGGG GAGCATGCAC CTTACAACGC TGGACTGTGC GGCCAGGGCC AATGTGGTGA TGGACTTTGCT TCTGCTTTCC GTGCAGCAGG GGATACAGAG GGATACAGAG GAGAGCCCT CCTGCCACCC TTCTTAGCTA TCCTAAGGCC TTCTTAGGTA TCCTAAGGCC TTGGCACCC TTGGCACCC TTGTTAGGTA TCCTAAGGCC TTGGCACCC TTGGCACC TTGGCACCC TTGGCACC TTGGCACCC TTGGCACC TTGGCACCC TTGGCACC TTG	3180 3240 3360 3420 3540 3540 3600 3720 3780 3960 4020 4020 4140 4260 4380 4440
50 55 60 65 70	TGACTTCTTT CCGGGAGGAG GACCAGCTGG CCCCAGTGT CCACCACTT ATGCTGTCTG CGAGTGCACT TGGTGCACA AAAACAAGCC CACCTCCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA AGATCTCTG AGGAACAAC GCAGCCAC AGACCAC GCAAGACCAC CATCCAGCCA TCCTTGGTT CATTTGGGTT CATTTGGGTT CATTTGGGTT Seq ID NO: Protein Act I MGPGPSRAPR QTERQORYLL DMWLGVTVAS HNEMCNSNTD DPDQGNLYI SQVGAYFGSA	ARGCGGACCC GAGCGCTACC CAGACTGGGA CCCTTTCTT TGGCTGGTAG GCCTTGGGG GCCTTGGGG GCCTGGGGA AAGAGGCTTC CTGACAGGGA AGAGGTGGGG GACCCAACAG TGAAGCCTC GACAGGGA AGAGGTGGGG TTCTCACACAG TTCTCACACAG GCCCAACAG GCCCAGCT TCTTGTGCCAG GCTGAGGCTA CCCAGCCCT TATATAGGC  11	GCTATTATCA CACCTCCAGG ACCAATACTA CCTATTTATC CAGCAGGCTC CAGCAGGCTC CCACCAGAGC GATCCATCTT GCAGCCCCG ATCCTGCCTA ACCATGCATC CCACCAGAGC CCACAGAGC CCACAGAGC CCACAGAGC ATCCTGCCTA GCACCACGT GCACCACGT GCACCACGT GCACCACGT GCACCATGCAC GACCATTGCAC GACCATTGCAC GACCATTGCC GTTCCAAAAA TCCATGGTAC TTCTCACCGC  I SEQUENCE INP_005492.1 IMVAAGGCVV PDGYTNRTGA AHRYTQVLWS TSGGFTQNTV LHGRNITIVT WQDLLVGAPY	GATCATGCCC GAGCACCTG CTGACGTCT ATAAGTTATG AGGCACATAC GCAGGGCCA GCAGGGGCCA GCAGGTGGGG AGGTTGTCTA GAGACACAC GCCGCTGGC AGGAGAA GCCTGGGCT CTGACACA CCAGCCTCCA TGTAGTAATA TCAGGGCCT CCCTCCCCC CCTCTCCTGA TGTAGCAGAC GACCAATAAA  31   SAFNLDTRFL VYLCPLTAHK GSEDQRRWG YFGAPGAYNW GAPREHRINGA YFERKEEVGG	AAGTACCACE CCACCAAGA CCCTGATCCC CCTCTGACAG ACCTCGTCACA ACCTCGTCACA ACCTCGTCACA ACCCTGCTCG CCTCTGCCAG ACGCCCTGCCGG ACGCCCTGCCGGCACACACACACACACACACACACACACA	CAGTGCGGAT AGCACTGGGT AGCACTGGT ACCCCCTCT TCCACAGGGG GAGCATGCAC CGCCAGCGCC AATGTGGTGA TGACTTTGCT CCAATTGACA TGGAGACCT CTTGCAGCAGG GGCATGCGG GGCATGCGG GGCATGCGG GGCATGCGG GGCATCAGG GGCATCAGG GGCATCAGG TCCTTAGCT TCCTAAGGCC TCCTTGCTTTGT  51 LFGYSVALHR RNDPGHHIIE LDSSDDWGTY EWBLSEYSYK EULERGVLEG TTSFAHPSLL	3180 3240 3360 3480 3540 3600 3720 3780 3960 4020 4020 4140 4260 4240 4320 4380 4440
50 55 60 65 70	TGACTTCTTT CCGGGAGGAG GACCAGCTG CCCCAGTGT CCACCACTT ATGCTGTCTG CGAGTGCACT TGGTGCATCA AAAACAAGC CACTCCCC GTCAAAACTA CCCATGCCG GGGGTGCTCA TGGTCCAG GGGTGCTCA TGCATCCTG AAGGAACAAA GATCCTCCAC GCAAGACCAC CATCCAGCCA TCCTTGGGTT CATTTGAGAA ACTCCCAGC TGCCTTCTTT Seq ID NO: Protein Act I MGPGPSRAPR QTERQORILLI DMWLGVIVAS HNEMCNSNTD DPEDQGNLYI SQUGAYTGSA	ARGCGGACCC GAGCGCTACC CAGACTGGGA CCCCTTTCTT TGGCTGGTAG GCCTTGCTG GAGAGGTGGC AAAGAGCCTC CTGACAGGGA AGAGGTGGGG GACCCAACAG GACCAACAG GACAGAGAGAGAG GACCAACAG GACAGAGAG GACCCAACAG GCCCCAGCT TTCTGTGCCAG GCTGAGGGAG CCCAGCCCT GTATATAGGC 11 APRIMICALA LAGAPRELAV YLETGMCQLG GTTAGACCCG GTTAGAGCTCT CCGGCCCT GTATATAGGC LSC LSC LSC LSC LSC LSC LSC LSC LSC LS	GCTATTATCA CACCTCCAGG ACCAATACTA CCTATTTATC CAGCAGGCTC CTCTTCCCACA GCCCTAGATG ATGGGCTCGC CACACAGAGC CCACCAGAGC CTCTTGCCCTA ATCCTGCCTA ATCCTGCCTA ACAGCACCTG ATCCTGCCTG ATCCTGCCTG GCACCACTGC GGACCATTGC GCACACTGCG GACCATTGA GAACCATGCG GCCTGGCTCTG GTTCCAAAAA TCCATGGTCTC TCTCCACGC In sequence NP_005492.1 21 LMWAAGGCUV PDGYTNTGAA AHRYTQUWS TSGGFTQNTV LHPRNTTIVT LHPRNTTIVT WQDLLVGAPY GQGFGDLAVG	GATCATGCCC GAGCACCCTC CTGACGTCT ATAAGTTATG AGGCACATTAC GCAGGGCCAG CACGTGGGGC CGTGTCTCAG GGAGGACAA GGCGCTGGC AGGTTGTCTA AGAAGAAGA AGAAAGAAG ACAGACTGAA GCCTGGGCTC TGGACAGCA TGTAGTAATA TCAGGGGCCT CCCTCCTCAT TGTAGCAGGG GACCAATAAA  31   SAFNLDTRFL VYLCPLTAHK GSEDQRMVG YFGAPGAYNW GAPRERHIMGA AYFERKEEVGG APFEGLGKVY	AAGTACCACE CCCACCAAGA CCCTGATCCC CCTCTGACAG ACCTCGTCAA CCCTGTCGCAG AGGCCCTGC CTCTGCCAG AGGCCCTGC CTCTGCCAG AGGCCCTGC CTCTGCCAG AGGCCCTGC CGCAGGAAGG CTCGCAGGAAG ACTGTGCTGG GATTTTGGGA ACTGTGCTGG GAAGGTGGAG ACGGCTCCCAG GCAGGGGGC AGAGGTGGAG ATTCCCTC CAGCTCCCAG  41    VVKEAGNPGS DDCERMNITV KCYVRGMDLE KGNSYMIQRK VFLLSQEAGG AIYEFMQAG IYHSSSKGLL	CAGTGCGGAT AGCACTGGGT AGCACTGGGT ACCCCTCTT TCCACAGGGG GAGCATCAC CTTACAACGC TGGACTGTGC GCCAGCGCC AATGTGGTGA TGACTTGCT CTTGCTTTCC GTGCAGCAGG GGATACAGGG GGATACAGGG GGATACAGGG GGATACAGGG TTCTTAGCTA TCCTAAGGCC TTCTTAGCTA TCCTAAGGCC TTGGCACCC TTTTGT  51   LFGYSVALHR KNDPGHHIIE LDSSDDWQTY EWDLSEYSYK DLERRQVLEG TTSPALPSLL RQPQQVIHGE	3180 3240 3360 3420 3540 3540 3600 3720 3780 3960 4020 4020 4140 4260 4320 4380 4440
50 55 60 65 70	TGACTTCTTT CCGGGAGGAG GACCAGCTG CCCCAGTGT CCACCACTT ATGCTGTCTG CGAGTGCACT TGGTGCATCA AAAACAAGC CACTCCCC GTCAAAACTA CCCATGCCG GGGGTGCTCA TGGTCCAG GGGTGCTCA TGCATCCTG AAGGAACAAA GATCCTCCAC GCAAGACCAC CATCCAGCCA TCCTTGGGTT CATTTGAGAA ACTCCCAGC TGCCTTCTTT Seq ID NO: Protein Act I MGPGPSRAPR QTERQORILLI DMWLGVIVAS HNEMCNSNTD DPEDQGNLYI SQUGAYTGSA	ARGCGGACCC GAGCGCTACC CAGACTGGGA CCCCTTTCTT TGGCTGGTAG GCCTTGCTG GAGAGGTGGC AAAGAGCCTC CTGACAGGGA AGAGGTGGGG GACCCAACAG GACCAACAG GACAGAGAGAGAG GACCAACAG GACAGAGAG GACCCAACAG GCCCCAGCT TTCTGTGCCAG GCTGAGGGAG CCCAGCCCT GTATATAGGC 11 APRIMICALA LAGAPRELAV YLETGMCQLG GTTAGACCCG GTTAGAGCTCT CCGGCCCT GTATATAGGC LSC LSC LSC LSC LSC LSC LSC LSC LSC LS	GCTATTATCA CACCTCCAGG ACCAATACTA CCTATTTATC CAGCAGGCTC CTCTTCCCACA GCCCTAGATG ATGGGCTCGC CACACAGAGC CCACCAGAGC CTCTTGCCCTA ATCCTGCCTA ATCCTGCCTA ACAGCACCTG ATCCTGCCTG ATCCTGCCTG GCACCACTGC GGACCATTGC GCACACTGCG GACCATTGA GAACCATGCG GCCTGGCTCTG GTTCCAAAAA TCCATGGTCTC TCTCCACGC In sequence NP_005492.1 21 LMWAAGGCUV PDGYTNTGAA AHRYTQUWS TSGGFTQNTV LHPRNTTIVT LHPRNTTIVT WQDLLVGAPY GQGFGDLAVG	GATCATGCCC GAGCACCCTC CTGACGTCT ATAAGTTATG AGGCACATTAC GCAGGGCCAG CACGTGGGGC CGTGTCTCAG GGAGGACAA GGCGCTGGC AGGTTGTCTA AGAAGAAGA AGAAAGAAG ACAGACTGAA GCCTGGGCTC TGGACAGCA TGTAGTAATA TCAGGGGCCT CCCTCCTCAT TGTAGCAGGG GACCAATAAA  31   SAFNLDTRFL VYLCPLTAHK GSEDQRMVG YFGAPGAYNW GAPRERHIMGA AYFERKEEVGG APFEGLGKVY	AAGTACCACE CCCACCAAGA CCCTGATCCC CCTCTGACAG ACCTCGTCAA CCCTGTCGCAG AGGCCCTGC CTCTGCCAG AGGCCCTGC CTCTGCCAG AGGCCCTGC CTCTGCCAG AGGCCCTGC CGCAGGAAGG CTCGCAGGAAG ACTGTGCTGG GATTTTGGGA ACTGTGCTGG GAAGGTGGAG ACGGCTCCCAG GCAGGGGGC AGAGGTGGAG ATTCCCTC CAGCTCCCAG  41    VVKEAGNPGS DDCERMNITV KCYVRGMDLE KGNSYMIQRK VFLLSQEAGG AIYEFMQAG IYHSSSKGLL	CAGTGCGGAT AGCACTGGGT AGCACTGGT ACCCCCTCT TCCACAGGGG GAGCATGCAC CGCCAGCGCC AATGTGGTGA TGACTTTGCT CCAATTGACA TGGAGACCT CTTGCAGCAGG GGCATGCGG GGCATGCGG GGCATGCGG GGCATGCGG GGCATCAGG GGCATCAGG GGCATCAGG TCCTTAGCT TCCTAAGGCC TCCTTGCTTTGT  51 LFGYSVALHR RNDPGHHIIE LDSSDDWGTY EWBLSEYSYK EULERGVLEG TTSFAHPSLL	3180 3240 3360 3480 3540 3600 3720 3780 3960 4020 4020 4140 4260 4240 4320 4380 4440
50 55 60 65 70	TGACTTCTTT CCGGGAGGAG GACCAGCTGG CCCCAGTGT CCACCACCTT ATGCTGTCTG CGAGTGCACCA TGGTGCATCA AAAACAAGCC CACCTCCCCT GTCAAAACTA CCCATGCAG GGCGTGCTA AAGGAACAAA GATCCTCGA GAATCCTCG GAAGACCAC CATCCAGCA TCCTTGGCTT CATTTAGGAA ACTCCCCAGC TGCCTTCTTT Seq ID NO: Protein Act 1   MGPGPSRAPR QTERQORYLL DMWLGYTVAS HNEMCNISNTD DPEDQGNLYI SQVGAYTGSAA LHGPSGSAFG KLGLPGLATF	ARGCGGACCC GAGCGCTACC CAGACTGGGA CCCCTTTCTT TGGCTGGTAG GCCTTGCTG GAGACTGGGA AAAGAGCCTC TTCACACAGGA AGAGGTGGGG GACCCAACAG GACCAACAG GACACAACAG GACACCAACAG GACACAACAG GACACAACAG GACACAACAG GACACAACAG GACACAACAG GACACAACAG GACACAACAG GACACAACAG GACACACAC	GCTATTATCA CACCTCAGG ACCATATTATC CAGCAGGCTC TCTTCCCACA ACCACAGAGC GATCCATCTT ACCACAGAGC GATCCATCT ACCACAGAGC CTCTTGGCCT ACCAGAGC CCGCACAGAGC CCGCACAGGC CCGCACAGGC CCGCACAGGC CTCCTGGCTC CCACTAGCAT GCACCACGA GAACCATCA GAACCATGCA GAACCATGCA TCCATGGTC TCTCACCGC IN SEQUENCE IN 005492.1 LMVAAGGCVV PDGYTNRTGA AHRYTQVLWS TSGGFTQNTV LHPRNITIVT WQDLLVGAPY TQDGFQDLAVG DENFYPDLLV	GATCATGCCC GAGCACCTC GAGCACCCTC ATAAGTTATG AGGCACATAC GCAGGGCCAG CACGTGGGGC CGTGTCTCAG GGAGGCACA GGCCGCTGC AGGATGAAG ACAGACTGAA GCCTGGCTCC CCTCCCCC CCTCCTCCCTGA TGTAGCAGGG GACCAATAAA  31   SAFNLDTRFL VYLCPLTAHK GSEDQRRMVG YFGAPGAYNW GAPRHRMGA YFERKEEVGG APFEGLGKVY GSLSDHIVLL	AAGTACCACE CCCACCAAGA CCCTGATCCC CCTCTGACAG ACCTCGTCAA CGCTGTGGAC CCACTGGTCAC CGCTGTGGAC CCTCTGCCAG AGGCCCTGC CGTGGGGCC CGGGGGCACT ACCCAGAAGG CTCGCAGGAG ACTGTGCTGG AATGTTGGGA ACTGTGCTGG GAATGTTGGGA ACGCTGCCCAG GAATGTCCCAG  41    VVKEAGNPGS DDCERNNITU KCYVRGNDLU KCYVRGNDLU VFLLSQEAGG AIYUFFNQAG IYHESSKGLL RARPVINIVE	CAGTGCGGAT AGCACTGGGT AGCACTGGGT ACCCCTCTT TCCACAGGGG GAGCATGCAC CTTACAACGC TGGACTGTGC CGCCAGCGCC AATGTGGTGA TGACTTGCT CCAATTGACA TGGAGGACCT CTTGCTTTCC GTGCAGCGG GGATACAGAG GAGAGACCT TCCTTAGCTA TCCTAGCTA TCCTAGCTA TCCTAGCTA TCCTTAGCTA TCCTTAGCTA TCCTTAGCTA TCCTTAGGCTA TCTTAGGTA TCCTTAGGCCC CCCCTCCTTG TTTGT  51	3180 3240 3360 3420 3540 3540 3600 3720 3780 4020 4020 4020 4140 4260 4320 4340 4340 4340 4340 4340 4340 434
50 55 60 65 70	TGACTTCTTT CCGGGAGGAG GACCAGCTG CCACCACTT ATGCTGTCTG CCACTGCACT TGGTGCACA AAACAAGCC CACTCCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA TGCATCTCTG AGGGACACA CATCCTCCC GGAATGCACC GCAAGACAC CATCCACCA GCAAGACCAC CATCCAGC GCAAGACCAC CATCCAGC TGCTTTT CATTTGAGAA ACTCCCCAGC TGCCTTCTTT Seq ID NO: Protein Act 1   MGPGGPSRAPR QTERQORYLL DMWLGVTVAS HNEMCNSNTD DPEDQGLYI SQVGAYPGSA LHGPSGSAFG KLGLPGLATF DPALCTATSC	ARGCGGACCC GAGCGCTACC CAGACTGGGA CCCCTTTCTT TGGCTGGTAG GCCCTGGGA AAGAGGCTTC CTGACAGGGA AAGAGGCTTC CTGACAGGGA AGAGGTGGGG GACCCAACAG TGAAGGCTCT GACAGGGA AGAGGAGGA TTCTCACTCA GGAGGGAACA GGAGGCCCAGCT TCTTGTGCCAG GCTGAGGCTA CCCAGCCCT TTTTTGCCAG GCTGAGGCTA LAGAGCACCC TCTTTTGCCAG GCTGAGGCTA CCCAGCT LAB Protei LABAPRELAU QGPAGRVLVC YLETGMCQUG GYTMCGSFI LALADLINIDG LSYASIGDIN CYSLSGQMDV VQVELCFAYN	GCTATTATCA CACCTCCAGG ACCATACTA CAGTATTATC CAGCAGGCTC CAGCAGGCTC CCACCAGAGG ATGCGCTAGATG ATGGGCTCGC ATCCTGCCTA ACCACGAGAC ACCAGGAACT CTCCTTCGCC CAGCACAGAG CCACAGAGAC CCACTACCAG GACCATTGAA GAACCATTGCA GACCATTGAC CTTCCACAGG GACCATTGAC GACCATTGAC TTCCACCGC  I SEQUENCE I SEQUENCE AHRYTQVLWS TSGGFTONTV LHPRNITIVT WQDLLVGAPY QDGFQDIAVG DENFYPDLLV QSAGNENYRR	GATCATGCCC GAGCACCTG CTGACGTCT ATAAGTTATG AGGCACATAC GCAGGGCCAG CACGTGGGG CACGTGGGG CACGTGGGA GGCGCTGGC AGGATTATT AGACACAC GCCGCTGGC AGGATGAAA GCCTGGGCT CTGACACAC TGTAGTAAT TCAGGGGCT CCCTCCCC CCTCTCCTGA TGTAGCAGAC GACCAATAAA  31   SAFNLDTRFL VYLCPLTAHK GSEDQRRWG YFGAFGAYNW GAPRRRIMGA YFERKEEVGG APFEGLGKVY GSLSDHIVLL NITLATTLEA	AAGTACCACE CCCACCAAGA CCCTGATCCC CCTCTGACAG ACCTCGTCACA ACCTCGTCACA CCCTCTGCCAG GCCCCTGCCAG GTCACTGGTCA TGGTGGGCC CGGGGGCACT TGGTGGGCC CTCCCAGGGA ACTGTGTGGA ACCCAGAAGG GATGTTGGGA GAAGGCCCA GGCAGGGGGC ATGGCTGCAG ATGGCTGCAG ATGGCTCCAG ATGCCTCCAG ATCCCTCCAG ATCCCTCAG ATCCCTCCAG ATCCCTCAG ATCCCTCCAG ATCCCTCAG ATCCCTCCAG ATCCCAG ATCCCTCCAG ATCCCCAG ATCCCCAG ATCCCCAG ATCCCCAG ATCCCCAG ATCCCAG ATCCCCAG ATCCCCAG ATCCCTCCAG ATCCCCAG ATCCCCAG ATCCCCAG ATCCC	CAGTGCGGAT AGCACTGGGT AGCACCTCCT TCCACAGGGG GAGCATGCAC CCTTACAAAGC TGGACTGTGC CGCCAGCGCC AATGTGGTGAT TGACTTTGCT CCAATTGACA TGGAGACCT CTTGCTTTCC GTGCAGCAG GGCATGCGGG GGATACAGAG GAGAGACCCT CCTGCCACCC TTCTTAGCTA TCCTAAGGCC TTCTTAGCTA TCCTAAGGCC TTCTTGT  51 LFGYSVALHR RNDPGHHITE LDSSDDWQTY EWDLSEYSYK EULSEYSYK EULSERGVLEG TTSFPAHPSILL RQPQQVIHGE KTLVPRPAVL FAGSESAVFH	3180 3240 3360 3420 3540 3540 3540 3780 3840 3990 4020 4080 4120 4260 4220 4380 4440
50 55 60 65 70	TGACTTCTTT CCGGGAGGAG GACCAGCTG CCACCACTT ATGCTGTCTG CGAGTGCACT TGGTGCATCA AAAACAAGC CACTCCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA TGCATCCTG AAGGAACAAA GATCCTCCAC GCAAGACCAC CATCCAGCCA TCCTTGGCTT CATTTGAGAA ACTCCCAGC TCCTTGGTT Seq ID NO: Protein Act	ARGCGGACCC GAGCGCTACC CAGACTGGGA CCCTTTCTT TGGCTGGTAG GCCTTGGGGA GCATTCCTGT CGGATGGTGC AAAGAGCCTC CTGACACGGA AGAGGTGGGG GCACTACACAG TGAAGCCTC GACAGGGA AGAGGTGGGG GACCCAACAG TGAAGCCTCT GACAGGGA AGAGGAGGAG GGACCCAACAG GCCCAGCT TTCTCTCTCACCA GGAGGGAGCC GACCCAGCT TCTTGTGCAG CCTGAGGCTA CCCAGCCCT TATATAGGC  148 Protei 1 1 APRIMICALA LAGAPRELAV GGPAGRVLVC YLETGMCQLG GYTMQVGSFI LALADLINDG LSVASIGDIN GYSLSGOMDV QVELCFAYN QKLEILIMDN	GCTATTATCA CACCTCCAGG ACCATACTA CAGCAGGCTC CAGCAGGGCTC CCACCAGAGGCTC GCACCACAGGC GATCCACT GCACCACAGGC ATCCTGCCTA ACAAGGAACT CTCCTTGGCC CGCAAACGTA CAAAGGAACT CCACTACCAG GACCATTGA GAACCATTGA GAACCATTGA GAACCATGCG GTTCCAAAAA TCCATGGTCT GTTCCACCGC In Sequence NP_005492.1 LMWAAGGCVV PDGYTNRTGA AHRYTQVLWS TSGGFTQNTV LHPRNTTIVT WQDLLUGAPY QDGFQDLAVG DENFYPDLLV QSAGNPNYRG LRDKURPIII	GATCATGCCC GAGCACCTG CTGACGTCT ATAAGTTATG AGGCACATAC GCAGGGCCAG GCAGGTGGGGC GGTGTCTCAG AGGACGACA AGGACGCACA AGGACGACA AGCACACACA	AAGTACCACE CCCACCAAGA CCCTGATCCC CCTCTGACAG ACCTCGTCACAG ACCTCGTCACAG ACGCTGCTCG CCTCTGCCAG AGGCCCCTGC GTCACTGGTAT TGGTGGGCCC CGGGGGCACT TGCTGGGAG ACTGTGCTGG CTCGCAGGGA ACTGTGCTGG GATTTTGGGA GGAGGGGGC AGAGGTGGAG ACTGTGCTGG GAATTCCCTC GAATTCCCTC CAGCTCCCAG  41    VVKEAGNPGS DDCERMITV KCYVRGNDLE KGNSYMIQRE VFLLSQEAGG AIYVFMQAG IYHSSSKGLL RARPVINIVE DDCRRPPILR PDRRPFLLRS	CAGTGCGGAT AGCACTGGGT AGCACTGGT ACCCCTCT TCCACAGGGG GAGCATCAC CTTACAAAGC TGGACTGTGC CGCCAGCGCC AATGTGGTGA TGACTTTGCT CCAATTGACA TGGAGGACT CTTGCTACCAGGG GGCATGCGG GGCATGCGG GGATACAGAG GAGAGACCT CCTGCCACCC TTCTTAGCTA TCCTAAGGCC TTCGTAGCAG TTGGCAGCCC CCCCTCTTG TTTGT  51   LFGYSVALHR KNDPGHHIIE LDSSDDMQTY EWBLSEYSYK DLERRQVLEG TSFFAHPSLL RQPQQVIHGE KTLVPRPAVL LFAGSESAVFH LDAYPILNQA	3180 3240 3360 3420 3540 3540 3720 3780 3960 4020 4020 4140 4260 4380 4440
50 55 60 65 70	TGACTTCTTT CCGGGAGGAG GACCAGCTG CCACCACTT ATGCTGTCTG CGAGTGCACT TGGTGCATCA AAAACAAGC CACTCCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA TGCATCCTG AAGGAACAAA GATCCTCCAC GCAAGACCAC CATCCAGCCA TCCTTGGCTT CATTTGAGAA ACTCCCAGC TCCTTGGTT Seq ID NO: Protein Act	ARGCGGACCC GAGCGCTACC CAGACTGGGA CCCTTTCTT TGGCTGGTAG GCCTTGGGGA GCATTCCTGT CGGATGGTGC AAAGAGCCTC CTGACACGGA AGAGGTGGGG GCACTACACAG TGAAGCCTC GACAGGGA AGAGGTGGGG GACCCAACAG TGAAGCCTCT GACAGGGA AGAGGAGGAG GGACCCAACAG GCCCAGCT TTCTCTCTCACCA GGAGGGAGCC GACCCAGCT TCTTGTGCAG CCTGAGGCTA CCCAGCCCT TATATAGGC  148 Protei 1 1 APRIMICALA LAGAPRELAV GGPAGRVLVC YLETGMCQLG GYTMQVGSFI LALADLINDG LSVASIGDIN GYSLSGOMDV QVELCFAYN QKLEILIMDN	GCTATTATCA CACCTCCAGG ACCATACTA CAGCAGGCTC CAGCAGGGCTC CCACCAGAGGCTC GCACCACAGGC GATCCACT GCACCACAGGC ATCCTGCCTA ACAAGGAACT CTCCTTGGCC CGCAAACGTA CAAAGGAACT CCACTACCAG GACCATTGA GAACCATTGA GAACCATTGA GAACCATGCG GTTCCAAAAA TCCATGGTCT GTTCCACCGC In Sequence NP_005492.1 LMWAAGGCVV PDGYTNRTGA AHRYTQVLWS TSGGFTQNTV LHPRNTTIVT WQDLLUGAPY QDGFQDLAVG DENFYPDLLV QSAGNPNYRG LRDKURPIII	GATCATGCCC GAGCACCTG CTGACGTCT ATAAGTTATG AGGCACATAC GCAGGGCCAG GCAGGTGGGGC GGTGTCTCAG AGGACGACA AGGACGCACA AGGACGACA AGCACACACA	AAGTACCACE CCCACCAAGA CCCTGATCCC CCTCTGACAG ACCTCGTCACAG ACCTCGTCACAG ACGCTGCTCG CCTCTGCCAG AGGCCCCTGC GTCACTGGTAT TGGTGGGCCC CGGGGGCACT TGCTGGGAG ACTGTGCTGG CTCGCAGGGA ACTGTGCTGG GATTTTGGGA GGAGGGGGC AGAGGTGGAG ACTGTGCTGG GAATTCCCTC GAATTCCCTC CAGCTCCCAG  41    VVKEAGNPGS DDCERMITV KCYVRGNDLE KGNSYMIQRE VFLLSQEAGG AIYVFMQAG IYHSSSKGLL RARPVINIVE DDCRRPPILR PDRRPFLLRS	CAGTGCGGAT AGCACTGGGT AGCACTGGT ACCCCTCT TCCACAGGGG GAGCATCAC CTTACAAAGC TGGACTGTGC CGCCAGCGCC AATGTGGTGA TGACTTTGCT CCAATTGACA TGGAGGACT CTTGCTACCAGGG GGCATGCGG GGCATGCGG GGATACAGAG GAGAGACCT CCTGCCACCC TTCTTAGCTA TCCTAAGGCC TTCGTAGCAG TTGGCAGCCC CCCCTCTTG TTTGT  51   LFGYSVALHR KNDPGHHIIE LDSSDDMQTY EWBLSEYSYK DLERRQVLEG TSFFAHPSLL RQPQQVIHGE KTLVPRPAVL LFAGSESAVFH LDAYPILNQA	3180 3240 3360 3420 3540 3540 3720 3780 3960 4020 4020 4140 4260 4380 4440
50 55 60 65 70	TGACTTCTTT CCGGGAGGAG GACCAGCTGG CCCCAGTGT CCACCACCTT ATGCTGTCTG CGAGTGCACT TGGTGCATCA AAAACAAGCC CACCTCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA TGCATCTCTG AAGGAACAAA GATCCTCAG CAGATGCCAC GAAGACCAC CATCCAGCA TCCTTGGCTT CATTTGAGAA ACTCCCAGC TGCCTTCTTT Seq ID NO: Protein Act 1   MGPGPSRAPR QTERQORYLL DMWLGVTVAS HNEMCNSNTD DPEDQGALYI SQVGAYFGSA LHGPSGSAFG KLGLPGLATF DPALCTATSC GFFSMPEMRC QALENHTEVQ	ARGCGGACCC GAGCGCTACC CAGACTGGGA CCAGACTGGGA CCCCTTTCTT TGGCTGGTGA GCATTCCTGT CGGATGGTGC AAAGAGCCTC CTGACACGGA AGAGGTGGGG GACCCAACAG GACCAACAG GACCAACAG GACACAACAG GACGCAACAG GACGCAACAG GACGCAACAG GCAGGGGAGGAGGAGG TTCTCACTCA CGAGGGCAAC CCCAGCT TCTTGCCAG GCTCAGGCTA CCCAGCCCT GTATATAGGC 11 APRIMICALA LAGAPRELAV QGPAGRVLVC GYTMOVGSFI LALADIANDGG GYTMOVGSFI LAVAGGGAGMU QKLELLLAMN QKLECTTTCT CTGGCAGC CCCTTTCTTCT CTGGCAGC CCCTTTCTTCT CTGGCAGC CCCTTTCTTCT CCGGATGGT CCGGATGG	GCTATTATCA CACCTCCAGG ACCAATACTA CCTATTTATC CAGCAGGCTC CTCTTCCCACA GCCCTAGATG ATGGGCTCGC CACCAGAGC CCACCAGAGC CTCTTGCCACA ATCCTGCCTA ACAAGGAACT CTCCTTGGCC CGGCAACATTC CCACTACAGG GAACCATTCA GAACCATTGAA GAACCATGGA GCACTGGACTG GTTCCAAAAA TCCATGGTCT I LMVAAGGCVV PDGYTNRTGA AHRYTQVLWS TSGGFTQNTV LHPRNTTIVT WQDLFVGAPY CQGAGNEPNYRR LRDKLRPIII CCESNLQMRAA	GATCATGCCC GAGCACCCTG CTGACGTCT ATAAGTTATG AGGCACATTAC GCAGGGCCAG CACGTGGGGC CGTGTCTCAG AGAAGCACAC AGCCTCGC AGGTTGTCTA AGAAGAAGA AGAAAGAAG ACAGACTGAA GCCTGGCTC TGGACAGCAC TGTAGTAATA TCAGGGGCCT CCTCTCCTGA TGTAGCAGGG GACCAATAAA  31   SAFNLDTRFL VYLCPLTAHK GSEDQRRMVG YFGAPGAYNW GAPRERRINGA YFGRESUGC AGSTGCTVL GSLSDHIVLL NITLAYTLEA SMYSLPLRM FVSEQQQKLS	AAGTACCACE CCCACCAAGA CCCTGATCCC CCTCTGACAG ACCTCGTCACAG ACCTCGTCACAG ACCTGGTCAC CCACTGCTCG CCTCTGCCAG AGGCCCTCG CTCACTGGTCA ACCCTGGTCA ACCCAGAAGG CTCGCAGGAA ACTGTGCTGG GATTTTGGGA ACTGTGCTGG GATGTTTGGGA ACTGTGCTGG GAAGGTGGAG ACAGGGGGACT CCCCTGCCTG GAATTCCCTC CAGCTCCCAG  41    VVKEAGNPGS DDCERNNITY VKCYVRGNDLE KGNSYMIQRK VFLLSQEAGG AIYSSSKGLL RARPVINIVE DDRRPPRLGLRS RLQYSRDVRK RLQYSRDVRK	CAGTGCGGAT AGCACTGGGT AGCACTGGGT ACCCCTCTT TCCACAGGGG GAGCATGCCC CTTACAACGC TGGACTTGGCT CGCCAGGGC AATGTGGTGA TGGACTTGCT CTTGCTTTCC GTGCAGCAGG GGATGCGG GGATGCGG GGATACAGAG GAGAGCCCT CCTGCCACCC TTCTTAGCTA TCCTAAGGCC TTCTTAGCTA TCCTAAGGCC TTGGCACCC TTGTAGGCC CCCCTCCTTG TTTGT  51  LFGYSVALHR KNDPGHHIIE LDSSDDMQTY EWDLSEYSYK DLERRQVLEG TTSPAHPSLL RQPQQVIHGE KTLVPRPAVL FAGSESAVEL LDASDDMGTY LGPGGSSAVEL LDASDDMGTY LGPGGSSAVEL LLLSINVTNT	3180 3240 3360 3420 3540 3540 3720 3780 4020 4020 4020 4140 4260 4260 4380 4440 60 120 180 240 300 360 4440
50 55 60 65 70	TGACTTCTTT CCGGGAGGAG GACCAGCTGG CCCCAGTGT CCACCACCTT ATGCTGTCCTG CCAGTGCACT TGGTGCATCA AAAACAAGCC CACTCCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA TGCATCTCTG AGGGACCAC CATCCTCCC GGAAGACAA GATCCTCCAC GCAAGACCAC CATCCAGCT CCTTGGCTT CATTTGAGAA ACTCCCCAGG TGCCTTCTTT Seq ID NO: Protein Act 1   MGPGPSRAPR QTERQORYLL DMWLGVTVAS HNEMCNSTD DPEDQGMLYI SQVGAYPGSA LEGPSGSAFG KLGLPGLATF CPALCTATSC GFFSMPEMRC QALENHTEVQ RTSERSGEDA	ARGCGGACCC GAGCGTACC CAGACTGGGA CCCTTTCTT TGGCTGTAG GCCCTGGGA GCCTTCCTGT CGGATGGTGC GAAGGGGA GCATTCCTGT TTGACACCTG TTGACAGGGA AGAGGTGGGG GACCCAACAG TGAAGCCTC GACAGGGAAA AGAGGGAAG TTCTCACTCA GGAGGGAGG TCTTCTCTCTCC GACCCCAGCT TCTTTGCCAG GCTGAGGCTA CCCAGCCT 148 Prote: 11  APRIMICALA LAGAPRELAV QGPAGRVLVC YLETGMCQLG GYTMYGSFI LALADLNING GYSLSGQMDV VQVELCFAYN QKLELLLIMDN FQKECGPIDNK HEALLTILVVE HEALLTLIVVE HEALLTLIVVE	GCTATTATCA CACCTCCAGG ACCATACTA CAGTAGATG CAGTAGATG CAGTAGATG CAGTAGATG GCCTAGATG ATGGGCTCG GATCCACCT GCACAGAGC ATCCTGCTA ACCACAGAGC CCACAGAGAC CCACAGAGAC CCACTAGATG CCACTAGATG GACCACTT GCAGCACCT GGCAACGTA GAACCATTGAA GAACCATTGAA GAACCATTGAC GCTGGCTCTG GTTCCAAAAA TCCATGGTAC TTCTCACCGC  n Sequence n Sequence p005492.1 21   LMVAAGGCVV PDGYTNRTGA AHRYTQVLWS TSGGFTQNTV LMPRNITIVT LMPRNI	GATCATGCCC GAGCACCTG CTGACGTCCT ATAAGTTATG AGGCACATAC GCAGGGCCAG CACGTGGGG CACGTGGGG CACGTGGGA GAGAGCACA GCCGCTGGC AGGATGACTAA GCCTGGGCTC CTGACAGACA CCAGCCTCCA TGTAGTAATA TCAGGGGCTC CTCTCCCCC CCTCTCCCCC CTCTCCCTGA TGTAGCAGACA GACCAATAAA  31   SAFNLDTRFL VYLCPLTAHK GSEDQRRWIG FYFAPGAYNW GAPRRHMGA YFERKEEVGG APFEGLGKVY GSLSDHIVLL NITLAYTLEA SMNYSLPLRM FVSEQQQKLS PGACQANETI	AAGTACCACE CCCACCAAGA CCCTGATCCC CCTCTGACAG ACCTCGTCACAG ACCTCGTCACAG ACCTCGTCACAG ACCTCGTCACAG CCTCTGCCAG GTCACTGGTCAT TGGTGGGCCC CGGGGGCACT ACCCAGAAGG CTCGCAGGAAC ACTGTCTGG GAATTTCGTGG GAATTCCCTC GAATTCCCTC GAATTCCCTC GCAGCTCCCAG  41     CCCTGCCTG CAGCTCCCAG ACTGCTCCCAG ACTGCTCCCAG ACTGCTCCCAG ACTGCTCCCAG ACTGCTCCCAG ACTGCTCCCAG ACTGCTCCCAG ACTCCCAG ACTCCAGA ACTCCAGA ACTCCCAG ACTCCAGA	CAGTGCGGAT AGCACTGGGT AGCACTGGT ACCCCTCTT TCCACAGGGG GAGCATGCAC CGCCAGCGCC TGGACTGTGC CGCCAGCGCC ATGGAGGACCT CTTGCATTGCT CCAATTGACA TGGAGACCT CTTGCTTTCC GTGCAGCAGG GGATACAGGG GGATACAGGG GGATACAGGG GGATACAGGG TTCTTAGCTA TCCTAAGGCC TTCTTAGCTA TCCTAAGGCC TTCTTAGT  51   LFGYSVALHR KNDPGHHITE LDSSDDWQTTY EWDLSEYSYK DLERRQVLEG TSFPAHPSLL RQPQQVIHGE KTLVPRPAVL PAGSESAVFH LDAYPILNQA LLLSINVTNT NQRMELLIAP	3180 3240 3360 3420 3540 3540 3540 3780 3780 3960 4020 4020 4140 4260 4320 4340 4340 4340 4340 4340 4360 4380 4360 4360 4360 4360 4360 4360 4360 436
50 55 60 65 70	TGACTTCTTT CCGGGAGGAG GACCAGCTGG CCCCAGTGT CCACCACCTT ATGCTGTCCTG CCAGTGCACT TGGTGCATCA AAAACAAGCC CACTCCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA TGCATCTCTG AGGGACCAC CATCCTCCC GGAAGACAA GATCCTCCAC GCAAGACCAC CATCCAGCT CCTTGGCTT CATTTGAGAA ACTCCCCAGG TGCCTTCTTT Seq ID NO: Protein Act 1   MGPGPSRAPR QTERQORYLL DMWLGVTVAS HNEMCNSTD DPEDQGMLYI SQVGAYPGSA LEGPSGSAFG KLGLPGLATF CPALCTATSC GFFSMPEMRC QALENHTEVQ RTSERSGEDA	ARGCGGACCC GAGCGTACC CAGACTGGGA CCCTTTCTT TGGCTGTAG GCCCTGGGA GCCTTCCTGT CGGATGGTGC GAAGGGGA GCATTCCTGT TTGACACCTG TTGACAGGGA AGAGGTGGGG GACCCAACAG TGAAGCCTC GACAGGGAAA AGAGGGAAG TTCTCACTCA GGAGGGAGG TCTTCTCTCTCC GACCCCAGCT TCTTTGCCAG GCTGAGGCTA CCCAGCCT 148 Prote: 11  APRIMICALA LAGAPRELAV QGPAGRVLVC YLETGMCQLG GYTMYGSFI LALADLNING GYSLSGQMDV VQVELCFAYN QKLELLLIMDN FQKECGPIDNK HEALLTILVVE HEALLTLIVVE HEALLTLIVVE	GCTATTATCA CACCTCCAGG ACCATACTA CAGTAGATG CAGTAGATG CAGTAGATG CAGTAGATG GCCTAGATG ATGGGCTCG GATCCACCT GCACAGAGC ATCCTGCTA ACCACAGAGC CCACAGAGAC CCACAGAGAC CCACTAGATG CCACTAGATG GACCACTT GCAGCACCT GGCAACGTA GAACCATTGAA GAACCATTGAA GAACCATTGAC GCTGGCTCTG GTTCCAAAAA TCCATGGTAC TTCTCACCGC  n Sequence n Sequence p005492.1 21   LMVAAGGCVV PDGYTNRTGA AHRYTQVLWS TSGGFTQNTV LMPRNITIVT LMPRNI	GATCATGCCC GAGCACCTG CTGACGTCCT ATAAGTTATG AGGCACATAC GCAGGGCCAG CACGTGGGG CACGTGGGG CACGTGGGA GAGAGCACA GCCGCTGGC AGGATGACTAA GCCTGGGCTC CTGACAGACA CCAGCCTCCA TGTAGTAATA TCAGGGGCTC CTCTCCCCC CCTCTCCCCC CTCTCCCTGA TGTAGCAGACA GACCAATAAA  31   SAFNLDTRFL VYLCPLTAHK GSEDQRRWIG FYFAPGAYNW GAPRRHMGA YFERKEEVGG APFEGLGKVY GSLSDHIVLL NITLAYTLEA SMNYSLPLRM FVSEQQQKLS PGACQANETI	AAGTACCACE CCCACCAAGA CCCTGATCCC CCTCTGACAG ACCTCGTCACAG ACCTCGTCACAG ACCTCGTCACAG ACCTCGTCACAG CCTCTGCCAG GTCACTGGTCAT TGGTGGGCCC CGGGGGCACT ACCCAGAAGG CTCGCAGGAAC ACTGTCTGG GAATTTCGTGG GAATTCCCTC GAATTCCCTC GAATTCCCTC GCAGCTCCCAG  41     CCCTGCCTG CAGCTCCCAG ACTGCTCCCAG ACTGCTCCCAG ACTGCTCCCAG ACTGCTCCCAG ACTGCTCCCAG ACTGCTCCCAG ACTGCTCCCAG ACTCCCAG ACTCCAGA ACTCCAGA ACTCCCAG ACTCCAGA	CAGTGCGGAT AGCACTGGGT AGCACTGGT ACCCCTCTT TCCACAGGGG GAGCATGCAC CGCCAGCGCC TGGACTGTGC CGCCAGCGCC ATGGAGGACCT CTTGCATTGCT CCAATTGACA TGGAGACCT CTTGCTTTCC GTGCAGCAGG GGATACAGGG GGATACAGGG GGATACAGGG GGATACAGGG TTCTTAGCTA TCCTAAGGCC TTCTTAGCTA TCCTAAGGCC TTCTTAGT  51   LFGYSVALHR KNDPGHHITE LDSSDDWQTTY EWDLSEYSYK DLERRQVLEG TSFPAHPSLL RQPQQVIHGE KTLVPRPAVL PAGSESAVFH LDAYPILNQA LLLSINVTNT NQRMELLIAP	3180 3240 3360 3420 3540 3540 3540 3780 3780 3960 4020 4020 4140 4260 4320 4340 4340 4340 4340 4340 4360 4380 4360 4360 4360 4360 4360 4360 4360 436
50 55 60 65 70	TGACTTCTTT CCGGGAGGAG GACCAGCTGG CCCCAGTGT CCACCACTT ATGCTGTCTG CGAGTGCACT TGGTGCACA AAAACAAGCC CACCTCCCCT GTCAAAACTA CCCATGCCAG GGCGTGCTCA TGCATCCTG AGGAACAAA GATCCTCCAG GCAAGACCAC CATCCAGCCA TCCTTGGGTT CATTTGAGAA ACTCCCCAGC TGCCTTCTTT Seq ID NO: Protein Aci I I MGPGPSRAPR QTERQORYLL DMWLGVTVAS HNEMCISNITU DPEDQGNLYI SQVGAYFGSA LEGPSGSAFG KLGLPGLATF DPALCTATSC QALENHTEVQ RTSERSEGDA EVIGVTLHTR	ARGCGGACCC GAGCGCTACC CAGACTGGGA CCCTTTCTT TGGCTGGTAG GCCTTGGGG GCATTCCTGT CGGATGGGG AAAGAGCCTC CTGACACGG AGAGTGGGG AGAGGTGGGG GCACTACAGG GACCAACAG GACCAACAG GACCAACAG GAGAGGAGGAG AGAGGAGGAG AGAGGAGGAG GCCCAGCT TCTGTGCCAG GCCCAGCCT 148 Protei 11    APRIMICALA APRIMICALA LAGAPRELAV CGPAGRUVC CYLTGMCQLG GYTAGTGCAG CYTAGTGCAG CYTAG	GCTATTATCA CACCTCCAGG ACCATACTA CAGCAGGCTC CAGCAGGCTC CCACAGGCTCC CCACAGAGC GATCCATCT GCAGCACGGC ATCCTGCCTA ACAAGGAACT CTCCTGCCTA CAAAGGAACT CCACTAGATG GAACCATCTG GCACCAGGC GCCAACGTA CAAAGGAACT CCACTACCAG GACACTTGAA GAACCATGCG GTTCCAAAAA TCCATGGTAC TTCTCACCGC I SEQUENCE NP_005492.1 21 LMVAAGGCVV PDGYTNRTGA AHRYTQVLWS TSGGFTQNTV LWPNITIVI WQDLLVGAPY QSAGNPNYRR LRDKLRPIII CCESNLOMRAA PALLLSSVRF SSHQDNLWPM	GATCATGCCC GAGCACCTG CTGACGTCT ATAAGTTATG AGGCACATAC GCAGGGCCAG GCAGGGCCAG GCAGGTGCGAG AGGTTGTCTA AGAAGAAG AGAAGACG ACGTGGGCT CTGACAGAA AGAAAGAAG ACAGACTGAA CCAGCCTCCA TGTAGTAATA TCAGGGCTC CCTTCCTCA TGTAGTAATA TCAGGGCTC CCTTCCTCA TGTAGCAGAG GACCACATAAA  31   SAFNLDTRFL VYLCPLTAHK GSEDQRRMVG YFGAPGAYNW GAPRHHMGA YFERKEEVGG APFEGLGKVY GSLSDHIVLL INITLAYTLEA SMYSLPLRM FVSEQQXILS FYSEQQXILS FYSEQQXILS FYSEQQXILS FGACQANETI ILILLYDYTL	AAGTACCACE CCACCAAGA CCCTGATCCC CCTCTGACAG ACCTCGTCACAG ACCTCGTCACAG ACCTCGTCGCAG CCACTGCTCG CCTCTGCCAG AGGCCCCTGC GTCACTGGAT TGGTGGGCCC CGGGGGCACT TGGTGGGCCC GGCAGGAAGG CTCGCAGGAAG ACTGTGTGGG AATGTTTGGGA GAAGGCCCA GGCAGGGGGC ACAGGTGGAG ACTGTCCCAG ATTCCCTC CAGCTCCCAG  41    VVKEAGNPGS DDCERMNITV KCYVRGNDLE KGNYMIQRG AIYHFNQAG IYHSSSKGLL RARPVINTE DRDRRPPRLR PDRPRLGLRS CTLSMWHER FCELGNPFKE QTSLSMWHER	CAGTGCGGAT AGCACTGGGT AGCACTGGGT ACCCCTCTT TCCACAGGGG GAGCATGCCC CTTACAACGC TGGACTTGGCT CGCCAGGGC AATGTGGTGA TGGACTTGCT CTTGCTTTCC GTGCAGCAGG GGATGCGG GGATGCGG GGATACAGAG GAGAGCCCT CCTGCCACCC TTCTTAGCTA TCCTAAGGCC TTCTTAGCTA TCCTAAGGCC TTGGCACCC TTGTAGGCC CCCCTCCTTG TTTGT  51  LFGYSVALHR KNDPGHHIIE LDSSDDMQTY EWDLSEYSYK DLERRQVLEG TTSPAHPSLL RQPQQVIHGE KTLVPRPAVL FAGSESAVEL LDASDDMGTY LGPGGSSAVEL LDASDDMGTY LGPGGSSAVEL LLLSINVTNT	3180 3240 3360 3420 3540 3540 3720 3780 4020 4020 4020 4140 4260 4260 4380 4440 60 120 180 240 300 360 4440

_	VLTCATGRAH SIPTINMENK	CVWLECPIPD TTWFSVDIDS	SDPGDRPSSP APVVTNVTVK ELVEELPAEI RYPPPGSTLP	ARVWNSTFIE ELWLVLVAVG	DYRDFDRVRV AGLLLLGLII	NGWATLFLRT	900 960 1020
5			ruence n#: NM_0064	124.1			
10	1	11	21	31	41	51	
10	000000000000000000000000000000000000000		GCCCCCCCC	TOCATOCCAG	Ca CCACCCCA	CCCACCCTC	60
			ATTGGGAGAT				120
			CACTGCCCCT				180
			CAAGATTGAA				240
15			GGATGACCCC				300
			CACCAAAGGG				360
			ATTTCTCTAC				420
			AGGAAAAATG GCTGGTGATC				480 540
20			CGTTGTCAGC				600
			GGGGCCAAC				660
			TCGGAGTGAG				720
			GTCCGTGTTG				780
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			TACCAACAAG				1020
			CCTCTGTTGG				1080
20			CATCGCCAAA				1140
30			CATCTTGCTC				1200
			CCTGGGCTCT				1260 1320
			GACCTTCATC				1380
			CGGCGTGATA				1440
35			CACCACCGCC				1500
			GATCGCCCTG				1560
			GTTCACTCGC				1620 1680
			CTGGTTCGCC				1740
40			CATCCTGGTA				1800
			ACTCCAGAAC				1860
			CGTCTCCAAG				1920
			CCGCGCGTGC				1980
45			GGACTTGGAG TAACATAACC				2040 2100
73			ATGCACGGCC				2160
			TTGCATGCTC				2220
	ACCTCGAGGA	GATTTGCTCC	CCATTAGCGA	ATGAAATTGA	TGCAGTCCTA	AAAAAAAA	
50	Com ID NO.	150 Protein					
30		cession #: 1			•		
	1	11	21	31	41	51	
	1	i	1	1	1	i	
55			AAGQQPTAPD				60
JJ			KWSERDTKGK SNPLLGLVIG				120 180
			LMQVGDRSEF				240
			PDLLKVITKP				300
			NCTSPSLCWT				360
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			TPLIGIGVIT				480 540
			LWYPIPFTRL			NFLPLWMRSL	600
						AQEGQDVPVK	660
65			SDSKTECTAL				
		151 DNA se					
		id Accessio uence: 11					
70	1	11	21	31 .	41	51	
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	ATGAACCGCA	GCCACCGGCA	CGGGGCGGG	AGCGGCTGCC	TGGGCACTAT	GGAGGTGAAG	60
	AGCAAGTTTG	GAGCTGAATT	TCGTCGGTTT	TCGCTGGAAA	GATCAAAACC	TGGAAAATTT CGTTTTGGTA	120 180
75	CCCTATCCAC	ATGGATTACT	ACAACATGTT	CCTATABATC	ATGATGATAA	TTATCACAAA	240
, 5	GCTGTTTCAA	CGGCCAATCC	ACTGCTTAGG	ATATTTATAC	AAAAGAAGGA	AGAAGCAGAC	300
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	CGTCCTGACA	ACCATAGAAA	AAAGCCACAT	ATAGTCATTA	GTATGCCCCA	AGACTTTAGA	420
80	CCTGTGTCTT	CTATTATAGA	CGTGGATATT	CTCCCAGAAA	CGCATCGTAG	GGTACGTCTT	480
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	GGTCTGGCTC	ALAGTACAC	ACTATTACC	GTTAATGATG	AAGTTTTAGA	AGTTAATGGC	660
	ATAGAAGTTT	CAGGGAAGAG	CCTTGATCA	GTAACAGACA	TGATGATTGC	AAATAGCCGT	720
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85	ACTTCTGGCA	GTTCCGGTC	GTCTACTGAT	AACAGCCTTC	TIGGCTACCC	ACAGCAGATT	840

5	AATGGAGTGC ACACAGATAG AGCTTAGCAG	CACAGCAGAT AGCTAAGCTT CCATAGCAAG	GGATGAAGAC TCCAAAAGCT TGAGTCTGGA CAGCTCAAAC AACAATCATA	GTTCCTAATA CAGAATGGCT ACGGAATTTG	CTGAGAGCCT TTATTCCCTC	GGAGTCATTA TAATGAAGTG	900 960 1020 1080
10		152 Proteir ession #: 2		31	41	51	
10	GYADIHGDLL RPDNHRKKPH	PINNDDNYHK IVISMPQDFR	SKFGAEFRRF AVSTANPLLR PVSSIIDVDI GLAQSTGLLA	IFIQKKEEAD LPETHRRVRL	YSAFGTDTLI YKYGTEKPLG	KKKNVLTNVL FYIRDGSSVR	60 120 180 240
15	NLIITVRPAN	QRNNVVRNSR VPNTESLESL	TSGSSGQSTD TQIELSFESG	NSLLGYPQQI	EPSFEPEDED	SEEDDIIIED	300 360
20	Nucleic Aci	153 DNA sec id Accession lence: 234	1 #: NM_0030	064.2			
	1	11	21	31	41	51	
25	TGCCCTGGGA AGTCTGTCCT	ACTCTGGCAC CCTAAGAAAT	CCATGAAGTC CTTGGGCTGT CTGCCCAGTG AGAAGAGATG	GGAAGGCTCT CCTTAGATAC	GGAAAGTCCT AAGAAACCTG	TCAAAGCTGG AGTGCCAGAG	60 120 180 240
30	TGGCCAATGT TGACTTGAAG ATTCCTGCCA	TTGATGCTTA TGTTGCATGG TATGGAGGAG	ACCCAACAAG ACCCCCCAA GCATGTGTGG GCTCTGGAGT	TTTCTGTGAG GAAATCCTGC CCTGCTCTGT	ATGGATGGCC GTTTCCCCTG GTGGTCCAGG	AGTGCAAGCG TGAAAGCTTG TCCTTTCCAC	300 360 420 480
			CTGATATCCT ATCAATGAAT				540
35		154 Protein cession #: 1 11		31	41	51	
40		KCLDPVDTPN	I WAVEGSGKSF PTRRKPGKCP				60 120
45	Nucleic Act		n #: NM_001	306.1			
73	1	uence: 199. 11 	21 	31 	41 	51 	
50	GCGCGCGCCG CGCCAGGCCC GGCCTTGCCG CTGGGCTGGC	TCGGTGAGTC AGCGGCCCCG CGGCAGCCAT TGGGCACCAT	GCAGGCGCAC AGTCCGTCCG GCCCCTCGTC GTCCATGGGC CGTGTGCTGC	TCCGTCCGTC TCCCCGCACC CTGGAGATCA GCGTTGCCCA	CGTCGGGGCG CGGAGCCACC CGGGCACCGC TGTGGCGCGT	CCGCAGCTCC CGGTGGAGCG GCTGGCCGTG GTCGGCCTTC	60 120 180 240 300 360
55	GTGCAGAGCA GACCTTCAGG CTAGTGGCGC	CCGGCCAGAT CGGCCCGCGC TGGTGGGCGC	GTCGCAGAAC GCAGTGCAAG CCTCATCGTG CCAGTGCACC	GTGTACGACT GTGGCCATCC AACTGCGTGC	CGCTGCTGGC TGCTGGCCGC AGGACGACAC	ACTGCCACAG CTTCGGGCTG GGCCAAGGCC	420 480 540
60	GTGTCCTGGT CAGAAGCGCG	CGGCCAACAC AGATGGGCGC	CGTGCTGTTC CATTATCCGG GGGCCTGTAC CTGCTCGTGT	GACTTCTACA GTGGGCTGGG CCCCCACGCG	ACCCCGTGGT CGGCCGCGGC AGAAGAAGTA	GCCCGAGGCG GCTGCAGCTG CACGGCCACC	600 660 720 780
	AAGGTCGTCT GACCGCAAGG CAACACCACC	ACTCCGCGCC ACTACGTCTA ACCACCACCG	GCGCTCCACC AGGGACAGAC CGAGCTGGAG	GGCCCGGGAG GCAGGGAGAC CGCGCACCAG	CCAGCCTGGG CCCACCACCA GCCATCCAGC	CACAGGCTAC CCACCACCAC GTGCAGCCTT	840 900 960
65	TCCCCAGCAG GCATGGACTG ACCACCCCGT	CCACGGCTTT TGAAACCTCA CGAGCCCCAT	GCGGGCCGGG CCCTTCTGGA	CAGTCGACTT GCACGGGGCC CCCCCATGTC	CGGGGCCCAG TGGGTGACCG GCGCTGGGCA	TGGGGCAGCT GGACCAACCT CCAATACTTG GGGACCGGCA	1020 1080 1140 1200
70		156 Protei cession #: 11	n sequence NP_001297.1 21	31	41	51	
75	MQCKVYDSLL GVLFLLAALL	ALAVLGWLGT ALPQDLQAAF TLVPVSWSAN	IVCCALPMWR	VSAFIGSNII AFGLLVALVO VPEAQKREMO	   TSQNIWEGLW   AQCTNCVQDD   AGLYVGWAAA	   MNCVVQSTGQ   TAKAKITIVA   ALQLLGGALL	60 120 180
80	Nucleic Ac	: 157 DNA se :id Accessionuence: 1	on #: NM_009	5564			
	1	11	21	31 	41 	51 	
85	ATGCCCCTAC CAGGACTCC	GTCTCCTGTY CCTCAGACC	   GCTGGGCCTX   GATCCCAGC	A GCCCTGTTGG CCACCTCTG	GGGCTCTGCA A GCAAGGTCCC	TGCCCAGGCC TCTGCAGCAG	60 120

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GACAAGAGCT ACAATGTCAC CTCCGTCCTG TTTAGGAAAA AGAAGTGTGA CTACTGGATC
                                                                                240
                                                                                300
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                                                                                360
 5
       CCTGGATTAA CGAGTTACCT CGTCCGAGTG GTGAGCACCA ACTACAACCA GCATGCTATG
       GTGTTCTTCA AGAAAGTTTC TCAAAACAGG GAGTACTTCA AGATCACCCT CTACGGGAGA
       ACCAAGGAGC TGACTTCGGA ACTAAAGGAG AACTTCATCC GCTTCTCCAA ATATCTGGGC
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10
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                                                                  51
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                              21
       MPLGLLWLGL ALLGALHAQA QDSTSDLIPA PPLSKVPLQQ NFQDNQFQGK WYVVGLAGNA
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       PGLTSYLVRV VSTNYNQHAM VFFKKVSQNR EYFKITLYGR TKELTSELKE NFIRFSKYLG
       LPENHIVEPV PIDOCIDG
       Seq ID NO: 159 DNA sequence
20
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       Coding sequence: 26..874
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       AGGAATCTGC GCTCGGGTTC CGCAGATGCA GAGGTTGAGG TGGCTGCGGG ACTGGAAGTC
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CATGAGGATT CTGCAGTTAA TCCTGCTTGC TCTGGCAACA GGGCTTGTAG GGGGAGAGAC
                                                                                120
                                                                                180
       CAGGATCATC AAGGGGTTCG AGTGCAAGCC TCACTCCCAG CCCTGGCAGG CAGCCCTGTT
                                                                                240
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                                                                                300
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                                                                                360
30
       GGAGGGCTGT GAGCAGACCC GGACAGCCAC TGAGTCCTTC CCCCACCCCG GCTTCAACAA
                                                                                420
       CAGCCTCCCC AACAAGACC ACCGCAATGA CATCATGCTG GTGAAGATGG CATCGCCAGT
                                                                                480
       CTCCATCACC TGGGCTGTGC GACCCCTCAC CCTCTCCTCA CGCTGTGTCA CTGCTGGCAC
       CAGCTGCCTC ATTTCCGGCT GGGGCAGCAC GTCCAGCCCC CAGTTACGCC TGCCTCACAC
                                                                                600
       CTTGCGATGC GCCAACATCA CCATCATTGA GCACCAGAAG TGTGAGAACG CCTACCCCGG
                                                                                660
       CAACATCACA GACACCATGG TGTGTGCCAG CGTGCAGGAA GGGGGCAAGG ACTCCTGCCA
                                                                                720
       GGGTGACTCC GGGGGCCCTC TGGTCTGTAA CCAGTCTCTT CAAGGCATTA TCTCCTGGGG
       CCAGGATCOG TGTGCGATCA CCCGAAAGCC TGGTGTCTAC ACGAAAGTCT GCAAATATGT
       GGACTGGATC CAGGAGACGA TGAAGAACAA TTAGACTGGA CCCACCCACC ACAGCCCATC
                                                                                900
       ACCCTCCATT TCCACTTGGT GTTTGGTTCC TGTTCACTCT GTTAATAAGA AACCCTAAGC
                                                                                960
40
       CAAGACCCTC TACGAACATT CTTTGGGCCT CCTGGACTAC AGGAGATGCT GTCACTTAAT
                                                                               1020
       AATCAACCTG GGGTTCGAAA TCAGTGAGAC CTGGATTCAA ATTCTGCCTT GAAATATTGT
       GACTCTGGGA ATGACAACAC CTGGTTTGTT CTCTGTTGTA TCCCCAGCCC CAAAGACAGC
       TCCTGGCCAT ATATCAAGGT TTCAATAAAT ATTTGCTAAA TGAGTG
45
       Seq ID NO: 160 Protein sequence
       Protein Accession #: NP_006844.1
                  11 .
                              21
                                                                  51
       MRILQLILLA LATGLVGGET RIIKGFECKP HSQPWQAALF EKTRLLCGAT LIAPRWLLTA
50
       AHCLKPRYIV HLGQHNLQKE EGCEQTRTAT ESFPHPGFNN SLPNKDHRND IMLVKMASPV
       SITWAVRPLT LSSRCVTAGT SCLISGWGST SSPQLRLPHT LRCANITIEE HQKCENAYPG
       NITDTMVCAS VQEGGKDSCQ GDSGGPLVCN QSLQGIISWG QDPCAITRKP GVYTKVCKYV
       DWIGETMKNN
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It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

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## WHAT IS CLAIMED IS:

1		1.	A method of detecting an ovarian cancer-associated transcript in a cell
2	from a patient	, the me	thod comprising contacting a biological sample from the patient with a
3	polynucleotide	e that se	lectively hybridizes to a sequence at least 80% identical to a sequence
4	as shown in Ta	ables 1-	26.
1		2.	The method of claim 1, wherein the biological sample comprises
2	isolated nuclei	ic acids.	
1		3.	The method of claim 2, wherein the nucleic acids are mRNA.
1		4.	The method of claim 2, further comprising the step of amplifying
2	nucleic acids b	efore th	ne step of contacting the biological sample with the polynucleotide.
i		5.	The method of claim 1, wherein the polynucleotide comprises a
2	sequence as sh		• • •
_	soquence as si	lown in	140105 1 20.
1		6.	The method of claim 1, wherein the polynucleotide is immobilized on
2	a solid surface	<b>.</b>	
1		7.	The method of claim 1, wherein the patient is undergoing a therapeutic
2	regimen to tre	at ovari	-
	Ü		
1		8.	The method of claim 1, wherein the patient is suspected of having
2	ovarian cance	r.	
1		9.	An isolated nucleic acid molecule consisting of a polynucleotide
2	sequence as sl	hown in	Tables 1-26.
1		10.	The nucleic acid molecule of claim 9, which is labeled.
1		11.	An expression vector comprising the nucleic acid of claim 9.
1		12.	A host cell comprising the expression vector of claim 11.
1		13.	An isolated polypeptide which is encoded by a nucleic acid molecule
2	having polyni	ucleotid	e sequence as shown in Tables 1-26.

1		14.	An antibody that specifically binds a polypeptide of claim 13.
1		15	The antibody of claim 14, further conjugated to an effector component.
1		16.	The antibody of claim 15, wherein the effector component is a
2	fluorescent lab	el.	·
1		17.	The antibody of claim 15, wherein the effector component is a
2	radioisotope o	r a cyto	toxic chemical.
1		18.	The antibody of claim 15, which is an antibody fragment.
1		19.	The antibody of claim 15, which is a humanized antibody
1		20.	A method of detecting an ovarian cancer cell in a biological sample
2	from a patient	, the me	thod comprising contacting the biological sample with an antibody of
3	claim 14.		•
1		21.	The method of claim 20, wherein the antibody is further conjugated to
2	an effector cor	mponen	t.
1		22.	The method of claim 21, wherein the effector component is a
2	fluorescent lab	oel.	
1		23.	A method for identifying a compound that modulates an ovarian
2	cancer-associa	ated pol	ypeptide, the method comprising the steps of:
3	•	(i) con	tacting the compound with an ovarian cancer-associated polypeptide,
4	the polypeptid	le encod	led by a polynucleotide that selectively hybridizes to a sequence at least
5	80% identical	to a sec	quence as shown in Tables 1-26; and
6		(ii) de	termining the functional effect of the compound upon the polypeptide.
1		24.	A drug screening assay comprising the steps of
2		(i) adn	ninistering a test compound to a mammal having ovarian cancer or a cell
3	isolated there	from;	
4		(ii) co	mparing the level of gene expression of a polynucleotide that selectively
5	hybridizes to	a seque	nce at least 80% identical to a sequence as shown in Tables 1-26 in a

6 treated cell or mammal with the level of gene expression of the polynucleotide in a control

- 7 cell or mammal, wherein a test compound that modulates the level of expression of the
- 8 polynucleotide is a candidate for the treatment of ovarian cancer.